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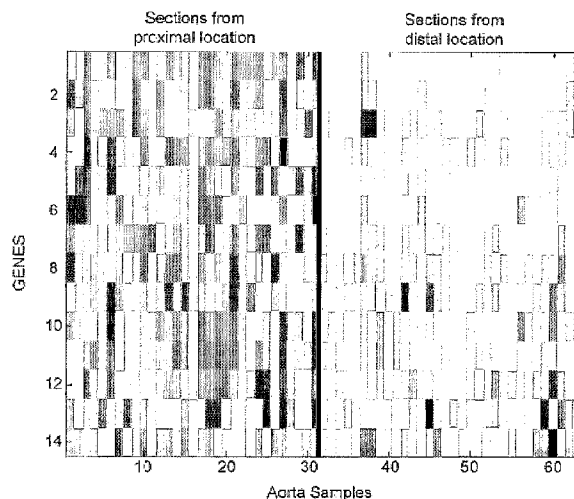
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(54) Title: **ATHEROSCLEROTIC PHENOTYPE DETERMINATIVE GENES AND METHODS FOR USING THE SAME**



(57) Abstract: Genes whose expression is correlated with and determinant of an atherosclerotic phenotype are provided. Genes whose expression is correlated with and determinant of an atherosclerotic susceptibility are also provided. Also provided are methods of using the subject atherosclerotic determinant genes or the atherosclerotic susceptibility genes in diagnosis and treatment methods, as well as drug screening methods. In addition, reagents and kits thereof that find use in practicing the subject methods are provided. Also provided are methods of determining whether a gene is correlated with a disease phenotype, where correlation is determined using at least one parameter that is not expression level and is preferably determined using a binary prediction tree analysis.

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## ATHEROSCLEROTIC PHENOTYPE DETERMINATIVE GENES AND METHODS FOR USING THE SAME

### CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part application of prior U.S. Application No. 10/291885, filed November 12, 2002, entitled "ATHEROSCLEROTIC PHENOTYPE DETERMINATIVE GENES AND METHODS FOR USING THE SAME," which claims the benefit of U.S. Provisional Application Nos. 60/334,709 filed November 9, 2001, 60/374,547 filed April 23, 2004, 60/420,784 filed October 24, 2002, 60/421,043 filed October 25, 2002 and 60/424,680 filed November 8, 2002. This application also claims priority under 35 USC 119(e) to U.S. Provisional Application No. 60/651462, filed August 4, 2004. The entire teachings of all these patent applications are incorporated herein by reference.

### FIELD OF THE INVENTION

The field of this invention is atherosclerosis.

### STATEMENT REGARDING FEDERALLY-SPONSORED RESEARCH OR DEVELOPMENT

The invention described herein was supported, in whole or in part, by Grant No. HL073042-02 from the National Heart, Lung and Blood Institute at the National Institutes of Health. The United States government has certain rights in the invention.

### BACKGROUND OF THE INVENTION

Atherosclerosis is the leading cause of morbidity and mortality in the industrialized world. While applicants have made substantial progress in the treatment and prevention of atherosclerosis and the related thromboembolic complications, there remains an urgent need to develop individualized prognostic tools and therapeutic plans. Progress in this direction will come with an improved understanding of the genetic foundations of the disease.

Atherosclerosis is a complex trait manifested by chronic inflammation that selectively affects arterial vessels and progressively destroys the structure of the vessel wall, leading to thromboembolic complications. The thromboembolic consequences of atherosclerosis, sudden cardiac death, myocardial infarction, and other ischemic organ damage such as stroke and ischemic renovascular disease, represent the major causes of death, morbidity and disability for developed countries and are spreading rapidly worldwide. In spite of substantial improvement in our understanding of risk for atherosclerosis and thromboembolic complications, improved predictive tools are needed to allow for early prevention in a fashion that is cost-effective.

The sequencing of the entire human genome promises to transform the study of human health by providing an opportunity to develop genomic knowledge that will eventually boost prevention, diagnosis and treatment of disease. Genome research in the post-sequencing era is now faced with massive, multi-disciplinary challenges to realize this promise. Most complex illnesses

result (i) from the combined action of gene variants that are considered as “normal”, as they do not destroy the function of the gene that they modify; (ii) from factors provided by the environment, and (iii) from a stochastic component that can be best defined as “chance”. The ensemble of genetic modifiers that enhance the impact of environmental factors on health represents the genetic susceptibility to ailments.

Because of the potential benefits of genetic approaches to diagnosis and treatment of atherosclerosis, there is intense interest in the identification of genes whose contribution is relevant to atherosclerosis. Ideally, one would like to test all variants of all genes for their contribution to atherosclerosis. However, such effort would be prohibitively expensive, and even if the resources were to become accessible, our current ability to analyze data would become limiting. Hence, the prioritization of contributory genes has become a necessity. A systematic approach to satisfy this need and provide such prioritization process has been defined and is based on gene expression that correlates with atherosclerosis. Hence, the present invention satisfies this need.

As with most complex illnesses, atherosclerosis results from the combined interaction of a genetic component and environmental factors. However, unlike classical Mendelian disorders, the genetic component is not attributable to single causative genes making it difficult to study by standard genetic and molecular biological approaches. Instead, it is anticipated that combinations of gene variants determine an individual's susceptibility to atherosclerosis by enhancing the impact of environmental factors.

The gene variants are often in the form of single nucleotide polymorphisms (SNPs). SNPs represent subtle variations in a gene's coding sequence or the associated regulatory regions resulting in a mild to moderate impact on the function or concentration of the encoded protein. The inheritance of unique combinations of genetic variants can have a dominant impact that fosters the pathogenesis of atherosclerosis. In principle, one would like to identify all variants of all genes and assay them for their contribution towards the genesis of atherosclerosis. Even if applicants were able to identify all variants, applicants would be limited by our ability to assay and analyze such a vast number of SNPs. Practically, one must take an approach that falls somewhere between an analysis restricted to known candidate genes identified on the basis of clinical and biological knowledge (functional candidate genes) and an investigation of the entire genomic complement of genes. See Nussbaum RL. Genetics in Medicine. New York: W.B. Saunders Company, 2001. Science 1996; 272:689-93.

Such an approach should involve prioritization based on programmatic qualification mechanisms.

Recent advances in the knowledge of the human genome, coupled with the development of technologies for large scale analysis of gene activity via DNA microarrays, now affords the opportunity to identify genes whose expression implies a role in a phenotype.

Therefore novel strategies for analyzing gene expression data to advance the understanding of the disease in relationship to gene expression, are needed to take advantage of the recent development of technologies. Further, new methods to predict and treat atherosclerosis based on the gene expression data obtained by such techniques are needed.

## SUMMARY OF THE INVENTION

The invention relates in part, to methods of diagnosing, or aiding in the diagnosis, of atherosclerosis. The invention also relates to determining the susceptibility, or aiding in determining the susceptibility, of developing atherosclerosis, such as in a mammal. Applicants have used a unique collection of human aorta samples, which exhibit a progression of atherosclerotic disease, coupled with novel strategies for analyzing gene expression data, to identify genes and metagenes whose expression closely relates to, and indeed predicts, the extent of fatty streaks and more advanced atherosclerotic lesions. Applicants believe this represents a novel approach to the identification of genes that contribute to atherosclerosis. Applicants have also analyzed gene expression data from different sections of aorta to identify genes and metagenes indicative of the susceptibility of vascular tissue to becoming atherosclerotic, or of the mammal from which the vascular sample was derived of developing atherosclerosis.

Genes whose expression is correlated with and determinant of an atherosclerotic phenotype are provided. Similarly, metagenes useful in binary prediction tree modeling to classify samples according to atherosclerotic phenotype are also provided. Genes whose expression is correlated with and determinant of susceptibility to atherosclerosis are provided. Similarly, metagenes useful in binary prediction tree modeling to classify samples according to their susceptibility to atherosclerosis are also provided.

The invention also provides methods of using the subject atherosclerotic determinant genes and metagenes in diagnosis and treatment methods, as well as in drug screening methods. In addition, reagents and kits thereof that find use in practicing the subject methods are provided. Also provided are methods of determining whether a gene is correlated with a disease phenotype, e.g., atherosclerosis, where correlation is determined using at least one parameter that is not expression level and is preferably determined using binary prediction tree analysis and metagene construction.

The invention also provides metagenes for atherosclerosis identified by the use of a binary prediction tree model, that characterize multiple patterns of expression of the genes across the samples.

One aspect of the invention provides a method of estimating whether a sample is from tissue having an atherosclerotic phenotype, said method comprising (a) obtaining an expression profile for said sample from at least two of said genes listed in Table I; (b) providing one or more predictive statistical tree models, each model including one or more nodes, each node representing a metagene, each node including a statistical predictive probability of the having an atherosclerotic phenotype, each metagene representing a dominant factor from a group of genes associated with having an atherosclerotic phenotype, wherein at least two genes in the group of genes are selected from those listed in Table I; and (c) determining an estimate of the sample having the atherosclerotic phenotype by averaging the predictions of one or more of the tree models applied to the expression profile of the sample. Steps (a) and (b) may be performed in any order.

In some embodiments, at least two of the genes are selected from those having Genbank



- accession numbers selected from Y09445, AF053233, U43185, AL050008, AB022718, L10333, M80634, AF044896, X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, AB014574, L13939, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271, J03011, D12485,
- 5 U88629, U75308, J03600, AF004709, AB002361, X90858, Z29067, U00952, M80254, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, L10678, Z98046, D79994, D87074, X81109, AL049946, U78556, M63603, X12451, U89606, AB029018, AF095791, X74039, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AB015718, X78817, AJ000534, M63835, M16336, U32324, M22324, X54162, U57911, M64571,
- 10 AC005546, AC005546, Y13622, L76191, U60060, AJ011497, D64142, D26350, X15414, D87434, X79204, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, U56833, J05070, AF093118, U12707, M55531, AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, X97074, D89016, AF022797, M33552, U09578, M21186,
- 15 M64925, U10906, U83993, AF022789, L35249, M61916, AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193, D84110, AJ006973, AB002318, U51333, U09577 and U00672.

- In some embodiments, at least two genes are preferred genes from table I. Preferred genes
- 20 from table II are genes having Genbank accession numbers selected from Y09445, AF053233, U43185, AL050008, AB022718, L10333, M80634, AF044896, X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, AB014574, L13939, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271, J03011, D12485, U88629, U75308, J03600, AF004709, AB002361, X90858, Z29067,
- 25 U00952, M80254, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, L10678, Z98046, D79994, D87074, X81109, AL049946, U78556, M63603, X12451, U89606, AB029018, AF095791, X74039, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AB015718, X78817, AJ000534, M63835, M16336, U32324, M22324, X54162, U57911, M64571, AC005546, AC005546, Y13622, L76191, U60060, AJ011497,
- 30 D64142, D26350, X15414, D87434, X79204, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, U56833, J05070, AF093118, U12707, M55531, AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, X97074, D89016, AF022797, M33552, U09578, M21186, M64925, U10906, U83993, AF022789, L35249, M61916,
- 35 AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193, D84110, AJ006973, AB002318, U51333, U09577 and U00672.

In some embodiments of the methods for estimating whether a sample is from tissue having an atherosclerotic phenotype, the tissue is a vascular tissue, such as aortic tissue. The tissue is

preferably mammalian tissue, such as human, primate or rodent tissue. In some embodiments, the sample is from a mammal suspected of having tissue having an atherosclerotic phenotype or from a mammal is at risk of being afflicted with atherosclerosis. Mammals at risk for being afflicted with atherosclerosis include those having traditional cardiovascular risk factors. Cardiovascular risk factors include but are not limited to cholesterol, HDL cholesterol, systolic blood pressure, cigarette smoking, exercise, alcohol, race, family history of premature coronary artery disease, and medication use, including aspirin, statins, B-blockers and hormone replacement therapy in women.

In some embodiments, the methods for estimating whether a sample is from tissue having an atherosclerotic phenotype are carried out in the context of determining if an agent has anti-atherosclerosis properties. For example, a mammal may be treated with a compound, and a sample is obtained from the mammal to determine if the compound can decrease an atherosclerosis phenotype. In some embodiments, the mammal is a rodent model of atherosclerosis, such as apolipoprotein E (apoE)-deficient C57BL/6 mice. In other embodiments, other mouse disease models are used, such as KK/Ay mice, an animal model of type II diabetes.

In some embodiments of the methods for estimating whether a sample is from tissue having an atherosclerotic phenotype, at least one metagene in at least one of the predictive statistical tree models is one of the 509 metagenes provided herein. In one embodiment, at least one of the metagenes (i) is one of the 509 metagenes and (ii) represents a dominant factor from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 genes associated with having an atherosclerotic phenotype. In another embodiment, at least one of the statistical tree models has two or more metagenes.

In some embodiments of the methods for estimating whether a sample is from tissue having an atherosclerotic phenotype, one or more predictive statistical tree models correctly classify samples with greater than 85%, 90%, 95%, 98% or 99% accuracy. In other embodiments, the one or more predictive statistical tree models correctly classify samples with an accuracy of up to 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%.

The invention also provides a method of predicting the susceptibility of a mammal for developing atherosclerosis, the method comprising: (a) obtaining an expression profile of at least two of said genes listed in Table II from a sample from the mammal; (b) providing one or more predictive statistical tree models, each model including one or more nodes, each node representing a metagene, each node including a statistical predictive probability of being susceptible to developing atherosclerosis, each metagene representing a dominant factor from a group of genes associated with susceptible to developing atherosclerosis, wherein at least two genes in the group of genes are selected from those listed in Table II; and (c) determining an estimate of the sample being susceptible to developing atherosclerosis by averaging the predictions of one or more of the tree models applied to the expression profile of the sample. Steps (a) and (b) may be performed in any order.

In some embodiments, the at least 2, 3, 4, 5, 6 or 7 of the genes are selected from genes having Genbank accession numbers selected from M68891, X51757, D83004, X06256, Z22865, X75918 and M55153.

In some embodiments of the methods for predicting the susceptibility of a mammal for developing atherosclerosis, the tissue is a vascular tissue, such as aortic tissue. The tissue is preferably mammalian tissue, such as human, primate or rodent tissue. In some embodiments, the sample is from a mammal suspected of having tissue susceptible to developing atherosclerosis.

5 Susceptible mammals include those having traditional cardiovascular risk factors.

In some embodiments, the methods for predicting the susceptibility of a mammal for developing atherosclerosis are carried out in the context of determining if an agent can modify the susceptibility of a mammal for developing atherosclerosis. For example, a mammal may be treated with a compound, and a sample is obtained from the mammal to determine if the compound can  
10 decrease the susceptibility of a mammal for developing atherosclerosis. In some embodiments, the mammal is a rodent, such as a rodent model of atherosclerosis. Mice atherosclerosis models include as apolipoprotein E (apoE)-deficient C57BL/6 mice. In other embodiments, other mouse disease models are used, such as KK/Ay mice, an animal model of type II diabetes.

In some embodiments of the methods for predicting the susceptibility of a mammal for developing atherosclerosis, at least one metagene in at least one of the predictive statistical tree  
15 models is one of the 509 metagenes provided herein. In one embodiment, at least one of the metagenes (i) is one of the 509 metagenes and (ii) represents a dominant factor from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 genes associated with having an atherosclerotic phenotype. In another embodiment, at least one of the statistical tree models has two  
20 or more metagenes.

In some embodiments of the methods for predicting the susceptibility of a mammal for developing atherosclerosis, one or more predictive statistical tree models correctly classify samples with greater than 85%, 90%, 95%, 98% or 99% accuracy. In other embodiments, the one or more predictive statistical tree models correctly classify samples with an accuracy of up to 90%, 91%,  
25 92%, 93%, 94% or 95%.

#### BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows an example prediction tree for cookie fat outcomes. The root node splits on predictor/factor 92, followed by two subsequent splits on additional predictors 330 and 305. The  $\Pi$   
30 values are point estimates of the predictive probabilities of high fat versus low fat at each of the nodes, with suffixes simply indexing nodes. The labels  $Z(0=1)$  indicate the numbers of low fat (0) and high fat (1) samples within each node, and the  $F\#$  symbols indicate the thresholds that define the predictor based splits within each node.

35 Figure 2 shows two predictive factors in cookie dough analysis. All samples are represented by index numbers 1 through 78. Training data are denoted by blue (low fat) and red (high fat), and validation data by cyan (low fat) and magenta (high fat). The two full lines (black) demark the thresholds on the two predictors in this example tree.

Figure 3 shows a scatter plot of cookie data on three factors in example tree. Samples are denoted by blue (low fat) and red (high fat), with training data represented by filled circles and validation data by open circles.

- 5 Figure 4 shows three ER related metagenes in 49 primary breast tumors. Samples are denoted by blue (ER negative) and red (ER positive), with training data represented by filled circles and validation data by open circles.

- 10 Figure 5 shows three ER related metagenes in 49 primary breast tumors. All samples are represented by index number in 1-78. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

- 15 Figure 6 shows honest predictions of ER status of breast tumors. Predictive probabilities are indicated, for each tumor, by the index number on the vertical probability scale, together with an approximate 90% uncertainty interval about the estimated probability. All probabilities are referenced to a notional initial probability (incidence rate) of 0.5 for comparison. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

- 20 Figure 7 shows cross-validation probability predictions of lymph node status. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of high risk (red) versus low risk (blue). Approximate 90% uncertainty(confidence) intervals about these estimated probabilities are indicated by vertical dashed lines.

- 25 Figure 8 shows gene expression patterns from the major metagene that predicts lymph node status. Samples are plotted by sample index number and by color (color coding as in Figure 7).

- 30 Figure 9 shows cross-validation probability predictions of 3-year recurrence. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of 3 year recurrence (red) versus 3 year recurrence free survival (blue). Approximate 90% uncertainty intervals about these estimated probabilities are indicated by vertical dashed lines.

- 35 Figure 10 shows a diagram of aorta processing. The thoracic aorta is harvested, divided along the ventral aspect and furthered sectioned as shown. The A and B strips are used for RNA extraction. The C strip is evaluated for Sudanophilia and raised lesion mapping.

Figure 11 shows a summary of results of cross validation analysis of disease burden analysis.

Samples are plotted by the probability that they are severely diseased (95% CI). Severely diseased samples are red and minimally diseased, blue.

Figure 12 shows a summary of results of cross validation analysis of aorta location. Samples are plotted by the probability that they are from the distal location in the aorta (95% CI). Distal sections are red and proximal sections, blue.

Figure 13 shows a graphical display of gene expression in the key metagene for aortic location. The image indicates the discrimination between aorta samples of distal sections and proximal sections by difference of shades.

#### DETAILED DESCRIPTION OF THE INVENTION

Genes whose expression is correlated with and determinant of an atherosclerotic phenotype or determinant of susceptibility to developing atherosclerosis are provided. The metagenes provided by the invention as useful in binary prediction tree statistical models to classify genes according to atherosclerotic phenotype or susceptibility to atherosclerosis. Also provided are methods of using the subject atherosclerotic determinant genes in diagnosis and treatment methods, as well as drug screening methods. In addition, reagents and kits thereof that find use in practicing the subject methods are provided. Also provided are methods of determining whether a gene is correlated with a disease phenotype, where correlation is determined using at least one parameter that is not expression level and is preferably determined using a binary prediction tree analysis.

Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an" and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or

both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

5 Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the subject components of the invention that are described in the  
10 publications, which components might be used in connection with the presently described invention.

As summarized above, the subject invention is directed to a collection of genes whose expression is correlated with atherosclerosis, i.e., that are atherosclerotic phenotype determinative genes, as well as methods for using the collection or subparts thereof in various applications. In further describing the invention, the collection of genes determinative of the atherosclerotic  
15 phenotype is described first in greater detail, followed by a review of the various different applications in which the collection finds use, including diagnostic, therapeutic and screening applications. Also reviewed are reagents and kits for use in practicing the subject methods. Finally, a review of various methods of identifying genes whose expression correlates with a given phenotype, such as atherosclerosis, is provided.

20

#### ATHEROSCLEROTIC PHENOTYPE DETERMINATIVE GENES

The subject invention provides a collection of atherosclerotic phenotype determinative genes. By atherosclerotic phenotype determinative genes is meant genes whose expression or lack thereof correlates with an atherosclerotic phenotype. Thus, atherosclerotic determinative genes  
25 include genes: (a) whose expression is correlated with an atherosclerotic phenotype, i.e., are expressed in cells and tissues thereof that have an atherosclerotic phenotype, and (b) whose lack of expression is correlated with an atherosclerotic phenotype, i.e., are not expressed in cells and tissues thereof that have an atherosclerotic phenotype. A cell is a cell with an atherosclerotic phenotype if it is obtained from vascular tissue that is determined to be atherosclerotic, e.g., by Sudan staining  
30 according to the method reported in the experimental section, below. Likewise, tissue is tissue with an atherosclerotic phenotype if it is vascular tissue or obtained from vascular tissue that is determined to be atherosclerotic, e.g., by Sudan staining according to the method reported in the experimental section, below.

By atherosclerotic susceptibility determinative genes is meant genes whose expression or  
35 lack thereof correlates with a susceptibility to developing an atherosclerotic phenotype.

The invention claims all collections and subsets thereof of atherosclerotic phenotype determinative genes as well as metagenes disclosed herewith. The subject collections of atherosclerotic phenotype determinative genes may be physical or virtual. Physical collections are those collections that include a population of different nucleic acid molecules, where the

atherosclerotic phenotype determinative genes are represented in the population, i.e., there are nucleic acid molecules in the population that correspond in sequence to the genomic, or more typically, coding sequence of the atherosclerotic phenotype determinative genes in the collection.

In many embodiments, the nucleic acid molecules are either substantially identical or  
5 identical in sequence to the sense strand of the gene to which they correspond, or are complementary to the sense strand to which they correspond, typically to an extent that allows them to hybridize to their corresponding sense strand under stringent conditions. An example of stringent hybridization conditions is hybridization at 50°C or higher and 0.1×SSC (15 mM sodium chloride/1.5 mM sodium citrate). Another example of stringent hybridization conditions is overnight incubation at 42°C in a  
10 solution: 50 % formamide, 5 × SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 × Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 × SSC at about 65°C. Stringent hybridization conditions are hybridization conditions that are at least as stringent as the above representative conditions, where conditions are considered to be at least as stringent if they are at  
15 least about 80% as stringent, typically at least about 90% as stringent as the above specific stringent conditions. Other stringent hybridization conditions are known in the art and may also be employed to identify nucleic acids of this particular embodiment of the invention.

The nucleic acids that make up the subject physical collections may be single-stranded or double-stranded. In addition, the nucleic acids that make up the physical collections may be linear or  
20 circular, and the individual nucleic acid molecules may include, in addition to an atherosclerotic phenotype determinative gene coding sequence, other sequences, e.g., vector sequences. A variety of different nucleic acids may make up the physical collections, e.g., libraries, such as vector libraries, of the subject invention, where examples of different types of nucleic acids include, but are not limited to, DNA, e.g., cDNA, etc., RNA, e.g., mRNA, cRNA, etc. and the like. The nucleic acids of  
25 the physical collections may be present in solution or affixed, i.e., attached to, a solid support, such as a substrate as is found in array embodiments, where further description of such diverse embodiments is provided below.

Also provided are virtual collections of the subject atherosclerotic phenotype determinative genes. By virtual collection is meant one or more data files or other computer readable data  
30 organizational elements that include the sequence information of the genes of the collection, where the sequence information may be the genomic sequence information but is typically the coding sequence information. The virtual collection may be recorded on any convenient computer or processor readable storage medium. The computer or processor readable storage medium on which the collection data is stored may be any convenient medium, including CD, DAT, floppy disk, RAM,  
35 ROM, etc, which medium is capable of being read by a hardware component of the device.

Also provided are databases of expression profiles of atherosclerotic phenotype determinative genes. Such databases will typically comprise expression profiles of various cells/tissues having atherosclerotic phenotypes, such as various stages of atherosclerosis, negative expression profiles, prognostic profiles, etc., where such profiles are further described below.

The expression profiles and databases thereof may be provided in a variety of media to facilitate their use. "Media" refers to a manufacture that contains the expression profile information of the present invention. The databases of the present invention can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present database information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure may be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.*

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means may comprise any manufacture comprising a recording of the present information as described above, or a memory access means that can access such a manufacture.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks expression profiles possessing varying degrees of similarity to a reference expression profile. Such presentation provides a skilled artisan with a ranking of similarities and identifies the degree of similarity contained in the test expression profile.

Specific atherosclerotic phenotype determinative genes of the subject invention are those listed in Table I. Specific atherosclerotic susceptibility determinative genes of the subject invention are those listed in Table II. The invention also provides metagenes indicative of atherosclerotic burden or susceptibility. The subject collections and subsets thereof, as well as applications directed to the use of the aforementioned subject collections only serve as an example to illustrate the invention.

The subject collections of atherosclerotic-determinative genes include at least 2 of the genes listed in Table I. Table I contains the following genes, designated by Genbank Accession Number:

J04765, AF052124, X15525, M94345, AB020687, U51240, Y09445, AF053233, U43185, AL050008, M12529, AB022718, Z24725, D13666, U50928, U46692, AF044253, J03909, L10333, M80634, M63138, J04430, AF044896, X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, X62078, AB014574, L13939, D90144, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271,



- AF014958, U58334, J03011, D12485, U22662, AF055008, D86964, U88629, U75308, J03600, AF004709, L15388, AB002361, X62744, AF072099, X90858, Z29067, U00952, J00194, M80254, M21121, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, AB014520, L10678, Z98046, D79994, U29615, D87074, X81109, AL049946, U78556,
- 5 U21931, M63603, D87433, AB029032, X12451, U89606, AB029018, M34423, AF095791, X03084, X74039, AB016811, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AF055581, AB015718, X78817, AJ000534, M63835, M16336, M32578, U32324, AF079167, M22324, D86961, X54162, U57911, M64571, AL023653, AL023653, AC005546, AC005546, M60028, Y13622, L76191, U83115, U60060, AJ011497, D64142, D26350, X15414,
- 10 D87434, X79204, M58285, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, AF055024, U56833, J05070, AF093118, U12707, M55531, AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, U15085, X97074, D89016, AF022797, M33552, U09578, M21186, M64925, AF029750, U10906, U83993, AF022789, L35249,
- 15 M61916, AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193, D84110, AJ006973, AB002318, U51333, U09577 and U00672.

- Preferred Table I genes consist of the following genes, designated by Genbank Accession Number: Y09445, AF053233, U43185, AL050008, AB022718, L10333, M80634, AF044896,
- 20 X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, AB014574, L13939, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271, J03011, D12485, U88629, U75308, J03600, AF004709, AB002361, X90858, Z29067, U00952, M80254, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, L10678, Z98046, D79994, D87074, X81109,
- 25 AL049946, U78556, M63603, X12451, U89606, AB029018, AF095791, X74039, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AB015718, X78817, AJ000534, M63835, M16336, U32324, M22324, X54162, U57911, M64571, AC005546, AC005546, Y13622, L76191, U60060, AJ011497, D64142, D26350, X15414, D87434, X79204, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, U56833, J05070, AF093118, U12707, M55531,
- 30 AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, X97074, D89016, AF022797, M33552, U09578, M21186, M64925, U10906, U83993, AF022789, L35249, M61916, AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193,
- 35 D84110, AJ006973, AB002318, U51333, U09577 and U00672.

Table II contains the following genes, designated by Genbank Accession Number: M26679, S82986, AF051323, J02947, M16937, K03000, M36711, D76435, M74297, M68891, U43328, X17360, X51757, U59831, D83004, L49169, L35545, U16799, M20560, X06256, Z22865, X75918, X16665, M97676, M55153. Preferred Table II genes consist of the following genes, designated by

Genbank Accession Number: M68891, X51757, D83004, X06256, Z22865, X75918, M55153.

In certain embodiments, the number of genes in the collection that are from Table I or Table II is at least 5, at least 10, at least 25, at least 50, at least 75 or more, including all of the genes listed in Table I or are preferred Table I genes. The subject collections may include only those genes  
 5 that are listed in Tables I and/or Table II, or they may include additional genes that are not listed in the tables. Where the subject collections include such additional genes, in certain embodiments the % number of additional genes that are present in the subject collections does not exceed about 50%, usually does not exceed about 25 %. In many embodiments where additional "non-Table" genes are included, a great majority of genes in the collection are atherosclerotic phenotype determinative  
 10 genes, where by great majority is meant at least about 75%, usually at least about 80 % and sometimes at least about 85, 90, 95 % or higher, including embodiments where 100% of the genes in the collection are atherosclerotic phenotype determinative genes.

In some embodiments, at least one of the genes in the collection is a gene whose function does not readily implicate it in the production of an atherosclerotic phenotype where such genes  
 15 include those genes that are listed in Table I but which have not been assigned a biological process (see section 2 of the experimental section V for a listing of atherosclerotic determinative genes which have been assigned a biological functions; those not listed are the ones without a biological function assigned). In many embodiments, the subject collections include two or more genes from this group, where the number of genes that are included from this group may be 5, 10, 20 or more, up to and  
 20 including all of the genes in this group. In some embodiments, the set comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 40 or 50 preferred genes from Table I.

In some embodiments, at least one of the genes in the collection is a gene whose function does not readily implicate it in susceptibility to atherosclerosis, where such genes include those genes that are listed in Table I but which have not been assigned a biological process (see section 3 of the  
 25 experimental section V for a listing of atherosclerotic susceptibility genes which have been assigned a biological functions; those not listed are the ones without a biological function assigned). In many embodiments, the subject collections include 2 or more genes from this group, where the number of genes that are included from this group may be 5, 10, 20 or more, up to and including all of the genes in this group. In some embodiments, the set comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20,  
 30 25, 30, 40 or 50 preferred genes from Table II.

#### METHODS OF USING THE SUBJECT COLLECTIONS OF ATHEROSCLEROTIC PHENOTYPE/SUSCEPTIBILITY DETERMINATIVE GENES

The subject collections find use in a number of different applications. Applications of  
 35 interest include, but are not limited to: (a) diagnostic applications, in which the collections of the genes are employed to either predict the presence of, or the probability for occurrence of, an atherosclerotic phenotype; (b) pharmacogenomic applications, in which the collections of genes are employed to determine an appropriate therapeutic treatment regimen, which is then implemented; and (c) therapeutic agent screening applications, where the collection of genes is employed to identify

atherosclerotic phenotype modulatory agent or to identify atherosclerotic susceptibility modulatory agents. Each of these different representative applications is now described in greater detail below.

#### **Diagnostic Applications**

5 In diagnostic applications of the subject invention, cells or collections thereof, e.g., tissues, as well as animals (subjects, hosts, etc., e.g., mammals, such as pets, livestock, and humans, etc.) that include the cells/tissues are assayed to determine the presence of and/or probability for development of, an atherosclerotic phenotype. As such, diagnostic methods include methods of determining the presence of an atherosclerotic phenotype. In certain embodiments, not only the presence but also the severity or stage of an atherosclerotic phenotype is determined. In addition, diagnostic methods also include methods of determining the propensity to develop an atherosclerotic phenotype, such that a determination is made that an atherosclerotic phenotype is not present but is likely to occur.

10 In practicing the subject diagnostic methods, a nucleic acid sample obtained or derived from a cell, tissue or subject that includes the same that is to be diagnosed is first assayed to generate an expression profile, where the expression profile includes expression data for at least two of the genes of Table I or Table II, or preferred genes within those tables, where the expression profile may include expression data for 5, 10, 20, 50, 75 or more of, including all of, the genes listed in Table I or Table II, or preferred genes within those tables. In many embodiments, the expression profile also includes expression data for at least 1 of the genes listed in Table I or Table II, or preferred genes within those tables, wherein the expression profile may include expression data for 2, 5, 10, 20 or more, including all of the genes listed in Table I or Table II, or preferred genes within those tables. The number of different genes whose expression data, i.e., presence or absence of expression, as well as expression level, that are included in the expression profile that is generated may vary, but is typically at least 2, and in many embodiments ranges from 2 to about 100 or more, sometimes from 3 to about 75 or more, including from about 4 to about 70 or more.

25 As indicated above, the sample that is assayed to generate the expression profile employed in the diagnostic methods is one that is a nucleic acid sample. The nucleic acid sample includes a plurality or population of distinct nucleic acids that includes the expression information of the atherosclerotic phenotype determinative genes of interest of the cell or tissue being diagnosed. The nucleic acid may include RNA or DNA nucleic acids, e.g., mRNA, cRNA, cDNA etc., so long as the sample retains the expression information of the host cell or tissue from which it is obtained. The sample may be prepared in a number of different ways, as is known in the art, e.g., by mRNA isolation from a cell, where the isolated mRNA is used as is, amplified, employed to prepare cDNA, cRNA, etc., as is known in the differential expression art. The sample is typically prepared from a cell or tissue harvested from a subject to be diagnosed, e.g., via biopsy of tissue, using standard protocols, where cell types or tissues from which such nucleic acids may be generated include any tissue in which the expression pattern of the to be determined atherosclerotic phenotype exists, including, but not limited, to, monocytes, endothelium, and/or smooth muscle.

The expression profile may be generated from the initial nucleic acid sample using any

convenient protocol. While a variety of different manners of generating expression profiles are known, such as those employed in the field of differential gene expression analysis, one representative and convenient type of protocol for generating expression profiles is array based gene expression profile generation protocols. Such applications are hybridization assays in which a nucleic acid that displays "probe" nucleic acids for each of the genes to be assayed/profiled in the profile to be generated is employed. In these assays, a sample of target nucleic acids is first prepared from the initial nucleic acid sample being assayed, where preparation may include labeling of the target nucleic acids with a label, e.g., a member of signal producing system. Following target nucleic acid sample preparation, the sample is contacted with the array under hybridization conditions, whereby complexes are formed between target nucleic acids that are complementary to probe sequences attached to the array surface. The presence of hybridized complexes is then detected, either qualitatively or quantitatively. Specific hybridization technology which may be practiced to generate the expression profiles employed in the subject methods includes the technology described in U.S. Patent Nos.: 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,800,992; the disclosures of which are herein incorporated by reference; as well as WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280. In these methods, an array of "probe" nucleic acids that includes a probe for each of the atherosclerotic phenotype determinative genes whose expression is being assayed is contacted with target nucleic acids as described above. Contact is carried out under hybridization conditions, e.g., stringent hybridization conditions as described above, and unbound nucleic acid is then removed. The resultant pattern of hybridized nucleic acid provides information regarding expression for each of the genes that have been probed, where the expression information is in terms of whether or not the gene is expressed and, typically, at what level, where the expression data, i.e., expression profile, may be both qualitative and quantitative.

Once the expression profile is obtained from the sample being assayed, the expression profile is compared with a reference or control profile to make a diagnosis regarding the atherosclerotic phenotype of the cell or tissue from which the sample was obtained/derived. The reference or control profile may be a profile that is obtained from a cell/tissue known to have an atherosclerotic phenotype, as well as a particular stage of atherosclerosis, and therefore may be a positive reference or control profile. In addition, the reference or control profile may be a profile from cell/tissue for which it is known that the cell/tissue ultimately developed an atherosclerotic phenotype, and therefore may be a positive prognostic control or reference profile. In addition, the reference/control profile may be from a normal cell/tissue and therefore be a negative reference/control profile.

In certain embodiments, the obtained expression profile is compared to a single reference/control profile to obtain information regarding the atherosclerotic phenotype of the cell/tissue being assayed. In yet other embodiments, the obtained expression profile is compared to two or more different reference/control profiles to obtain more in depth information regarding the atherosclerotic phenotype of the assayed cell/tissue. For example, the obtained expression profile

may be compared to a positive and negative reference profile to obtain confirmed information regarding whether the cell/tissue has an atherosclerotic or normal phenotype. Furthermore, the obtained expression profile may be compared to a series of positive control/reference profiles each representing a different stage/level of atherosclerosis, so as to obtain more in depth information regarding the particular atherosclerotic phenotype of the assayed cell/tissue. The obtained expression profile may be compared to a prognostic control/reference profile, so as to obtain information about the propensity of the cell/tissue to develop an atherosclerotic phenotype.

The comparison of the obtained expression profile and the one or more reference/control profiles may be performed using any convenient methodology, where a variety of methodologies are known to those of skill in the array art, e.g., by comparing digital images of the expression profiles, by comparing databases of expression data, etc. Patents describing ways of comparing expression profiles include, but are not limited to, U.S. Patent Nos. 6,308,170 and 6,228,575, the disclosures of which are herein incorporated by reference. Methods of comparing expression profiles are also described above.

The comparison step results in information regarding how similar or dissimilar the obtained expression profile is to the control/reference profiles, which similarity/dissimilarity information is employed to determine the atherosclerotic phenotype of the cell/tissue being assayed. For example, similarity with a positive control indicates that the assayed cell/tissue has an atherosclerotic phenotype. Likewise, similarity with a negative control indicates that the assayed cell/tissue does not have an atherosclerotic phenotype.

Depending on the type and nature of the reference/control profile(s) to which the obtained expression profile is compared, the above comparison step yields a variety of different types of information regarding the cell/tissue that is assayed. As such, the above comparison step can yield a positive/negative determination of an atherosclerotic phenotype of an assayed cell/tissue. In addition, where appropriate reference profiles are employed, the above comparison step can yield information about the particular stage of an atherosclerotic phenotype of an assayed cell/tissue. Furthermore, the above comparison step can be used to obtain information regarding the propensity of the cell or tissue to develop an atherosclerotic phenotype.

In many embodiments, the above obtained information about the cell/tissue being assayed is employed to diagnose a host, subject or patient with respect to the presence of, state of or propensity to develop, atherosclerosis. For example, where the cell/tissue that is assayed is determined to have an atherosclerotic phenotype, the information may be employed to diagnose a subject from which the cell/tissue was obtained as having atherosclerosis.

#### **Pharmaco/Surgicogenomic Applications**

Another application in which the subject collections of atherosclerotic phenotype determinative genes finds use is in pharmacogenomic and/or surgicogenomic applications. In these applications, a subject/host/patient is first diagnosed for an atherosclerotic phenotype, e.g., presence or absence of atherosclerosis, propensity to develop atherosclerosis, etc., using a protocol such as the

diagnostic protocol described in the preceding section.

The subject is then treated using a pharmacological and/or surgical treatment protocol, where the suitability of the protocol for a particular subject/patient is determined using the results of the diagnosis step. A variety of different pharmacological and surgical treatment protocols are known to those of skill in the art. Such protocols include, but are not limited to: surgical treatment protocols, including bypass grafting, endarterectomy, and percutaneous transluminal angioplasty (PCTA). Pharmacological protocols of interest include treatment with a variety of different types of agents, including but not limited to: thrombolytic agents, growth factors, cytokines, nucleic acids (e.g. gene therapy agents); etc.

#### Assessment Of Therapy (Therapeutics)

Another application in which the subject collections of atherosclerotic phenotype determinative genes and/or atherosclerotic phenotype susceptibility genes find use is in monitoring or assessing a given treatment protocol. In such methods, a cell/tissue sample of a patient undergoing treatment for an atherosclerosis disease condition is monitored using the procedures described above in the diagnostic section, where the obtained expression profile is compared to one or more reference profiles to determine whether a given treatment protocol is having a desired impact on the disease being treated. For example, periodic expression profiles are obtained from a patient during treatment and compared to a series of reference/controls that includes expression profiles of various atherosclerotic stages and normal expression profiles. An observed change in the monitored expression profile towards a normal profile indicates that a given treatment protocol is working in a desired manner.

#### Therapeutic Agent Screening Applications

The present invention also encompasses methods for identification of agents having the ability to modulate an atherosclerotic phenotype, e.g., enhance or diminish an atherosclerotic phenotype, which finds use in identifying therapeutic agents for atherosclerosis.

Identification of compounds that modulate an atherosclerotic phenotype can be accomplished using any of a variety of drug screening techniques. The screening assays of the invention are generally based upon the ability of the agent to modulate an expression profile of atherosclerotic phenotype determinative genes.

The term "agent" as used herein describes any molecule, e.g., protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 Daltons. Candidate agents comprise functional groups necessary for structural

interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, etc. to produce structural analogs.

Exemplary candidate agents of particular interest include, but are not limited to, antisense polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (e.g., receptors and other molecule stably-associated with the outer cell membrane).

Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cell or tissue known to have an atherosclerotic phenotype with a candidate agent, and assessing the effect upon a gene expression profile made up of atherosclerotic phenotype determinative genes. The effect can be detected using any convenient protocol, where in many embodiments the diagnostic protocols described above are employed. Generally such assays are conducted in vitro, but many assays can be adapted for in vivo analyses, e.g., in an animal model of the diabetes.

#### **Screening For Drug Targets**

In another embodiment, the invention contemplates identification of genes and gene products from the subject collections of atherosclerotic determinative genes or of atherosclerosis susceptibility genes as therapeutic targets. In some respects, this is the converse of the assays described above for identification of agents having activity in modulating (e.g., decreasing or increasing) an atherosclerotic phenotype, and is directed towards identifying genes that are atherosclerotic phenotype determinative genes, e.g., the genes appearing in Table I, as therapeutic targets or directed towards identifying genes that are atherosclerotic susceptibility determinative genes, e.g., the genes appearing in Table II, as therapeutic targets

In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate an atherosclerotic phenotype (*e.g.*, inhibit or suppress an atherosclerotic phenotype). For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a gene appearing in Table I or Table II or preferred genes within these tables.

Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cell that expresses or overexpresses a candidate gene, *e.g.*, a gene found in Table I, is contacted with the known atherosclerotic agent, the effect upon a atherosclerotic phenotype and a biological activity of the candidate gene product assessed. The biological activity of the candidate gene product can be assayed by examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as detected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product.

Inhibition or suppression of the atherosclerotic phenotype indicates that the candidate gene product is a suitable target for atherosclerotic therapy. Assays described herein and/or known in the art can be readily adapted in for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal model of atherosclerosis.

#### REAGENTS AND KITS

Also provided are reagents and kits thereof for practicing one or more of the above described methods. The subject reagents and kits thereof may vary greatly. Reagents of interest include reagents specifically designed for use in production of the above described expression profiles of atherosclerotic phenotype determinative genes.

One type of such reagent is an array probe nucleic acids in which the atherosclerotic phenotype determinative genes of interest are represented. A variety of different array formats are known in the art, with a wide variety of different probe structures, substrate compositions and attachment technologies. Representative array structures of interest include those described in U.S. Patent Nos.: 5,143,854; 5,288,644; 5,324,633; 5,432,049; 5,470,710; 5,492,806; 5,503,980; 5,510,270; 5,525,464; 5,547,839; 5,580,732; 5,661,028; 5,800,992; the disclosures of which are herein incorporated by reference; as well as WO 95/21265; WO 96/31622; WO 97/10365; WO 97/27317; EP 373 203; and EP 785 280. In many embodiments, the arrays include probes for at least 2 of the genes listed in Table I or Table II, or preferred genes listed therein. In certain embodiments, the number of genes that are from Table I that is represented on the array is at least 5, at least 10, at least 25, at least 50, at least 75 or more, including all of the genes listed in Table I and/or Table II. The subject arrays may include only those genes that are listed in Table I and/or Table II, or they may include additional genes that are not listed in Table I and Table II. Where the subject arrays include probes for such additional genes, in certain embodiments the number % of additional genes that are



represented does not exceed about 50%, usually does not exceed about 25 %. In many embodiments where additional "non-Table I or Table II" genes are included, a great majority of genes in the collection are atherosclerotic phenotype determinative genes, where by great majority is meant at least about 75%, usually at least about 80 % and sometimes at least about 85, 90, 95 % or higher, including embodiments where 100% of the genes in the collection are atherosclerotic phenotype determinative genes. In many embodiments, at least one of the genes represented on the array is a gene whose function does not readily implicate it in the production of an atherosclerotic phenotype, where such genes include those genes listed in Table I and/or Table II. In many embodiments, the subject arrays include 2 or more genes from Table I and/or Table II, where the number of genes that are included from Table I may be 5, 10, 20 or more, up to an including all of the genes listed in Table I and/or Table II.

Another type of reagent that is specifically tailored for generating expression profiles of atherosclerotic phenotype determinative genes is a collection of gene specific primers that is designed to selectively amplify such genes. Gene specific primers and methods for using the same are described in U.S. Patent No. 5,994,076, the disclosure of which is herein incorporated by reference. Of particular interest are collections of gene specific primers that have primers for at least 2 of the genes listed in Table I and/or Table II, above. In certain embodiments, the number of genes that are from Table I and/or Table II that have primers in the collection is at least 5, at least 10, at least 25, at least 50, at least 75 or more, including all of the genes listed in Table I and/or Table II. The subject gene specific primer collections may include only those genes that are listed in Table I and/or Table II, or they may include primers for additional genes that are not listed in Table I and/or Table II. Where the subject gene specific primer collections include primers for such additional genes, in certain embodiments the number % of additional genes that are represented does not exceed about 50%, usually does not exceed about 25 %. In many embodiments where additional "non-Table I and/or Table II" genes are included, a great majority of genes in the collection are atherosclerotic phenotype determinative genes, where by great majority is meant at least about 75%, usually at least about 80 % and sometimes at least about 85, 90, 95 % or higher, including embodiments where 100% of the genes in the collection are atherosclerotic phenotype determinative genes. In many embodiments, at least one of the genes represented on collection of gene specific primers is a gene whose function does not readily implicate it in the production of an atherosclerotic phenotype, where such genes include those genes listed in Table I and/or Table II. In many embodiments, the subject gene specific primer collections include 2 or more genes from Table I and/or Table II, where the number of genes that are included from Table I and/or Table II may be 5, 10, 20 or more, up to an including all of the genes listed in Table I and/or Table II.

The kits of the subject invention may include the above described arrays and/or gene specific primer collections. The kits may further include one or more additional reagents employed in the various methods, such as primers for generating target nucleic acids, dNTPs and/or rNTPs, which may be either premixed or separate, one or more uniquely labeled dNTPs and/or rNTPs, such as biotinylated or Cy3 or Cy5 tagged dNTPs, gold or silver particles with different scattering spectra,

or other post synthesis labeling reagent, such as chemically active derivatives of fluorescent dyes, enzymes, such as reverse transcriptases, DNA polymerases, RNA polymerases, and the like, various buffer mediums, *e.g.* hybridization and washing buffers, prefabricated probe arrays, labeled probe purification reagents and components, like spin columns, etc., signal generation and detection reagents, *e.g.* streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

In addition to the above components, the subject kits will further include instructions for practicing the subject methods. These instructions may be present in the subject kits in a variety of forms, one or more of which may be present in the kit. One form in which these instructions may be present is as printed information on a suitable medium or substrate, *e.g.*, a piece or pieces of paper on which the information is printed, in the packaging of the kit, in a package insert, etc. Yet another means would be a computer readable medium, *e.g.*, diskette, CD, etc., on which the information has been recorded. Yet another means that may be present is a website address which may be used via the internet to access the information at a removed site. Any convenient means may be present in the kits.

#### COMPOUNDS AND METHODS FOR TREATMENT OF CARDIOVASCULAR DISEASE

Also provided are methods and compositions whereby cardiovascular disease symptoms may be ameliorated. The subject invention provides methods of ameliorating, *e.g.*, treating, an atherosclerotic disease conditions, by modulating the expression of one or more target genes or the activity of one or more products thereof, where the target genes are one or more of the atherosclerotic phenotype determinative genes of Table I, the preferred genes of Table I, or the genes in Table I to which no function has been assigned. The subject invention provides methods of decreasing the susceptibility to atherosclerotic disease by modulating the expression of one or more target genes or the activity of one or more products thereof, where the target genes are one or more of the atherosclerotic susceptibility determinative genes of Table II, the preferred genes of Table II, or the genes in Table II to which no function has been assigned.

Certain cardiovascular diseases are brought about, at least in part, by an excessive level of gene product, or by the presence of a gene product exhibiting an abnormal or excessive activity. As such, the reduction in the level and/or activity of such gene products would bring about the amelioration of cardiovascular disease symptoms. Techniques for the reduction of target gene expression levels or target gene product activity levels are discussed below.

Alternatively, certain other cardiovascular diseases are brought about, at least in part, by the absence or reduction of the level of gene expression, or a reduction in the level of a gene product's activity. As such, an increase in the level of gene expression and/or the activity of such gene products would bring about the amelioration of cardiovascular disease symptoms. Techniques for increasing target gene expression levels or target gene product activity levels are discussed below.

#### COMPOUNDS THAT INHIBIT EXPRESSION, SYNTHESIS

#### OR ACTIVITY OF MUTANT TARGET GENE ACTIVITY

As discussed above, target genes involved in cardiovascular disease disorders can cause such disorders via an increased level of target gene activity. A variety of techniques may be utilized to inhibit the expression, synthesis, or activity of such target genes and/or proteins. For example, 5 compounds such as those identified through assays described which exhibit inhibitory activity, may be used in accordance with the invention to ameliorate cardiovascular disease symptoms. As discussed, above, such molecules may include, but are not limited to small organic molecules, peptides, antibodies, and the like. Inhibitory antibody techniques are described, below.

For example, compounds can be administered that compete with an endogenous ligand for 10 the target gene product, where the target gene product binds to an endogenous ligand. The resulting reduction in the amount of ligand-bound gene target will modulate endothelial cell physiology. Compounds that can be particularly useful for this purpose include, for example, soluble proteins or peptides, such as peptides comprising one or more of the extracellular domains, or portions and/or analogs thereof, of the target gene product, including, for example, soluble fusion proteins such as Ig- 15 tailed fusion proteins. (For a discussion of the production of Ig-tailed fusion proteins, see, for example, U.S. Pat. No. 5,116,964.). Alternatively, compounds, such as ligand analogs or antibodies, that bind to the target gene product receptor site, but do not activate the protein, (e.g., receptor-ligand antagonists) can be effective in inhibiting target gene product activity. Furthermore, antisense and ribozyme molecules which inhibit expression of the target gene may also be used in accordance with 20 the invention to inhibit the aberrant target gene activity. Such techniques are described, below. Still further, also as described, below, triple helix molecules may be utilized in inhibiting the aberrant target gene activity.

#### INHIBITORY ANTISENSE, RIBOZYME AND TRIPLE HELIX APPROACHES

25 Among the compounds which may exhibit the ability to ameliorate cardiovascular disease symptoms are antisense, RNA interference molecules (RNAi), ribozyme, and triple helix molecules. Such molecules may be designed to reduce or inhibit mutant target gene activity. Techniques for the production and use of such molecules are well known to those of skill in the art.

Anti-sense RNA and DNA molecules act to directly block the translation of mRNA by 30 hybridizing to targeted mRNA and preventing protein translation. With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the target gene nucleotide sequence of interest, are preferred.

“RNA interference” or “RNAi” is a term initially applied to a phenomenon observed in plants and worms where double-stranded RNA (dsRNA) blocks gene expression in a specific and 35 post-transcriptional manner. Current research indicates that RNAi appears to involve mRNA degradation. Despite some uncertainty regarding the mechanism of action, RNAi provides a useful method of inhibiting gene expression *in vitro* or *in vivo*. RNAi constructs comprise double stranded RNA that can specifically block expression of a target gene. “RNAi construct” is a generic term used herein to include small interfering RNAs (siRNAs, around 19-30 nucleotides in length), hairpin

5 RNAs, and other RNA species which can be cleaved *in vivo* to form siRNAs. RNAi constructs also include expression vectors (also referred to as RNAi expression vectors) capable of giving rise to transcripts which form dsRNAs or hairpin RNAs in cells, and/or transcripts which can produce siRNAs *in vivo*. RNAi constructs contain a nucleotide sequence that hybridizes under physiologic  
10 conditions of the cell to the nucleotide sequence of at least a portion of the mRNA transcript for the gene to be inhibited (*i.e.*, the "target" gene). The double-stranded RNA need only be sufficiently similar to natural RNA that it has the ability to mediate RNAi. Thus, the invention has the advantage of being able to tolerate sequence variations that might be expected due to genetic mutation, strain polymorphism or evolutionary divergence. The number of tolerated nucleotide mismatches between  
15 the target sequence and the RNAi construct sequence is no more than 1 in 5 base pairs, or 1 in 10 base pairs, or 1 in 20 base pairs, or 1 in 50 base pairs. Mismatches in the center of the siRNA duplex are most critical and may essentially abolish cleavage of the target RNA. In contrast, nucleotides at the 3' end of the siRNA strand that is complementary to the target RNA do not significantly contribute to specificity of the target recognition. Exemplary methods of making and delivering  
either long or short RNAi constructs can be found, for example, in WO01/68836 and WO01/75164. RNAi constructs can be synthesized using methods well known in the art to synthesize or recombinantly produce RNA molecules.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme  
20 molecule to complementary target RNA, followed by an endonucleolytic cleavage. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see U.S. Pat. No. 5,093,246, which is incorporated by reference herein in its entirety. As such within the scope of the invention are engineered hammerhead motif ribozyme molecules that  
25 specifically and efficiently catalyze endonucleolytic cleavage of RNA sequences encoding target gene proteins. Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the molecule of interest for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site  
30 may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate sequences may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription  
35 should be single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules

provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

It is possible that the antisense, RNAi, ribozyme, and/or triple helix molecules described herein may reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by both normal and mutant target gene alleles. To ensure that substantially normal levels of target gene activity are maintained, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal activity may be introduced into cells via gene therapy methods such as those described, below, that do not contain sequences susceptible to whatever antisense, RNAi, ribozyme, or triple helix treatments are being utilized. Alternatively, it may be preferable to co-administer normal target gene protein into the cell or tissue to maintain the requisite level of cellular or tissue target gene activity.

Anti-sense RNA and DNA, RNAi constructs, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Various well-known modifications to the DNA molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

### 35 ANTIBODIES FOR TARGET GENE PRODUCTS

Antibodies that are both specific for target gene protein and interfere with its activity may be used to inhibit target gene function. Such antibodies may be generated using standard techniques known in the art against the proteins themselves or against peptides corresponding to portions of the proteins. Such antibodies include but are not limited to polyclonal, monoclonal, Fab fragments,

single chain antibodies, chimeric antibodies, etc.

In instances where the target gene protein is intracellular and whole antibodies are used, internalizing antibodies may be preferred. However, lipofectin liposomes may be used to deliver the antibody or a fragment of the Fab region which binds to the target gene epitope into cells. Where fragments of the antibody are used, the smallest inhibitory fragment which binds to the target protein's binding domain is preferred. For example, peptides having an amino acid sequence corresponding to the domain of the variable region of the antibody that binds to the target gene protein may be used. Such peptides may be synthesized chemically or produced via recombinant DNA technology using methods well known in the art (e.g., see Creighton, 1983, supra; and Sambrook *et al.*, 1989, supra). Alternatively, single chain neutralizing antibodies which bind to intracellular target gene epitopes may also be administered. Such single chain antibodies may be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population by utilizing, for example, techniques such as those described in Marasco *et al.* (Marasco, W. *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90:7889-7893).

In some instances, the target gene protein is extracellular, or is a transmembrane protein. Antibodies that are specific for one or more extracellular domains of the gene product, for example, and that interfere with its activity, are particularly useful in treating cardiovascular disease. Such antibodies are especially efficient because they can access the target domains directly from the bloodstream. Any of the administration techniques described, below which are appropriate for peptide administration may be utilized to effectively administer inhibitory target gene antibodies to their site of action.

#### METHODS FOR RESTORING TARGET GENE ACTIVITY

Target genes that cause cardiovascular disease may be underexpressed within cardiovascular disease situations. Alternatively, the activity of target gene products may be diminished, leading to the development of cardiovascular disease symptoms. Described in this Section are methods whereby the level of target gene activity may be increased to levels wherein cardiovascular disease symptoms are ameliorated. The level of gene activity may be increased, for example, by either increasing the level of target gene product present or by increasing the level of active target gene product which is present.

For example, a target gene protein, at a level sufficient to ameliorate cardiovascular disease symptoms may be administered to a patient exhibiting such symptoms. Any of the techniques discussed, below, may be utilized for such administration. One of skill in the art will readily know how to determine the concentration of effective, non-toxic doses of the normal target gene protein, utilizing techniques known to those of ordinary skill in the art.

Additionally, RNA sequences encoding target gene protein may be directly administered to a patient exhibiting cardiovascular disease symptoms, at a concentration sufficient to produce a level of target gene protein such that cardiovascular disease symptoms are ameliorated. Any of the techniques discussed, below, which achieve intracellular administration of compounds, such as, for

example, liposome administration, may be utilized for the administration of such RNA molecules. The RNA molecules may be produced, for example, by recombinant techniques as is known in the art.

Further, patients may be treated by gene replacement therapy. One or more copies of a normal target gene, or a portion of the gene that directs the production of a normal target gene protein with target gene function, may be inserted into cells using vectors which include, but are not limited to adenovirus, adeno-associated virus, and retrovirus vectors, in addition to other particles that introduce DNA into cells, such as liposomes. Additionally, techniques such as those described above may be utilized for the introduction of normal target gene sequences into human cells.

Cells, preferably, autologous cells, containing normal target gene expressing gene sequences may then be introduced or reintroduced into the patient at positions which allow for the amelioration of cardiovascular disease symptoms. Such cell replacement techniques may be preferred, for example, when the target gene product is a secreted, extracellular gene product.

#### PHARMACEUTICAL PREPARATIONS AND METHODS OF ADMINISTRATION

The identified compounds that inhibit target gene expression, synthesis and/or activity can be administered to a patient at therapeutically effective doses to treat or ameliorate cardiovascular disease. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of cardiovascular disease.

##### 1. Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the  $LD_{50}$  (the dose lethal to 50% of the population) and the  $ED_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio  $LD_{50}/ED_{50}$ . Compounds which exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the  $ED_{50}$  with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the  $IC_{50}$  (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

### FORMULATIONS AND USE

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Suitable vehicles and their formulation inclusive of various proteins are described, for example, in the book *Remington's Pharmaceutical Sciences* (Mack Publishing Company, Easton, Pa., USA 1985) or *Handbook of Pharmaceutical Excipients*, 4<sup>th</sup> ed. (Ed. Rowe *et al.*, Pharmaceutical Press, Grayslake, IL, USA 2003), the contents of which are incorporated herein by reference.

Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-*p*-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner. For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of *e.g.* gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active



ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other  
5 glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an  
10 emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be  
15 accompanied by instructions for administration.

#### METHODS OF IDENTIFYING ATHEROSCLEROTIC PHENOTYPE/SUSCEPTIBILITY DETERMINATIVE GENES

Also provided are methods of identifying atherosclerotic phenotype determinative genes,  
20 *i.e.*, genes whose expression is associated with a disease phenotype, or of identifying atherosclerotic susceptibility determinative genes, *i.e.*, genes whose expression is associated with an atherosclerotic susceptibility phenotype.

In these methods, an expression profile for a nucleic acid sample obtained from a source having the atherosclerotic phenotype, or a sample to be tested for susceptibility, is prepared using the  
25 gene expression profile generation techniques described above, with the only difference being that the genes that are assayed are candidate genes and not genes necessarily known to be atherosclerotic phenotype/susceptibility determinative genes. Next, the obtained expression profile is compared to a control profile, *e.g.*, obtained from a source that does not have an atherosclerotic phenotype.

Following this comparison step, genes whose expression correlates with said the  
30 atherosclerotic phenotype/susceptibility are identified. A feature of the subject invention is that the correlation is based on at least one parameter that is other than expression level. As such, a parameter other than whether a gene is up or down regulated is employed to find a correlation of the gene with the atherosclerotic phenotype.

One expression analysis approach may include a Bayesian analysis of binary prediction tree  
35 models for retrospectively sampled outcomes as illustrated in the following three exemplary analyses.

Bayesian analysis is an approach to statistical analysis that is based on the Bayes law, which states that the posterior probability of a parameter *p* is proportional to the prior probability of parameter *p* multiplied by the likelihood of *p* derived from the data collected. This increasingly popular methodology represents an alternative to the traditional (or frequentist probability) approach:

whereas the latter attempts to establish confidence intervals around parameters, and/or falsify a-priori null-hypotheses, the Bayesian approach attempts to keep track of how a-priori expectations about some phenomenon of interest can be refined, and how observed data can be integrated with such a-priori beliefs, to arrive at updated posterior expectations about the phenomenon. Bayesian analysis have been applied to numerous statistical models to predict outcomes of events based on available data. These include standard regression models, e.g. binary regression models, as well as to more complex models that are applicable to multi-variate and essentially non-linear data.

Another such model is commonly known as the tree model which is essentially based on a decision tree. Decision trees can be used in clarification, prediction and regression. A decision tree model is built starting with a root node, and training data partitioned to what are essentially the "children" nodes using a splitting rule. For instance, for clarification, training data contains sample vectors that have one or more measurement variables and one variable that determines that class of the sample. Various splitting rules have been used; however, the success of the predictive ability varies considerably as data sets become larger. Furthermore, past attempts at determining the best splitting for each node is often based on a "purity" function calculated from the data, where the data is considered pure when it contains data samples only from one class. Most frequently, used purity functions are entropy, gini-index, and towsing rule. A statistical predictive tree model to which Bayesian analysis is applied may consistently deliver accurate results with high predictive capabilities.

#### 20 Development of the Tree Clarification Model: Model Context and Methodology

Data  $\{Z_i, \mathbf{x}_i\}$  ( $i = 1, \dots, n$ ) are available on a binary response variable  $Z$  and a  $p$ -dimensional covariate vector  $\mathbf{x}$ : The 0/1 response totals are fixed by design. Each predictor variable  $x_j$  could be binary, discrete or continuous.

#### 25 1. Bayes' factor measures of association

At the heart of a classification tree is the assessment of association between each predictor and the response in subsamples, and we first consider this at a general level in the full sample. For any chosen single predictor  $x$ ; a specified threshold  $\tau$  on the levels of  $x$  organizes the data into the  $2 \times 2$  table.

	$Z = 0$	$Z = 1$	
$x \leq \tau$	$n_{00}$	$n_{01}$	$N_0$
$x > \tau$	$n_{10}$	$n_{11}$	$N_1$
	$M_0$	$M_1$	

30

With column totals fixed by design, the categorized data is properly viewed as two Bernoulli sequences within the two columns, hence sampling

$$p(n_{0z}, n_{1z} | M_z, \theta_{z,\tau}) = \theta_{z,\tau}^{n_{0z}} (1 - \theta_{z,\tau})^{n_{1z}}$$

for each column  $z = 0, 1$ . Here, of course,  $\theta_{0,\tau} = Pr(x \leq \tau | Z = 0)$  and  $\theta_{1,\tau} = Pr(x \leq \tau | Z = 1)$ . A test of association of the thresholded predictor with the response will now be based on assessing the difference between these Bernoulli probabilities.

The natural Bayesian approach is via the Bayes' factor  $B_\tau$  comparing the null hypothesis  $\theta_{0,\tau} = \theta_{1,\tau}$  to the full alternative  $\theta_{0,\tau} \neq \theta_{1,\tau}$ . We adopt the standard conjugate beta prior model and require that the null hypothesis be nested within the alternative. Thus, assuming  $\theta_{0,\tau} \neq \theta_{1,\tau}$ , we take  $\theta_{0,\tau}$  and  $\theta_{1,\tau}$  to be independent with common prior  $Be(a_\tau, b_\tau)$  with mean  $m_\tau = a_\tau / (a_\tau + b_\tau)$ . On the null hypothesis  $\theta_{0,\tau} = \theta_{1,\tau}$ , the common value has the same beta prior. The resulting Bayes' factor in favour of the alternative over the null hypothesis is then simply

$$B_\tau = \frac{\beta(n_{00} + a_\tau, n_{10} + b_\tau) \beta(n_{01} + a_\tau, n_{11} + b_\tau)}{\beta(N_0 + a_\tau, N_1 + b_\tau) \beta(a_\tau, b_\tau)}.$$

As a Bayes' factor, this is calibrated to a likelihood ratio scale. In contrast to more traditional significance tests and also likelihood ratio approaches, the Bayes' factor will tend to provide more conservative assessments of significance, consistent with the general conservative properties of proper Bayesian tests of null hypotheses (See Sellke, T., Bayarri, M.J. and Berger, J.O., Calibration of p-values for testing precise null hypotheses, *The American Statistician*, **55**, 62-71, (2001) and references therein).

In the context of comparing predictors, the Bayes' factor  $B_\tau$  may be evaluated for all predictors and, for each predictor, for any specified range of thresholds. As the threshold varies for a given predictor taking a range of (discrete or continuous) values, the Bayes' factor maps out a function of  $\tau$  and high values identify ranges of interest for thresholding that predictor. For a binary predictor, of course, the only relevant threshold to consider is  $\tau = 0$ .

15

## 2. Model consistency with respect to varying thresholds

A key question arises as to the consistency of this analysis as we vary the thresholds. By construction, each probability  $\theta_{z,\tau}$  is a non-decreasing function of  $\tau$ , a constraint that must be formally represented in the model. The key point is that the beta prior specification must formally reflect this. To see how this is achieved, note first that  $\theta_{z,\tau}$  is in fact the cumulative distribution function of the predictor values  $x$ ; conditional on  $Z = z$ ; ( $z = 0, 1$ ); evaluated at the point  $x = \tau$ . Hence the sequence of beta priors,  $Be(a_\tau, b_\tau)$  as  $\tau$  varies, represents a set of marginal prior distributions for the corresponding set of values of the cdfs. It is immediate that the natural embedding is in a non-parametric Dirichlet process model for the complete cdf. Thus the threshold-specific beta priors are consistent, and the resulting sets of Bayes' factors comparable as  $\tau$  varies, under a Dirichlet process prior with the betas as margins. The required constraint is that the prior mean values  $m_\tau$  are themselves values of a cumulative distribution function on the range of  $x$ , one that defines the prior mean of each  $\theta_\tau$  as a function. Thus, we simply rewrite the beta parameters ( $\alpha_\tau, b_\tau$ ) as  $\alpha_\tau = \alpha m_\tau$  and  $b_\tau = \alpha(1 - m_\tau)$  for a specified prior mean cdf  $m_\tau$ , and where  $\alpha$  is the prior precision (or "total mass") of the

underlying Dirichlet process model. Note that this specializes to a Dirichlet distribution when  $\chi$  is discrete on a finite set of values, including special cases of ordered categories (such as arise if  $\chi$  is truncated to a predefined set of bins), and also the extreme case of binary  $\chi$  when the Dirichlet is a simple beta distribution.

5

### 3. Generating a tree

The above development leads to a formal Bayes' factor measure of association that may be used in the generation of trees in a forward-selection process as implemented in traditional classification tree approaches. Consider a single tree and the data in a node that is a candidate for a binary split. Given the data in this node, construct a binary split based on a chosen (predictor, threshold) pair  $(\chi, \tau)$  by (a) finding the (predictor, threshold) combination that maximizes the Bayes' factor for a split, and (b) splitting if the resulting Bayes' factor is sufficiently large. By reference to a posterior probability scale with respect to a notional 50:50 prior, Bayes' factors of 2.2, 2.9, 3.7 and 5.3 correspond, approximately, to probabilities of .9, .95, .99 and .995, respectively. This guides the choice of threshold, which may be specified as a single value for each level of the tree. We have utilized Bayes' factor thresholds of around 3 in a range of analyses, as exemplified below. Higher thresholds limit the growth of trees by ensuring a more stringent test for splits.

The Bayes' factor measure will always generate less extreme values than corresponding generalized likelihood ratio tests (for example), and this can be especially marked when the sample sizes  $M_0$  and  $M_1$  are low. Thus the propensity to split nodes is always generally lower than with traditional testing methods, especially with lower samples sizes, and hence the approach tends to be more conservative in extending existing trees. Post-generation pruning is therefore generally much less of an issue, and can in fact generally be ignored.

Index the root node of any tree by zero, and consider the full data set of  $n$  observations, representing  $M_z$  outcomes with  $Z = z$  in 0, 1. Label successive nodes sequentially: splitting the root node, the left branch terminates at node 1, the right branch at node 2; splitting node 1, the consequent left branch terminates at node 3, the right branch at node 4; splitting node 2, the consequent left branch terminates at node 5, and the right branch at node 6, and so forth. Any node in the tree is labelled numerically according to its "parent" node; that is, a node  $j$  splits into two children, namely the (left, right) children  $(2j + 1; 2j + 2)$ : At level  $m$  of the tree ( $m = 0; 1; \dots$ ) the candidate nodes are, from left to right, as  $2^m - 1; 2^m; \dots; 2^{m+1} - 2$ .

Having generated a "current" tree, we run through each of the existing terminal nodes one at a time, and assess whether or not to create a further split at that node, stopping based on the above Bayes' factor criterion. Unless samples are very large (thousands) typical trees will rarely extend to more than three or four levels.

### 4. Inference and prediction with a single tree

Suppose we have generated a tree with  $m$  levels; the tree has some number of terminal nodes up to the maximum possible of  $L = 2^{m+1} - 2$ . Inference and prediction involves computations for

*branch probabilities* and the predictive probabilities for new cases that these underlie. We detail this for a specific path down the tree, i.e., a sequence of nodes from the root node to a specified terminal node.

First, consider a node  $j$  that is split based on a (predictor, threshold) pair labeled  $(\chi_j, \tau_j)$ , (note that we use the node index to label the chosen predictor, for clarity). Extend the notation of Section 2.1 to include the subscript  $j$  indexing this node. Then the data at this node involves  $M_{0j}$  cases with  $Z = 0$  and  $M_{1j}$  cases with  $Z = 1$ . Based on the chosen (predictor, threshold) pair  $(\chi_j, \tau_j)$  these samples split into cases  $n_{00j}, n_{01j}, n_{10j}, n_{11j}$  as in the table of Section 2.1, but now indexed by the node label  $j$ . The implied conditional probabilities  $\theta_{z,\tau_j} = \Pr(\chi_j \leq \tau_j | Z = z)$ , for  $z = 0, 1$  are the *branch probabilities* defined by such a split (note that these are also conditional on the tree and data subsample in this node, though the notation does not explicitly reflect this for clarity). These are uncertain parameters and, following the development of Section 2.1, have specified beta priors, now also indexed by parent node  $j$ , i.e.,  $Be(a_{\tau_j}, b_{\tau_j})$ . Assuming the node is split, the two sample Bernoulli setup implies conditional posterior distributions for these branch probability parameters: they are independent with posterior beta distributions

$$\theta_{0,\tau_j} \sim Be(a_{\tau_j} + n_{00j}, b_{\tau_j} + n_{01j}) \text{ and } \theta_{1,\tau_j} \sim Be(a_{\tau_j} + n_{10j}, b_{\tau_j} + n_{11j}).$$

These distributions allow inference on branch probabilities, and feed into the predictive inference computations as follows.

Consider predicting the response  $Z^*$  of a new case based on the observed set of predictor values  $\mathbf{x}^*$ . The specified tree defines a unique path from the root to the terminal node for this new case. To predict requires that we compute the posterior predictive probability for  $Z^* = 1/0$ . We do this by following  $\mathbf{x}^*$  down the tree to the implied terminal node, and sequentially building up the relevant likelihood ratio defined by successive (predictor, threshold) pairs.

For example and specificity, suppose that the predictor profile of this new case is such that the implied path traverses nodes 0, 1, 4, 9, terminating at node 9. This path is based on a (predictor, threshold) pair  $(\chi_0, \tau_0)$  that defines the split of the root node,  $(\chi_1, \tau_1)$  that defines the split of node 1, and  $(\chi_4, \tau_4)$  that defines the split of node 4. The new case follows this path as a result of its predictor values, in sequence:

$(x_0^* \leq \tau_0)$ ,  $(x_1^* > \tau_1)$  and  $(x_4^* \leq \tau_4)$ . The implied likelihood ratio for  $Z^* = 1$  relative to  $Z^* = 0$  is then the product of the ratio of branch probabilities to this terminal node, namely

$$\lambda^* = \frac{\theta_{1,\tau_0,0}}{\theta_{0,\tau_0,0}} \times \frac{(1 - \theta_{1,\tau_1,1})}{(1 - \theta_{0,\tau_1,1})} \times \frac{\theta_{1,\tau_4,0}}{\theta_{0,\tau_4,0}}.$$

Hence, for any specified prior probability  $\Pr(Z^* = 1)$ , this single tree model implies that, as a function of the branch probabilities, the updated probability  $\pi^*$  is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{\Pr(Z^* = 1)}{\Pr(Z^* = 0)}.$$

Hence, for any specified prior probability  $\pi \Pr(Z^* = 1)$ , this single tree model implies that, as a function the branch probabilities, the updated probability  $\pi^*$  is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \frac{\lambda^* \Pr(Z^* = 1)}{\Pr(Z^* = 0)}$$

The case-control design provides no information about  $\Pr(Z^* = 1)$  so it is up to the user to specify this or examine a range of values; one useful summary is obtained by simply taking a 50:50 prior odds as benchmark, whereupon the posterior probability is

$$\pi^* = \lambda^* / (1 + \lambda^*).$$

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Prediction follows by estimating  $\pi^*$  based on the sequence of conditionally independent posterior distributions for the branch probabilities that define it. For example, simply “plugging-in” the conditional posterior means of each  $\theta$ . will lead to a plug-in estimate of  $\lambda^*$  and hence  $\pi^*$ . The full posterior for  $\pi^*$  is defined implicitly as it is a function of the  $\theta$ .. Since the branch probabilities follow beta posteriors, it is trivial to draw Monte Carlo samples of the  $\theta$ . and then simply compute the corresponding values of  $\lambda^*$  and hence  $\pi^*$  to generate a posterior sample for summarization. This way, we can evaluate simulation-based posterior means and uncertainty intervals for  $\pi^*$  that represent predictions of the binary outcome for the new case.

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## 20 5. Generating and weighting multiple trees

In considering potential (predictor, threshold) candidates at any node, there may be a number with high Bayes’ factors, so that multiple possible trees with difference splits at this node are suggested. With continuous predictor variables, small variations in an “interesting” threshold will generally lead to small changes in the Bayes’ factor – moving the threshold so that a single observation moves from one side of the threshold to the other, for example. This relates naturally to the need to consider thresholds as parameters to be inferred; for a given predictor  $x$ , multiple candidate splits with various different threshold values  $\tau$  reflects the inherent uncertainty about  $\tau$ , and indicates the need to generate multiple trees to adequately represent that uncertainty. Hence, in such a situation, the tree generation can spawn multiple copies of the “current” tree, and then each will split the current node based on a different threshold for this predictor. Similarly, multiple trees may be spawned this way with the modification that they may involve different predictors.

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In problems with many predictors, this naturally leads to the generation of many trees, often with small changes from one to the next, and the consequent need for careful development of tree-managing software to represent the multiple trees. In addition, there is then a need to develop inference and prediction in the context of multiple trees generated this way. The use of “forests of trees” has recently been urged by Breiman, L., Statistical Modeling: The two cultures (with discussion), *Statistical Science*, 16 199-225 (2001), and our perspective endorses this. The rationale here is quite simple: node splits are based on specific choices of what we regard as parameters of the overall predictive tree model, the (predictor, threshold) pairs. Inference based on any single tree

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chooses specific values for these parameters, whereas statistical learning about relevant trees requires that we explore aspects of the posterior distribution for the parameters (together with the resulting branch probabilities).

- 5 Within the current framework, the forward generation process allows easily for the computation of the resulting relative likelihood values for trees, and hence to relevant weighting of trees in prediction. For a given tree, identify the subset of nodes that are split to create branches. The overall marginal likelihood function for the tree is then the product of component marginal likelihoods, one component from each of these split nodes. Continue with the notation of Section 2.1 but now, again, indexed by any chosen node  $j$ : Conditional on splitting the node at the defined
- 10 (predictor, threshold) pair  $(x_j, \tau_j)$ , the marginal likelihood component is

$$m_j = \int_0^1 \int_0^1 \prod_{z=0,1} p(n_{0zj}, n_{1zj} | M_{zj}, \theta_{z,\tau_j,j}) p(\theta_{z,\tau_j,j}) d\theta_{z,\tau_j,j}$$

where  $p(\theta_{z,\tau_j,j})$  is the  $Bc(a_{\tau,j}, b_{\tau,j})$  prior for each  $z = 0, 1$ . This clearly reduces to

$$m_j = \prod_{z=0,1} \frac{\beta(n_{0zj} + a_{\tau,j}, n_{1zj} + b_{\tau,j})}{\beta(a_{\tau,j}, b_{\tau,j})}.$$

- The overall marginal likelihood value is the product of these terms over all nodes  $j$  that define branches in the tree. This provides the relative likelihood values for all trees within the set of trees generated. As a first reference analysis, we may simply normalize these values to provide
- 15 relative posterior probabilities over trees based on an assumed uniform prior. This provides a reference weighting that can be used to both assess trees and as posterior probabilities with which to weight and average predictions for future cases.

#### Example 1: Analysis of Biscuit Dough Data

- 20 A first example concerns the application of biscuit dough data (publicly available at Osborne, B.G., Fearn, T., Miller, A.R. and Douglas, S., Applications of near infrared reflectance spectroscopy to compositional analysis of biscuits and biscuit doughs, *J. Sci. Food Agric.*, **35**, 99-105 (1984); Brown, P.J., Fearn, T. and Vannucci, M., The choice of variables in multivariate regression: A non-conjugate Bayesian decision theory approach, *Biometrika*, **86**, 635-648 (1999)) in which
- 25 interest lies in relating aspects of near infrared ("NIR") spectra of dough to the fat content of the resulting biscuits. The data set provides 78 samples, of which 39 are taken as training data and the remaining 39 as validation cases to be predicted, precisely as in Brown *et al* (1999). The binary outcome is 0/1 according to whether the measured fat content exceeds a threshold, where the threshold is the mean of the sample of fat values. As predictors, each  $x_i$  comprises 300 values of the
- 30 spectrum of dough sample  $i$ , augmented by the set of singular factors (principal components) of the 78 sample spectra, so that  $p = 378$ ; with singular factors indexed 301; : : : 378.

The analysis was developed repeatedly, exploring aspects of model fit and prediction of the validation sample as the number of control parameters were varied. The particular parameters of key

interest varied were the Bayes' factor thresholds that define splits, and controls on the number of such splits that may be made at any one node. It was determined that across ranges of these control parameters, that there was a good degree of robustness. The Bayes' factor threshold was fixed at 3 on the log scale, after which and two-level trees were explored allowing at most 10 splits of the root node and then at most 4 splits of each of nodes 1 and 2. This allowed up to 160 trees, with this analysis generating 148 trees.

Many of the trees identified had one or two of the predictors in common, and represent variation in the threshold values for those predictors. Figures 1-3 display some summaries. Figure 1 represents one of the 148 trees, split at the root node by the spectral predictor labeled factor 92 (corresponding to a wavelength of 1566 nm). Multiple wavelength values appear in the 148 trees, with values close to this appearing commonly, reflecting the underlying continuity of the spectra. The key second level predictor is factor 305, one of the principal component predictors. The data are scatter plotted on these two predictors in Figure 2 with corresponding levels of the predictor-specific thresholds from this tree marked.

The data appears also against the three predictors in this tree in Figure 3. Evidently there is substantial overlap in predictor space between the 0/1 outcomes, and cases close to the boundaries defined by any single tree are hard to accurately predict. Nevertheless, in terms of posterior predictive probabilities for the 39 validation samples, accuracy is good. By simply establishing the predictive probability threshold at 0.5 it is determined that 18 of 20 (90%) low fat (blue) cases are "correctly" predicted, as are 19 of 20 (95%) high fat (red) cases.

Predictive accuracy is high in this example with considerable overlap between predictor patterns among the two outcome groups. This is a positive example of the use of the predictive tree approach in a context where standard methods, such as logistic regression, would be less useful. Furthermore, we end with a note that the 50:50 split of the 78 samples into training and validation sets followed the previous authors as references. Curious about this, we reran the analysis 500 times, each time randomly splitting the data 50:50 into training and validation samples. Predictive accuracy, as measured above, was generally not so good as reported for the initial sample split, varying from a little below 50% to 100% across this set of 500 analyses. The average accuracy for low fat (blue) cases was 80%, and that for high fat (red) cases 76%.

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#### Example 2: Metagene Expression Profiling to Predict Estrogen Receptor Status of Breast Cancer Tumors

This example illustrates not only predictive utility but also exploratory use of the tree analysis framework in exploring data structure. Here, the tree analysis is used to predict estrogen receptor ("ER") status of breast tumors using gene expression data. Prior analyses of such data involved binary regression models which utilized Bayesian generalized shrinkage approaches to factor regression. Specifically, prior statistical models involved the use of probit linear regression linking principal components of selected subsets of genes to the binary (ER positive/negative) outcomes. See West, M., Blanchette, C., Dressman, H., Ishida, S., Spang, R., Zuzan, H., Marks, J.R.



and Nevins, J.R. Utilization of gene expression profiles to predict the clinical status of human breast cancer. *Proc. Natl. Acad. Sci.*, **98**, 11462-11467 (2001). However, the tree model presents some distinct advantages over Bayesian linear regression models in the analysis of large non-linear data sets such as these.

5 Primary breast tumors from the Duke Breast Cancer SPORE frozen tissue bank were selected for this study on the basis of several criteria. Tumors were either positive for both the estrogen and progesterone receptors or negative for both receptors. Each tumor was diagnosed as invasive ductal carcinoma and was between 1.5 and 5 cm in maximal dimension. In each case, a diagnostic auxiliary lymph node dissection was performed. Each potential tumor was examined by  
10 hematoxylin/eosin staining and only those that were > 60% tumor (on a per-cell basis), with few infiltrating lymphocytes or necrotic tissue, were carried on for RNA extraction. The final collection of tumors consisted of 13 estrogen receptor (ER)+ lymph node (LN)+ tumors, 12 ER LN+ tumors, 12 ER+ LN tumors, and 12 ER LN tumors

The RNA was derived from the tumors as follows: Approximately 30 mg of frozen breast  
15 tumor tissue was added to a chilled BioPulverizer H tube (Bio101) (Q-Biogene, La Jolla, CA). Lysis buffer from the Qiagen (Chatsworth, CA) RNeasy Mini kit was added, and the tissue was homogenized for 20 sec in a MiniBeadbeater (Biospec Products, Bartlesville, OK). Tubes were spun briefly to pellet the garnet mixture and reduce foam. The lysate was transferred to a new 1.5-ml tube by using a syringe and 21-gauge needle, followed by passage through the needle 10 times to shear  
20 genomic DNA. Total RNA was extracted by using the Qiagen RNeasy Mini kit. Two extractions were performed for each tumor, and total RNA was pooled at the end of the RNeasy protocol, followed by a precipitation step to reduce volume. Quality of the RNA was checked by visualization of the 28S:18S ribosomal RNA ratio on a 1% agarose gel. After the RNA preparation, the samples were subject to Affymetrix GENECHIP analysis.

25 Affymetrix GENECHIP Analysis: The targets for Affymetrix DNA microarray analysis were prepared according to the manufacturer's instructions. All assays used the human HuGeneFL GENECHIP microarray. Arrays were hybridized with the targets at 45°C for 16 h and then washed and stained by using the GENECHIP Fluidics. DNA chips were scanned with the GENECHIP scanner, and signals obtained by the scanning were processed by GENECHIP Expression Analysis  
30 algorithm (version 3.2) (Affymetrix, Santa Clara, CA).

The same set of  $n = 49$  samples used in the binary regression analysis described in West et al (2001) is analyzed in this study, using predictors based on *metagene* summaries of the expression levels of many genes. Metagenes are useful aggregate, summary measures of gene expression profiles. The evaluation and summarization of large-scale gene expression data in terms of lower  
35 dimensional factors of some form is utilized for two main purposes: first, to reduce dimension from typically several thousand, or tens of thousands of genes to a more practical dimension; second, to identify multiple underlying "patterns" of variation across samples that small subsets of genes share, and that characterize the diversity of patterns evidenced in the full sample. Although, the analysis is conducive to the use of various factor model approaches known to those skilled in the art, a cluster-

factor approach is used here to define empirical metagenes. This defines the predictor variables  $x$  utilized in the tree model. Metagenes may be obtained by combining clustering with empirical factor methods. The metagene summaries used in the ER example were based on the following steps:

Assume a sample of  $n$  profiles of  $p$  genes;

- 5 (1) Screen genes to reduce the number by eliminating genes that show limited variation across samples or that are evidently expressed at low levels that are not detectable at the resolution of the gene expression technology used to measure levels. This removes noise and reduces the dimension of the predictor variable;
- (2) Cluster the genes using  $k$ \_means, correlated-based clustering. Any standard statistical package  
10 may be used. This analysis uses the xcluster software created by Gavin Sherlock  
(<http://genomewww.stanford.edu/sherlock/cluster.html>). A large number of clusters are targeted so as to capture multiple, correlated patterns of variation across samples, and generally small numbers of genes within clusters;
- (3) Extract the dominant singular factor (principal component) from each of the resulting clusters.  
15 Again, any standard statistical or numerical software package may be used for this; this analysis uses the efficient, reduced singular value decomposition function ("SVD") in the Matlab software environment.

- In the analysis of the ER data, the original data was developed using Affymetrix arrays with 7129 sequences, of which 7070 were used (following removal of Affymetrix controls from the data.).
- 20 The expression estimates used were  $\log_2$  values of the signal intensity measures computed using the dChip software for post-processing Affymetrix output data (See Li, C. and Wong, W.H. Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc. Natl. Acad. Sci.*, **98**, 31-36 (2001). With a target of 500 clusters, the xcluster software implementing the correlation-based  $k$ \_means clustering produced  $p = 491$  clusters. The corresponding  $p$  metagenes  
25 were then evaluated as the dominant singular factors of each of these cluster, as referenced above.

- The data comprised 40 training samples and 9 validation cases. Among the latter, 3 were initial training samples that presented conflicting laboratory tests of the ER protein levels, so casting into question their actual ER status; these were therefore placed in the validation sample to be predicted, along with an initial 6 validation cases selected at random. These three cases are numbers  
30 14, 31 and 33. The color coding in the graphs is based on the first laboratory test (immunohistochemistry). Additional samples of interest are cases 7, 8 and 11, cases for which the DNA microarray hybridizations were of poor quality, with the resulting data exhibiting major patterns of differences relative to the rest.

- The metagene predictor has dimension  $p = 491$ : the analysis generated trees based on a  
35 Bayes' factor threshold of 3 on the log scale, allowing up to 10 splits of the root node and then up to 4 at each of nodes 1 and 2. Some pertinent summaries appear in the following figures. Figures 4 and 5 display 3-D and pairwise 2-D scatterplots of three of the key metagenes, all clearly strongly related to the ER status and also correlated. However, there are in fact five or six metagenes that quite strongly associate with ER status and it is evident that they reflect multiple aspects of this major

biological pathway in breast tumors. In the study reported in West *et al* (2001), Bayesian probit regression models were utilized with singular factor predictors which identified a single major factor predictive of ER. That analysis identified ER negative tumors 16, 40 and 43 as difficult to predict based on the gene expression factor model; the predictive probabilities of ER positive versus negative for these cases were near or above 0.5, with very high uncertainties reflecting real ambiguity.

In contrast to the more traditional regression models, the current tree model identifies several metagene patterns that together combine to define an ER profile of tumors, and that when displayed as in Figures 4 and 5 isolate these three cases as quite clearly consistent with their designated ER negative status in some aspects, yet conflicting and much more in agreement with the ER positive patterns on others. Metagene 347 is the dominant ER signature; the genes involved in defining this metagene include two representations of the ER gene, and several other genes that are coregulated with, or regulated by, the ER gene. Many of these genes appeared in the dominant factor in the regression prediction. This metagene strongly discriminates the ER negatives from positives, with several samples in the mid-range.

Thus, it is no surprise that this metagene shows up as defining root node splits in many high-likelihood trees. This metagene also clearly defines these three cases – 16, 40 and 43 – as appropriately ER negative. However, a second ER associated metagene, number 352, also defines a significant discrimination. In this dimension, however, it is clear that the three cases in question are very evidently much more consistent with ER positives; a number of genes, including the ER regulated PS2 protein and androgen receptors, play roles in this metagene, as they did in the factor regression; it is this second genomic pattern that, when combined together with the first as is implicit in the factor regression model, breeds the conflicting information that fed through to ambivalent predictions with high uncertainty.

The tree model analysis here identifies multiple interacting patterns and allows easy access to displays such as those shown in Figures 4 to 6 that provide insights into the interactions, and hence to interpretation of individual cases. In the full tree analysis, predictions based on averaging multiple trees are in fact dominated by the root level splits on metagene 347, with all trees generated extending to two levels where additional metagenes define subsidiary branches. Due to the dominance of metagene 347, the three interesting cases noted above are perfectly in accord with ER negative status, and so are well predicted, even though they exhibit additional, subsidiary patterns of ER associated behavior identified in the figures.

Figure 6 displays summary predictions. The 9 validation cases are predicted based on the analysis of the full set of 40 training cases. Predictions are represented in terms of point predictions of ER positive status with accompanying, approximate 90% intervals from the average of multiple tree models. The training cases are each predicted in an honest, cross-validation sense: each tumor is removed from the data set, the tree model is then refitted completely to the remaining 39 training cases only, and the hold-out case is predicted, *i.e.*, treated as a validation sample. Excellent predictive performance is observed for both these one-at-a-time honest predictions of training samples and for the out of sample predictions of the 9 validation cases. One ER negative, sample 31,

is firmly predicted as having metagene expression patterns completely consistent with ER positive status. This is in fact one of the three cases for which the two laboratory tests conflicted. The other two such cases, however agree with the initial ER negative test result - number 33, for which the predictions firmly agree with the initial ER negative test result, and number 14, for which the predictions agree with the initial ER positive result though not quite so forcefully. The lack of conformity of expression patterns in some cases (Case 8, 11 and 7) are due to major distortions in the data on the DNA microarray due to hybridization problems.

#### Example 3: Prediction of Lymph Node Metastases and Cancer Recurrence

This study assesses complex, multivariate patterns in gene expression data from primary breast tumor samples that can accurately predict nodal metastatic states and relapse for the individual patient using the statistical tree model of the invention.

DNA microarray data on samples of primary breast tumors was generated to which non-linear statistical analyses embodied by the tree model of the invention was applied to evaluate multiple patterns of interactions of groups of genes that have true predictive value, at the individual patient level, with respect to lymph node metastasis and cancer recurrence. For both lymph node metastasis and cancer recurrence, patterns of gene expression (metagenes) were identified that associate with outcome. Much more importantly, these patterns were capable of honestly predicting outcomes in individual patients with about 90% accuracy, based on a simple threshold of 0.5 probability in each case. The metagenes that predict lymph node metastasis and recurrence identify distinct groups of genes, suggesting different biological processes underlying these two characteristics of breast cancer.

Patients and biopsy specimens: The analyses of gene expression phenotypes drew samples from 171 primary tumor biopsies at the Koo Foundation Sun Yat-Sen Cancer Center (KF-SYSCC) in Taipei, Taiwan, collected and banked from 1991 to 2001. Samples from eleven patients who received preoperative chemotherapy and one with *in-situ* carcinoma were excluded from analysis. These 159 samples represent a heterogeneous population, though patient selection was enriched with cases of longer-term follow-up and observed recurrences. By September 2002, 62 patients developed recurrence whereas 97 remain disease free.

Microarray analysis: Tumor total RNA was extracted with Qiagen RNEasy kits, and assessed for quality with an Agilent Lab-on-a-Chip 2100 Bioanalyzer. Hybridization targets were prepared from total RNA according to Affymetrix protocols and hybridized to Affymetrix Human U95 GeneChip arrays See West M, Blanchette C, Dressman H, Huang E, Ishida S, Spang R et al. Predicting the clinical status of human breast cancer by using gene expression profiles, *Proc Natl Acad Sci*, 98:11462-11467 (2001).

Statistical analysis: This analysis again used the predictive statistical tree model. The method first screens genes to reduce noise, applies k-means correlation-based clustering targeting a large number of clusters, and then uses singular value decompositions ("SVD") to extract the single dominant factor (principal component) from each cluster. This generated 496 cluster-derived singular

factors (metagenes) that characterize multiple patterns of expression of the genes across samples. The strategy aimed to extract multiple such patterns while reducing dimension and smoothing out gene-specific noise through the aggregation within clusters. Formal predictive analysis then uses these metagenes in a Bayesian classification tree analysis. This generates multiple recursive partitions of the sample into subgroups (the "leaves" of the classification tree), and associates Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate weights, across many such tree models. Iterative out-of-sample, cross-validation predictions are then performed leaving each tumor out of the data set one at a time, refitting the model from the remaining tumors and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world prognostic context where prediction of new cases as they arise is the major goal.

Although, clinico-pathologic parameters such as the presence or absence of positive auxiliary nodes represent the best means available to classify patients into broad subgroups by recurrence and survival, such methods remain an imperfect tool. Among patients with no detectable lymph node involvement, a population thought to be in a low risk category, between 22 and 33% develop recurrent disease after a 10-year follow-up. See Polychemotherapy for early breast cancer: an overview of the randomized trials, Early Breast Cancer Trialists' Collaborative Group, *Lancet*; 352:930-942 (2001). Thus, properly identifying individuals out of this group who are at risk for recurrence is beyond the current capabilities of most predictive diagnostics.

The question of lymph node diagnosis is part of the broader issue of more accurately predicting breast cancer disease course and recurrence. Recently, genomic-scale measures of gene expression, using microarrays and other technologies have opened a new avenue for cancer diagnosis. They identify patterns of gene activity that sub-classify tumors, and such patterns may correlate with the biological and clinical properties of the tumors. The utility of such data in improving prognosis will rely on analytical methods that accurately predict the behavior of the tumors based on expression patterns. Credible predictive evaluation is critical in establishing valid and reproducible results and implicating expression patterns that do indeed reflect underlying biology. This predictive perspective is a key step towards integrating complex data into the process of prognosis for the individual patient, a step that can be accomplished through the practice of the present invention.

Furthermore, an ultimate goal is to integrate molecular and genomic information with traditional clinical risk factors, including lymph node status, patient age, hormone receptor status, and tumor size, in comprehensive models for predicting disease outcomes. Rather than supplant traditional clinical appraisal, genomic data adds data to traditional risk factors, and assessing individuals based on combinations of relevant traditional risk factors with identified genomic factors could potentially improve predictions. The present invention allows this goal to be realized by demonstrating the ability of genomic data to accurately predict lymph node involvement and disease recurrence in defined patient subgroups. Most importantly, these predictions are relevant for the individual patient and can provide a quantitative measure of the probability for the clinical phenotype and outcome of disease. Such predictions may ultimately facilitate treating patients as individuals

rather than as unidentifiable members of a risk profile.

The binary prediction tree model was applied to the analysis of gene expression patterns in primary breast tumors that predict lymph node metastasis, as well as tumor recurrence. The first study compares traditional "low-risk" versus "high-risk" patients, primarily based on age, primary tumor size, lymph node status, and Estrogen receptor ("ER") status. Among ER positive individuals, the "high-risk" clinical profile is represented by advanced lymph node metastases (10 or more positive nodes); the "low-risk profile" identifies node-negative women of age greater than 40 years with tumor size below 2cm. The number of samples in the tumor collection that met these criteria reduced down to 18 high-risk and 19 low-risk cases. Expression data were generated and metagenes identified and used in the Bayesian statistical tree analysis. Figure 7 displays summary predictions from the resulting total of 37 cross-validation analyses. For each individual tumor, this graph illustrates the predicted probability for "high-risk" versus "low-risk" (red versus blue) together with an approximate 90% confidence interval, based on analysis of the 36 remaining tumors performed successively 37 times as each tumor prediction is made. It is important to recognize that each sample in the data set, when assayed in this manner, constitutes a validation set that accurately assesses the robustness of the predictive model. The metagene model accurately predicts metastatic potential; about 90% of cases are accurately predicted based on a simple threshold at 0.5 on the estimated probability in each case. Case number 7 is in the intermediate zone, exhibiting patterns of expression of the selected metagenes that relate equally well to those of "high-" and "low-risk" cases, while case 22 is a clinical "high-risk" case with genomic expression patterns that relate more closely to "low-risk" cases. In contrast, node negative patients 5 and 11 have gene expression patterns more strongly indicative of "high-risk", and are key cases for follow-up investigations.

Clinical features of these "discordant" cases are illuminating, and suggestive of how a broader investigation of clinical data combined with molecular model-based predictions may aid in the eventual decision-making process. Although case 22 did in fact recur, 6 years post-surgery; this patient's clinical classification as high risk for recurrence based on purely clinical parameters was moderated by a lower risk based on metagenes, as demonstrated by this patient having survived recurrence-free for a longer time. Thus the lower probability prediction assigned to patient 22 based on the gene expression profiles is reflected in the clinical behavior of her disease. The "low-risk" patient 7 recurred at 31 months, and patient 11 at 38 months, whereas case 5 is currently disease-free after only 12 months of follow-up. Again, case 7, and to some degree case 11, thus partly corroborate the predictions based on genomic criteria. data. With such predictions as part of a prognostic model, more intensive or innovative post-surgical therapy should perhaps have been recommended for these two cases.

A critical aspect of the analyses described here is allowing the complexity of distinct gene expression patterns to enter the predictive model. Tumors are graphed against metagene levels for three of the highest scoring metagene factors as shown in Figure 8. This analysis highlights the need to analyze multiple aspects of gene expression patterns. For example, if the low-risk cases 1, 3 and 11 are assessed against metagene 146 alone, their levels are more consistent with high-risk cases.

However, when additional dimensions are considered, the picture changes. The second frame (upper right) shows that low-risk is consistent with low levels of metagene 130 or high levels of metagene 146; hence, cases 1 and 3 are not inconsistent in the overall pattern, though case 11 is consistent. An analysis that selects one set of genes, summarized here as one metagene, as a "predictor" would be potentially misleading, as it ignores the broader picture of multiple interlocked genomic patterns that together characterize a state. In the predictions, these two metagenes play key roles: low levels of metagene 146 coupled with higher levels of metagene 130 are strongly predictive of high-risk cases. Combined use of multiple metagenes, in the context of the tree selection model building process, ultimately yields a pattern that has the capacity to accurately predict the clinical outcome.

The second analysis concerns 3 year recurrence following primary surgery among the challenging and varied subset of patients with 1-3 positive lymph nodes. Such patients typically receive adjuvant chemotherapy alone, but more than 20% suffer relapse within five years. Hence, improved prognosis for this heterogeneous group is of critical importance; patients identified with a high probability of relapse could be targeted for more intensive treatment. The dataset provided 52 ER-positive cases in this lymph node category (34 non-recurrent, 18 recurrent). The aggregate predictions from the sets of generated statistical tree models defines a rather accurate picture; once again, there is an approximate 90% overall predictive accuracy in the 52 separate one-at-a-time, cross-validation prediction assessments as shown in Figure 9. Based on the gene expression analysis, the 3 year non-recurrent cases 6 and 23, having profiles more akin to recurrent cases, would be candidates for intensive treatment. These patients did receive adjuvant chemotherapy based on additional clinical risk factors (especially tumor size). Thus traditional clinical risk factors other than lymph node status also indicate higher risk of recurrence for these two cases, consistent with the molecular predictions. Each actually survived recurrence-free for over three years; case 6 recurred at 42 months and case 23 remains disease-free after over 6 years. Cases with low genomic criteria for recurrence would be 36, 38 and 42. They, however, experienced recurrence within three years. These are cases that, under prognosis informed by only the genomic model, would have been indicated as more benign and not candidates for intensive treatment, whereas such a treatment might have proven to be more beneficial.

The tree model identified subsets of genes related to the metagene predictors of lymph node involvement. These are replete with those involved in cellular immunity, including a high proportion of genes that function in the interferon pathway. They include genes that are induced by interferon such as various chemokines and chemokine receptors (Rantes, CXCL10, CCR2), other interferon-induced genes (IFI30, IFI35, IFI27, IFIT1, IFIT4, IFITM3), as well as interferon effectors (2'-5' oligoA synthetase), and genes encoding proteins mediating the induction of these genes in response to interferon (STAT1 and IRF1). This connection is intriguing given the role of interferon as a mediator of the anti-tumor response and, together with the fact that many genes involved in T cell function (TCRA, CD3D, IL2R, MHC) are also included within the group that predict lymph node metastasis. This may reflect the distinct nature of these tumors that have acquired a metastatic potential that elicits an anti-tumor response that is ultimately unsuccessful or an aberration of the

normal anti-tumor response.

Genes implicated in recurrence prediction as identified by the tree model do not exhibit such a striking functional clustering but do include many examples previously associated with breast cancer. Moreover, this group of genes is clearly distinct set from those that predict lymph node involvement. They include genes associated with cell proliferation control, both cell cycle specific activities (CDKN2D, Cyclin F, E2F4, DNA primase, DNA ligase), more general cell growth and signaling activities (MK2, JAK3, MAPK8IP, and EF1 $\alpha$ ), and a number of growth factor receptors and G-protein coupled receptors, some of which have been shown to facilitate breast tumor growth (EpoR). Possibly, the poor prognosis with respect to survival reflects a more vigorous proliferative capacity of the tumor.

Thus, the genes implicated in the prediction of lymph node metastasis and overall recurrence of disease, although clearly representing interrelated phenomena, nevertheless reflect the participation of distinct biological processes. The tree model is thus flexible in that regard as it only selects those metagenes that are most relevant to the prediction in hand. By contrast, traditional statistical testing perspectives that focus on significant differences at a population parameter level may say little of practical significance in terms of an individual patient's prognosis. Furthermore, the tree model takes into account the relevant multiple features of the complex patterns of gene expression, especially in a context such as breast cancer where multiple, interacting biological and environmental processes define physiological states, and individual dimensions provide only partial information. The tree model of the present invention assesses the complex, multivariate patterns in gene expression data from primary tumor biopsies, exploring the value of such patterns in predicting lymph node metastasis and relapse, two critically important aspects of breast cancer, at the individual patient level. The tree model identifies multivariate patterns of gene expression that, in this realistic context of substantial patient heterogeneity, deliver predictive accuracy of about 90%. The probabilistic models highlight cases where uncertainty is high, and generate subsets of implicated genes that relate to the biology of metastasis and tumor evolution.

To ascertain the success of the tree model, an out-of-sample predictive assessment via cross-validation is always conducted. Any selection of gene, metagene or clinical variables must be part of each cross-validation analysis. The results of such "feature selection" will vary each time a tumor is analyzed, and can dramatically impact on predictive accuracy. Analyses that select a set of predictors based on the entire dataset, including the individual to be predicted, in advance of predictive evaluation are inappropriate, and lead to misleadingly over-optimistic conclusions about predictive value. For breast cancer recurrence, the results provide evidence for gene expression profiles associated with recurrence in a homogeneous cohort of low risk patients. There are, however, several distinctions. First is the evaluation of models on the basis of accuracy in prediction at the individual level, with predictions made in formal probabilistic terms. Second, multiple, related and interacting biological patterns, here represented as separate and distinct metagenes, together represent a clinical state. Reducing high-dimensional genomic data to a single index may sacrifice opportunity for understanding complex interactions (see Figure 2) that are truly predictive. Thirdly, applicants



believe that the integration of molecular profiles with clinical risk factors—rather than the replacement of clinical data with molecular data—will define the major step towards personalized prognosis utilizing genomic data, hence the need for stratification using clinical variables.

The above gene expression analysis approach to the identification of atherosclerotic phenotype determinative genes may be combined with one or more additional selection protocols in a “multi-prong” gene selection approach for identifying genes associated with an atherosclerotic phenotype. Additional selection protocols that can be employed in conjunction with the subject selection protocol include: (1) selection protocols that identify all currently known genes that are associated with atherosclerosis (e.g., as determined by using existing biological and clinical databases, e.g., by performing a thorough review of the published literature concerning biological research on atherosclerosis mechanism and clinical research related to drugs that have shown a beneficial, or detrimental, effect on patients with atherosclerotic clinical manifestations); (2) genes that have been identified as associated with atherosclerosis using human genetic studies, e.g., genetic linkage analysis (for example, one analyzes the genome of individuals who have presented with premature coronary heart disease (CAD, hard manifestations of CAD before 45 for men and before 50 for women, such as myocardial infarction or bypass surgery), and their siblings and studies markers within the genome of these individuals that co-segregate with the disease process. The localization of such markers across the entire genome allows for identification of “hot spots” that contain 10-300 genes. These genes become candidates for further analysis); (3) genes that have been identified as associated with atherosclerosis using mouse genetic studies, e.g., using mouse models of human disease (Using established mouse models of atherosclerosis, such as ApoE knock-out mice, one searches for “modifiers” that alter the development of the disease process, either increase or reduce, that come into play upon changing the genetic background of the mice. The modifiers thus identified, or their human equivalents, in turn, become candidate genes for further studies on human atherosclerosis); (4) genes that have been identified as associated with atherosclerosis using epigenetic and methylation studies (It is known that with aging, gene expression can be altered, yet the mechanism(s) for such altered expression remains an enigma. Changes in methylation of CpG islands within the promoter region of a multitude of genes can result in altered transcription of such genes, and applicants have shown that such changes can occur in cardiovascular tissues with aging. Typically, methylation of the CpG island within the promoter of a gene results in silencing of this gene. Such changes in DNA methylation have been called “epigenetic” as they do not represent necessarily inherited changes. Applicants have been surveying the genome of human aortas for the presence of genes whose methylation is altered within atherosclerotic regions compared to normal aorta tissue. The technique that applicants have used for this survey is called restriction landmark genome scanning, or RLGS. Applicants have already identified two genes, nucleolin and monocarboxylate transporter 3 (MCT3) that are differently methylated between normal and diseased aorta tissues. These genes have become members of our pool of “candidates”); (6) Genes identified by our previous analysis using Bayesian analysis approach. Where the above expression analysis approach is combined with one or more additional approaches to identify genes that are

atherosclerotic phenotype determinative genes, the initial genes identified using each disparate selection protocol may be combined into a single set for further use, as described below, using a number of different combination protocols. For example, each of the initially identified subsets may be additively combined to produce a master set of genes for further use. Alternatively, only the  
 5 common genes of one or more subsets may be placed in the final set of genes for further use. For example, where one develops five initial subsets of genes using five different selection criteria, such as the specific criteria listed above, only those genes common to at least two or more, three or more, or four or more of the initial subsets, including all of the initial subsets, may be chosen for inclusion in the final set.

10 The resultant final or master set of genes may be used as a collection of atherosclerotic phenotype determinative genes as described above. In addition, such a set may be used as an initial set or "library" of candidate genes for further study to identify SNPs that cause or are otherwise associated with an atherosclerotic phenotype.

Figure 6 provides a flow diagram showing a selection procedure as described above as it  
 15 would be used to identify atherosclerotic phenotype determinative gene variants, e.g., SNPs, which are then used, either singly or in combination, in a variety of different applications, including the applications described above in connection with the specific atherosclerotic phenotype determinative genes identified herein.

While the above selection approach of the subject invention is described above in terms of  
 20 the identification of atherosclerotic phenotype determinative genes, included within the scope of the invention is the use of the above approach to identify genes that are determinative of other phenotypes, including other disease phenotypes, such as cancer, etc.

The following examples are offered by way of illustration and not by way of limitation.

## 25 EXPERIMENTAL

### I. Tissue/Sample Procurement for Gene Expression Analysis

A serious challenge at the inception of this study was to find human arterial material that would be suitable for study of various stages of atherosclerosis and concurrent gene expression profiling. Although the most straightforward approach to the analysis of disease tissue would be the  
 30 collection of material from individuals who have either succumbed to heart disease or those who are undergoing a heart transplant, this has the significant disadvantage of utilizing tissue at the end-stage of disease. Many previous studies have demonstrated that atherosclerosis is a long-term process associated with aging, with development of disease preceding the development of overt signs of disease. Hence, it is likely that end-stage tissue would not reflect events associated with initiation  
 35 and progression of disease, but instead molecular events that reflect response to injury and associated repair processes.

The aortas of heart donors were collected at organ harvest in University of Wisconsin solution on ice to minimize post-mortem changes. Figure 10 shows the aorta sectioning. Strips A and B were frozen in liquid nitrogen for RNA extraction. Strip C was preserved in formalin for scoring

atherosclerotic burden. The Pathobiological Determinants of Atherosclerosis in Youth study (PDAY) investigators showed that atherosclerosis displays increasing severity from proximal to distal locations. Also, they found sagittal symmetry with respect to disease burden across the longitudinal midline that approached 0.995. The mirroring of disease allowed us to ascribe the clinical atherosclerosis phenotype from one side to the gene expression pattern of the other. Early atherosclerotic plaques were assessed with imaging processing software by quantifying the area of Sudan IV staining. Advanced disease was quantified using PDAY methodologies to evaluate raised lesions. The data were expressed as a ratio of affected area over total surface of the studied section. Permission to procure these tissues was obtained from the North Carolina Organ Donor Services executive committee and approved by the institutional review board of the Duke University Medical Center.

## II. RNA Preparation, Microarray Processing, Gene Expression Analysis

Techniques for microarray assays have been previously reported. See Huang E et al., Gene expression profiling for prediction of clinical characteristics of breast cancer. *Recent Progress in Hormone Research*, 2003;55:55-73; West M, et al., Predicting the clinical status of human breast cancer by using gene expression profiles. *Proc. Nat'l Acad. Sci. USA*, 2001;98:11462-11467. Briefly, aortic tissue was ground in liquid nitrogen. The RNA was extracted by the Trizol protocol and further purified with the Qiagen RNeasy kit. Quality was assessed with the Agilent Bioanalyzer and Affymetrix Test3 chips. The targets for microarray analysis were hybridized to U95Av2 Affymetrix microarrays and processed with the GENECHIP system. The signal intensity values were converted to a log2 scale following quantile normalization. Quantitative real-time PCR reactions were performed on 13 aorta samples and compared to microarray expression measures with a high degree of correlation across these genes. Replicate microarray assays were performed also showing a high degree of correlation in signal intensities (data not shown).

## III. Design of phenotyping studies.

Applicants prioritized genes by their ability to predict two clinical phenotypes: disease extent and aorta location. Disease extent was scored by combining Sudan IV staining and raised lesion data. The "minimally diseased" group showed less than 5% Sudan IV staining and contained no raised lesions. The "severely diseased" group contained both raised lesions and extensive Sudan IV staining. Applicants analyzed sections from two identical locations in all the aortas, a proximal and distal section. From this pool, applicants identified 15 minimally diseased and 16 severely diseased sections for this analysis. Nine of these sections came from single aortas. The size of a particular section used in the analysis was quite small, on average 10mm by 5mm, making Sudanophilia and raised lesion content homogeneous throughout the section.

The second phenotype was the location of the section within the thoracic aorta as a surrogate for disease susceptibility. This assumption is based on the conclusive evidence from the PDAY study that progression of disease advances from the distal to proximal areas of the aorta suggesting that distal regions are more susceptible to disease development. See Cornhill JF, et al. Topography of

human aortic sudanophilic lesions. Monogr. Atheroscler. 1990;15:13-19. As stated above, applicants analyzed sections from identical locations in all the aortas. There were 31 proximal (1A) sections and 32 distal (4B) sections in our analysis of aorta location. Applicants used the same pool of aorta sections for both analyses.

#### 5 IV. Statistical analysis.

Statistical analysis was performed utilizing the metagene construction and binary prediction tree analysis used previously in our analysis of gene expression patterns predictive of breast cancer outcomes. Huang E et al., *Lancet*. 2003;361:1590-1596; Huang E. et al., *Nature Genetics*. 2003;34:226-230. The initial step filtered out genes whose maximum expression did not exceed the  
 10 median value of expression or did not vary more than 1-fold across the samples to remove genes with extremely low levels of expression or little variance. After the filter was applied, 7,470 of 12,563 total genes remained in the analysis.

Next, applicants clustered the genes into groups based on their expression patterns with the notion that related genes share similar variances in expression using k-means clustering. This  
 15 algorithm randomly places genes into a predetermined number of groups. The genes are then shuffled among the groups in an iterative fashion to maximize the distinction between each groups. The number of designated clusters was also then varied iteratively to further maximize differences between the clusters. The resulting clusters contained anywhere from 20 to 50 genes and represented a unique gene expression pattern.

Singular value decomposition was performed on each cluster to generate a single factor, called a metagene. The metagene is the dominant expression pattern of a cluster and represents a group of genes that share a common gene expression signature in the context of a particular experimental condition. The metagenes are then used in binary decision trees to partition the samples into subgroups. In the trees, a metagene is used at a branch point to partition samples to one of two  
 25 classifications based upon similarity or dissimilarity of a sample's gene expression pattern to the metagene. Each tree had several of these branches, and hundreds of trees were generated to determine the metagenes that did the best job of partitioning the samples. Within each metagene, applicants then identified the genes that lend the most weight to the dominant expression pattern.

To guard against over-fitting given the disproportionate number of variables to samples,  
 30 applicants performed honest, out-of-sample cross validation analysis to test the stability and predictive capability of our model. Each aorta section was left out of the data set one at a time. The model was refitted (both the metagene factors and the partitions used) using the remaining samples, and the phenotype of the held out case was then predicted and the certainty of the classification is calculated.

35 Candidate gene annotation was performed using the Duke Integrated Genomics database.

#### V. Results

##### 1. Assessment of atherosclerosis burden in aorta samples

Two analyses were performed: a comparison of minimally vs. severely diseased sections,

and a comparison of proximal and distal sections of the thoracic aorta. The first analysis identified gene signatures associated with atherosclerotic severity. The two groups of aorta sections used were significantly different. There was significantly less Sudan IV staining ( $1.0\% \pm 0.0\%$  vs.  $19.3\% \pm 5.0\%$ ), and raised lesions ( $0.0\% \pm 0.0\%$  vs.  $42.4\% \pm 7.5\%$ ) in the minimally diseased samples, as

5 shown in the following table:

	Minimally Diseased	Severely Diseased	p value <sup>3</sup>
Male Gender (%)	50	50	NS
Age mean (range)	38.2 (20-62)	55.6 (39-64)	<0.0005
Sudan IV Staining <sup>1</sup> mean ( $\pm$ sem)	$1.0\% \pm 0.0\%$	$19.3\% \pm 5.0\%$	<0.0005
Raised Lesion <sup>2</sup> mean ( $\pm$ sem)	$0.0\% \pm 0.0\%$	$42.4\% \pm 7.5\%$	<0.000003

<sup>1</sup>Sudan IV Staining: percent of the total aorta that is stained.

<sup>2</sup>Raised Lesion: percent of the total aorta that contains raised lesions.

<sup>3</sup>Student T-test

10 . The second analysis identified gene signatures associated with the proximal and distal locations within the thoracic aorta as a possible metric of atherosclerotic susceptibility. There were no significant difference in the characteristics of the two locations in either Sudan IV staining ( $12.4\% \pm 3.0\%$  vs.  $12.6\% \pm 3.1\%$ ) or raised lesions ( $10.1\% \pm 4.7\%$  vs.  $13.2\% \pm 5.3\%$ ). There was also no significant difference in the gender or ages of the donor pools as shown on the following table:

	Low Susceptibility/ 1A	High Susceptibility/ 4B	p value <sup>3</sup>
Male Gender (%)	43.5	42.9	NS
Age mean (range)	39.2 (17-62)	44.6 (17-62)	0.21
Sudan IV Staining <sup>1</sup> mean ( $\pm$ sem)	$12.4\% \pm 3.0\%$	$12.6\% \pm 3.1\%$	0.95
Raised Lesion <sup>2</sup> mean ( $\pm$ sem)	$10.1\% \pm 4.7\%$	$13.2\% \pm 5.3\%$	0.66

15 <sup>1</sup>Sudan IV Staining: percent of the total aorta that is stained.

<sup>2</sup>Raised Lesion: percent of the total aorta that contains raised lesions.

<sup>3</sup>Student T-test

## 2. Metagene patterns predictive of extent of atherosclerotic lesions

Figure 11 displays the results from the analysis of disease severity where the predictive model correctly classifies 93.5% (29 of 31 sections) of the sections as minimally or severely diseased based solely upon their gene expression profiles. This figure shows results of the hold-one-out cross validation analysis where applicants construct the model from 30 samples and use it to predict the phenotype of the 31<sup>st</sup> sample. The plot represents the probability that the unknown sample is severely diseased. The red numbers represent the severely diseased section with 95% confidence intervals; the blue numbers represent minimally diseased samples.

The gene prioritization process identified a set of 208 genes whose expression patterns provide the power to discriminate and predict disease states in our aorta samples as shown on Table I below which includes Genbank Deposit numbers and Unigene designations:

Table I: Genes associated with disease burden

Genbank	Gene Symbol	Gene Name	UniGene
J04765	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	Hs.313
AF052124	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	Hs.313
X15525	ACP2	acid phosphatase 2, lysosomal	Hs.75589
M94345	CAPG	capping protein (actin filament), gelsolin-like	Hs.82422
AB020687	SLC21A9	solute carrier family 21 (organic anion transporter), member 9	Hs.7884
U51240	LAPTM5	Lysosomal-associated multispanning membrane protein-5	Hs.79356
Y09445	TBX5	T-box 5	Hs.50947
AF053233	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	Hs.172684
U43185	STAT5A	signal transducer and activator of transcription 5A	Hs.167503
AL050008	BRMS1	breast cancer metastasis-suppressor 1	Hs.100426
M12529	APOE	apolipoprotein E	Hs.169401
AB022718	DEPP	decidual protein induced by progesterone	Hs.93675
Z24725	MIG2	mitogen inducible 2	Hs.75260
D13666	OSF-2	osteoblast specific factor 2 (fasciclin I-like)	Hs.136348
U50928	PKD2	polycystic kidney disease 2 (autosomal dominant)	Hs.82001
U46692	CSTB	cystatin B (stefin B)	Hs.695
AF044253	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	Hs.298184
J03909	IFI30	interferon, gamma-inducible protein 30	Hs.14623
L10333	RTN1	reticulon 1	Hs.99947

		fibroblast growth factor receptor 2 (bacteria-expressed	
		kinase, keratinocyte growth factor receptor, craniofacial	
		dysostosis 1, Crouzon syndrome, Pfeiffer syndrome,	
M80634	FGFR2	Jackson-Weiss syndrome)	Hs.278581
M63138	CTSD	cathepsin D (lysosomal aspartyl protease)	Hs.343475
J04430	ACP5	acid phosphatase 5, tartrate resistant	Hs.1211
AF044896	ICB-1	basement membrane-induced gene	Hs.10649
X78565	TNC	tenascin C (hexabrachion)	Hs.289114
AB011143	GAB2	GRB2-associated binding protein 2	Hs.30687
X69819	ICAM3	intercellular adhesion molecule 3	Hs.99995
J02947	SOD3	superoxide dismutase 3, extracellular	Hs.2420
U78095	SPINT2	serine protease inhibitor, Kunitz type, 2	Hs.31439
D67029	SEC14L1	SEC14-like 1 ( <i>S. cerevisiae</i> )	Hs.75232
AF013249	LAIR1	leukocyte-associated Ig-like receptor 1	Hs.115808
X62078	GM2A	GM2 ganglioside activator protein	Hs.289082
AB014574	KIAA0674	KIAA0674 protein	Hs.14799
L13939	AP1B1	adaptor-related protein complex 1, beta 1 subunit	Hs.331602
D90144	SCYA3	small inducible cytokine A3	Hs.73817
L06797	CXCR4	chemokine (C-X-C motif), receptor 4 (fusin)	Hs.89414
D89077	SLA	Src-like-adaptor	Hs.75367
Y08374	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	Hs.75184
		superoxide dismutase 1, soluble (amyotrophic lateral	
X02317	SOD1	sclerosis 1 (adult))	Hs.75428
AB002365	KIAA0367	KIAA0367 protein	Hs.23311
AF084481	WFS1	Wolfram syndrome 1 (wolframin)	Hs.26077
		thromboxane A synthase 1 (platelet, cytochrome P450,	
D34625	TBXAS1	subfamily V)	Hs.2001
AB011103	KIF5C	kinesin family member 5C	Hs.6641
AF041259	ZNF217	zinc finger protein 217	Hs.155040
J05037	SDS	serine dehydratase	Hs.76751
AF056087	SFRP1	secreted frizzled-related protein 1	Hs.7306
		solute carrier family 16 (monocarboxylic acid	
U81800	SLC16A3	transporters), member 3	Hs.85838
AL050262	TLR1	toll-like receptor 1	Hs.2474
AB018271	BPAG1	bullous pemphigoid antigen 1 (230/240kD)	Hs.198689
AF014958	CCRL2	chemokine (C-C motif) receptor-like 2	Hs.302043
U58334	TP53BP2	tumor protein p53 binding protein, 2	Hs.44585

			<a href="http://dig.cgt.duke.edu/cgi-bin/">http://dig.cgt.duke.edu/cgi-bin/</a>
J03011	IGLC6	immunoglobulin lambda constant 6 (Kern+Oz- marker)	
D12485	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	Hs.11951
U22662	NR1H3	nuclear receptor subfamily 1, group H, member 3	Hs.347353
AF055008	GRN	granulin	Hs.180577
D86964	DOCK2	dedicator of cyto-kinesis 2	Hs.17211
U88629	ELL2	ELL-related RNA polymerase II, elongation factor	Hs.98124
		TAF4 RNA polymerase II, TATA box binding protein	
U75308	TAF4	(TBP)-associated factor, 135 kD	Hs.24644
J03600	ALOX5	arachidonate 5-lipoxygenase	Hs.89499
AF004709	MAPK13	mitogen-activated protein kinase 13	Hs.178695
L15388	GPRK5	G protein-coupled receptor kinase 5	Hs.211569
AB002361	KIAA0363	KIAA0363 protein	Hs.96633
X62744	HLA-DMA	major histocompatibility complex, class II, DM alpha	Hs.77522
		leukocyte immunoglobulin-like receptor, subfamily B	
AF072099	LILRB4	(with TM and ITIM domains), member 4	Hs.67846
X90858	UP	uridine phosphorylase	Hs.77573
Z29067	NEK3	NIMA (never in mitosis gene a)-related kinase 3	Hs.2236
U00952	HPIP	hematopoietic PBX-interacting protein	Hs.8068
J00194	HLA-DRA	major histocompatibility complex, class II, DR alpha	Hs.76807
M80254	PPIF	peptidylprolyl isomerase F (cyclophilin F)	Hs.173125
M21121	SCYA5	small inducible cytokine A5 (RANTES)	Hs.241392
AF030339	PLXNC1	plexin C1	Hs.286229
AJ007395	SIGLEC7	sialic acid binding Ig-like lectin 7	Hs.355493
AF013570	MYH11	myosin, heavy polypeptide 11, smooth muscle	Hs.78344
		CD36 antigen (collagen type I receptor, thrombospondin	
Z22555	CD36L1	receptor)-like 1	Hs.180616
L22524	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	Hs.2256
Y07512	PRKG1	protein kinase, cGMP-dependent, type I	Hs.2689
		integrin, alpha X (antigen CD11C (p150), alpha	
Y00093	ITGAX	polypeptide)	Hs.51077
AB007889	KIAA0429	KIAA0429 gene product	Hs.77694
Y08136	ASM3A	acid sphingomyelinase-like phosphodiesterase	Hs.42945
AB014520	KIAA0620	KIAA0620 protein	Hs.301685
L10678	PFN2	profilin 2	Hs.91747



Z98046	MAGED2	melanoma antigen, family D, 2	Hs.4943
D79994	KIAA0172	KIAA0172 protein	Hs.77546
U29615	CHIT1	chitinase 1 (chitotriosidase)	Hs.91093
D87074	KIAA0237	KIAA0237 gene product	Hs.78748
X81109	DXS1357E	accessory protein BAP31	Hs.291904
AL049946	DKFZp564I1922	adlican	Hs.72157
U78556	CRA	cisplatin resistance associated	Hs.166066
U21931	FBP1	fructose-1,6-bisphosphatase 1	Hs.574
M63603	PLN	phospholamban	Hs.85050
D87433	STAB1	stabilin 1	Hs.301989
AB029032	KIAA1109	KIAA1109 protein	Hs.6606
X12451	CTSL	cathepsin L	Hs.78056
U89606	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	Hs.38041
AB029018	KIAA1095	KIAA1095 protein	Hs.177635
M34423	GLB1	galactosidase, beta 1	Hs.79222
AF095791	TACC2	transforming, acidic coiled-coil containing protein 2	Hs.272023
		complement component 1, q subcomponent, beta	
X03084	C1QB	polypeptide	Hs.8986
X74039	PLAUR	plasminogen activator, urokinase receptor	Hs.179657
AB016811	ARL7	ADP-ribosylation factor-like 7	Hs.111554
		runt-related transcription factor 1 (acute myeloid	
X90976	RUNX1	leukemia 1; aml1 oncogene)	Hs.129914
U00802	DBN1	drebrin 1	Hs.89434
		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short	
X96752	HADHSC	chain	Hs.8110
Z49107	LGALS9	lectin, galactoside-binding, soluble, 9 (galectin 9)	Hs.81337
AL080235	RIS1	Ras-induced senescence 1	Hs.35861
AF051851	SVIL	supervillin	Hs.154567
AF062075	LPXN	leupaxin	Hs.49587
		sema domain, immunoglobulin domain (Ig), short basic	
AB000220	SEMA3C	domain, secreted, (semaphorin) 3C	Hs.171921
AF055581	LNK	lymphocyte adaptor protein	Hs.13131
AB015718	STK10	serine/threonine kinase 10	Hs.16134
X78817	ARHGAP4	Rho GTPase activating protein 4	Hs.3109
AJ000534	SGCE	sarcoglycan, epsilon	Hs.110708
M63835	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	Hs.77424
M16336	CD2	CD2 antigen (p50), sheep red blood cell receptor	Hs.89476

M32578	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	Hs.375570
U32324	IL11RA	interleukin 11 receptor, alpha	Hs.64310
AF079167	OLR1	oxidised low density lipoprotein (lectin-like) receptor 1	Hs.77729
		alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	Hs.1239
M22324	ANPEP		
D86961	LHFPL2	lipoma HMGIC fusion partner-like 2	Hs.79299
X54162	LMOD1	leiomodulin 1 (smooth muscle)	Hs.79386
U57911	C11orf8	chromosome 11 open reading frame 8	Hs.46638
M64571	MAP4	microtubule-associated protein 4	Hs.239298
AL023653	CXorf9	chromosome X open reading frame 9	Hs.61469
		X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	Hs.57922
AL023653	XPNPEP2		
AC005546	FLJ20244	hypothetical protein FLJ20244	Hs.158947
AC005546	LYL1	lymphoblastic leukemia derived sequence 1	Hs.46446
M60028	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	Hs.73931
Y13622	LTBP4	latent transforming growth factor beta binding protein 4	Hs.85087
L76191	IRAK1	interleukin-1 receptor-associated kinase 1	Hs.182018
U83115	AIM1	absent in melanoma 1	Hs.161002
U60060	FEZ1	fasciculation and elongation protein zeta 1 (zyglin I)	Hs.79226
AJ011497	CLDN7	claudin 7	Hs.278562
D64142	H1FX	H1 histone family, member X	Hs.109804
D26350	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	Hs.238272
		aldo-keto reductase family 1, member B1 (aldose reductase)	Hs.75313
X15414	AKR1B1		
D87434	KIAA0247	KIAA0247 gene product	Hs.82426
		spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	Hs.74520
X79204	SCA1		
M58285	HEM1	hematopoietic protein 1	Hs.132834
AB014513	LDB3	LIM domain binding 3	Hs.49998
U63127	TIC	SEC7 homolog	Hs.110121
S59184	RYK	RYK receptor-like tyrosine kinase	Hs.79350
X53587	ITGB4	integrin, beta 4	Hs.85266
Z84718	GSTT1	glutathione S-transferase theta 1	Hs.77490
		solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	Hs.62185
AF030409	SLC9A6		
J04621	SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-	Hs.1501

		associated, fibroglycan)	
AF055024	ASB1	ankyrin repeat and SOCS box-containing 1	Hs.153489
U56833	VBP1	von Hippel-Lindau binding protein 1	Hs.198307
		matrix metalloproteinase 9 (gelatinase B, 92kD	
J05070	MMP9	gelatinase, 92kD type IV collagenase)	Hs.151738
AF093118	FBLN5	fibulin 5	Hs.11494
U12707	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Hs.2157
		solute carrier family 2 (facilitated glucose/fructose	
M55531	SLC2A5	transporter), member 5	Hs.33084
AB019527	LDOC1	leucine zipper, down-regulated in cancer 1	Hs.45231
X62055	PTPN6	protein tyrosine phosphatase, non-receptor type 6	Hs.63489
		ubiquitin-conjugating enzyme E2N (UBC13 homolog,	
D83004	UBE2N	yeast)	Hs.75355
X76534	GPNMB	glycoprotein (transmembrane) nmb	Hs.82226
		T-cell, immune regulator 1, ATPase, H <sup>+</sup> transporting,	
U45285	TCIRG1	lysosomal V0 protein a isoform 3	Hs.46465
X63657	FVT1	follicular lymphoma variant translocation 1	Hs.74050
L09708	C2	complement component 2	Hs.2253
AB020316	UST	uronyl-2-sulfotransferase	Hs.134015
AF112219	ESD	esterase D/formylglutathione hydrolase	Hs.82193
Y14768	BAT1	HLA-B associated transcript 1	Hs.55296
		nuclear factor of kappa light polypeptide gene enhancer	
Y14768	NFKBIL1	in B-cells inhibitor-like 1	Hs.2764
Y14768	LTB	lymphotoxin beta (TNF superfamily, member 3)	Hs.890
Y14768	LTA	lymphotoxin alpha (TNF superfamily, member 1)	Hs.36
		ATPase, H <sup>+</sup> transporting, lysosomal 13kD, V1 subunit G	
Y14768	ATP6V1G2	isoform 2	Hs.249227
Y14768	AIF1	allograft inflammatory factor 1	Hs.76364
			<a href="http://dig.cgt.duke.edu/cg">http://dig.cgt</a>
			<a href="http://dig.cgt.duke.edu/cg">.duke.edu/cg</a>
AL031846	CBX7	chromobox homolog 7	<a href="#">i-bin/</a>
AL031846	DJ742C19.2	phorbolin-1-related	Hs.226307
AF036927	ADCY9	adenylate cyclase 9	Hs.20196
D49400	ATP6V1F	ATPase, H <sup>+</sup> transporting, lysosomal 14kD, V1 subunit F	Hs.78089
M55210	LAMC1	laminin, gamma 1 (formerly LAMB2)	Hs.214982
U15085	HLA-DMB	major histocompatibility complex, class II, DM beta	Hs.1162

X97074	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	Hs.119591
D89016	ARHGEF16	Rho guanine exchange factor (GEF) 16	Hs.87435
AF022797	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	Hs.10082
M33552	LSP1	lymphocyte-specific protein 1	Hs.56729
U09578	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	Hs.227789
M21186	CYBA	cytochrome b-245, alpha polypeptide	Hs.68877
M64925	MPP1	membrane protein, palmitoylated 1 (55kD)	Hs.1861
AF029750	TAPBP	TAP binding protein (tapasin)	Hs.179600
U10906	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	Hs.238990
U83993	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	Hs.321709
AF022789	USP12	ubiquitin specific protease 12	Hs.42400
L35249	ATP6V1B2	ATPase, H <sup>+</sup> transporting, lysosomal 56/58kD, V1 subunit B, isoform 2	Hs.1697
M61916	LAMB1	laminin, beta 1	Hs.82124
AB011155	DLG5	discs, large (Drosophila) homolog 5	Hs.170290
X91809	RGS19	regulator of G-protein signaling 19	Hs.22698
U20158	LCP2	lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD)	Hs.2488
S59049	RGS1	regulator of G-protein signaling 1	Hs.75256
U13991	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30 kD	Hs.89657
X93498	SH3BGR	SH3 domain binding glutamic acid-rich protein	Hs.47438
M87770	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	Hs.278581
AL050139	FLJ13910	hypothetical protein FLJ13910	Hs.75277
M73720	CPA3	carboxypeptidase A3 (mast cell)	Hs.646
U35451	CBX1	chromobox homolog 1 (HP1 beta homolog Drosophila )	Hs.77254
M32315	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	Hs.256278
Y13710	SCYA18	small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated	Hs.16530
AB008109	RGS5	regulator of G-protein signaling 5	Hs.24950
M60830	EVI2B	ecotropic viral integration site 2B	Hs.5509
X71874	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	Hs.9661

AB007972	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	Hs.130760
X16663	HCLS1	hematopoietic cell-specific Lyn substrate 1	Hs.14601
M63193	ECGF1	endothelial cell growth factor 1 (platelet-derived)	Hs.73946
D84110	RBPMS	RNA-binding protein gene with multiple splicing	Hs.80248
AJ006973	TOM1	target of myb1 (chicken)	Hs.9482
AB002318	TLN2	talin 2	Hs.150443
U51333	HK3	hexokinase 3 (white cell)	Hs.159237
U09577	HYAL2	hyaluronoglucosaminidase 2	Hs.76873
U00672	IL10RA	interleukin 10 receptor, alpha	Hs.327

These genes in Table I encode proteins previously suspected to play a role in atherosclerosis including apolipoprotein E (*apoE*), osteopontin, and the oxidized LDL receptor 1 (*olr1*). Applicants performed a query against gene ontology databases to determine the important biological processes represented in the analysis. Applicants found that the genes reflected processes that applicants would infer from our current understanding of atherosclerosis such as cell cycle regulation and inflammatory response. Genes in these categories without direct links to atherosclerosis could be novel candidates for study. Such genes include *capp*, *gm2* ganglioside activator protein, matrix metalloproteinase 9 (*mmp9*) and chemokine (C-C motif) receptor-like 2 (*ccrl2*).

10 Genes from table I were classified according to biological process as follows:

Apoptosis: accessory protein BAP31, dedicator of cyto-kinesis 2, hematopoietic protein 1, secreted frizzled-related protein 1, tumor necrosis factor receptor superfamily, member 1B, tumor protein p53 binding protein, 2.

15 Cell Adhesion: basement membrane-induced gene, bullous pemphigoid antigen 1, cathepsin D, claudin 7, fasciculation and elongation protein zeta 1, fibulin 5, glycoprotein, integrin, alpha X, intercellular adhesion molecule 3, laminin, beta 1, osteoblast specific factor 2, sialic acid binding Ig-like lectin 7, tenascin C.

20 Cell Motility: GRB2-associated binding protein 2, KIAA0429 gene product, lymphocyte-specific protein 1, myosin, heavy polypeptide 11, smooth muscle, plasminogen activator, urokinase receptor, profilin 2, talin 2

25 Cell Growth and Proliferation: cell proliferation, breast cancer metastasis-suppressor 1, follicular lymphoma variant translocation 1  
 Immune Response: accessory protein BAP31, capping protein, gelsolin-like, cathepsin L, CD2 antigen (p50), sheep red blood cell receptor, complement component 1, q subcomponent, complement component 2, dedicator of cyto-kinesis 2, immunoglobulin lambda constant 6, leukocyte immunoglobulin-like receptor, lymphocyte cytosolic protein 2, MHC, class II, DM alpha, MHC, class II, DM beta, MHC, class II, DQ beta 1, MHC, class II, DR alpha, MHC, class II, DR beta 1, osteopontin, TAP binding protein, Wiskott-Aldrich syndrome.

Inflammatory Response: allograft inflammatory factor 1, arachidonate 5-lipoxygenase,

ATPase, H<sup>+</sup> transporting, lysosomal 13kD, carboxypeptidase A3, chemokine (C-X-C motif), receptor 4, granulin, HLA-B associated transcript 1, interleukin 10 receptor, alpha, interleukin 11 receptor, alpha, lymphotoxin alpha (TNF superfamily, member 1), lymphotoxin beta (TNF superfamily, member 3), small inducible cytokine A3, small inducible cytokine A5, small inducible cytokine subfamily A, m 18, thromboxane A synthase 1, tumor necrosis factor receptor superfamily, member 1B.

Chemotaxis: endothelial cell growth factor 1, lymphocyte-specific protein 1, plasminogen activator, urokinase receptor.

Cell Signaling: adenylate cyclase 9, ADP-ribosylation factor-like 7, chemokine (C-X-C motif), receptor 4, cyclin-dependent kinase inhibitor 1B, discs, large (Drosophila) homolog 5, fibroblast growth factor receptor 2, mitogen-activated protein kinase 13, mitogen-activated protein kinase-activated protein kinase 3, osteopontin, regulator of G-protein signaling 1, regulator of G-protein signaling 19, regulator of G-protein signaling 5, Rho GTPase activating protein 4, SH3 domain binding glutamic acid-rich protein, Src-like-adaptor, tumor protein p53 binding protein, 2.

Regulation of Transcription: chromobox homolog 1, endothelial cell growth factor 1, H1 histone family, member X, hematopoietic cell-specific Lyn substrate 1, integrin, beta 4, KIAA0363 protein, KIAA0363 protein, nuclear receptor subfamily 1 group H member 3, TAF10 RNA polymerase II, TATA box binding protein, TAF4 RNA polymerase II, TATA box binding protein, T-box 5, zinc finger protein 217.

Extracellular Matrix Structural Component: chitinase 1, hyaluronoglucosaminidase 2, laminin, beta 1, stabilin 1, syndecan 2.

Cytoskeleton/Structural Component: leiomodulin 1, Lysosomal-associated multispanning membrane protein-5, reticulon 1, Rho GTPase activating protein 4, sarcoglycan, epsilon, solute carrier family 16, member 3, vesicle-associated membrane protein 8, Wolfram syndrome 1 Lipid Metabolism: apolipoprotein E, L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain.

Proteolysis: alanyl aminopeptidase, cathepsin L, matrix metalloproteinase 7, matrix metalloproteinase 9, proteasome subunit, beta type, 10, protein phosphatase 1, regulatory subunit 2B

Carbohydrate Metabolism: aldo-keto reductase family 1, member B1, fructose-1,6-bisphosphatase 1, galactosidase, beta 1, hexokinase 3, solute carrier family 2 member 5.

### 3. Metagene patterns predictive of susceptibility to atherosclerosis

In our second analysis, applicants were able to predict the location of a sample within the thoracic aorta with 93.6% accuracy (59 of 63 sections correctly classified). The location may be a surrogate for disease susceptibility. Figure 12 is a plot of the hold-one-out cross validation analysis that shows the probability that an unknown sample is from the distal aorta with 95% confidence intervals. The red numbers represent samples from the distal location; the blue numbers are from the proximal aorta. Figure 13 shows expression levels by color display of the genes in the key predictive metagene and illustrates the differential expression patterns between proximal and distal tissues.

Twenty-five genes were identified that provided the predictive power in the analysis. These

are listed in Table II, as follows:

Table II: Genes associated with disease susceptibility

Genbank	Gene Symbol	Gene Name	UniGene
M26679	HOXA5	homeo box A5	<a href="#">Hs.37034</a>
S82986	HOXC6	homeo box C6	<a href="#">Hs.820</a>
AF051323	SCAP2	src family associated phosphoprotein 2	<a href="#">Hs.52644</a>
J02947	SOD3	superoxide dismutase 3, extracellular	<a href="#">Hs.2420</a>
M16937	HOXB7	homeo box B7	<a href="#">Hs.819</a>
K03000	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	<a href="#">Hs.76392</a>
		transcription factor AP-2 alpha (activating enhancer binding	
M36711	TFAP2A	protein 2 alpha)	<a href="#">Hs.334334</a>
D76435	ZIC1	Zic family member 1 (odd-paired homolog, Drosophila)	<a href="#">Hs.41154</a>
M74297	HOXA4	homeo box A4	<a href="#">Hs.77637</a>
M68891	GATA2	GATA binding protein 2	<a href="#">Hs.367725</a>
U43328	CRTL1	cartilage linking protein 1	<a href="#">Hs.2799</a>
X17360	HOXD4	homeo box D4	<a href="#">Hs.278255</a>
X51757	HSPA6	heat shock 70kD protein 6 (HSP70B')	<a href="#">Hs.3268</a>
U59831	FOXD1	forkhead box D1	<a href="#">Hs.96028</a>
D83004	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	<a href="#">Hs.75355</a>
L49169	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	<a href="#">Hs.75678</a>
L35545	PROCR	protein C receptor, endothelial (EPCR)	<a href="#">Hs.82353</a>
U16799	ATP1B1	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide	<a href="#">Hs.78629</a>
M20560	ANXA3	annexin A3	<a href="#">Hs.1378</a>
X06256	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	<a href="#">Hs.149609</a>
Z22865	DPT	dermatopontin	<a href="#">Hs.80552</a>
X75918	NR4A2	nuclear receptor subfamily 4, group A, member 2	<a href="#">Hs.82120</a>
X16665	HOXB2	homeo box B2	<a href="#">Hs.2733</a>
M97676	MSX1	msh homeo box homolog 1 (Drosophila)	<a href="#">Hs.1494</a>
		transglutaminase 2 (C polypeptide, protein-glutamine-gamma-	
M55153	TGM2	glutamyltransferase)	<a href="#">Hs.8265</a>

Some of the genes identified in this analysis, such as superoxide dismutase 3 (*sod3*) and protein C receptor (*procr*) have previously been associated with atherosclerosis. Interestingly, many genes that populate the dominant metagene have cellular roles that could be associated with atherosclerotic disease initiation such as homeobox-containing genes and *gata2*. An analysis of the biological processes represented by our gene list showed a preponderance of candidates relevant to regulation of transcription and signal transduction within our short list.

Genes from table II were classified according to biological process as follows:

Regulation of Cell Cycle: FBJ murine osteosarcoma viral oncogene homolog B.

Regulation of Transcription: nuclear receptor subfamily 4, group A, member 2, homeo box A4, msh homeo box homolog 1, transcription factor AP-2 alpha, forkhead box D1, homeo box B7, homeo box D4, homeo box C6.

- 5       Signal Transduction: src family associated phosphoprotein 2, Zic family member 1.  
       Inflammatory Response: protein C receptor, endothelial.  
       Cell Adhesion: Dermatopectin, cartilage linking protein 1, integrin alpha 5.  
       Development: homeo box B2.

- 10      From the aorta samples, 508 metagenes were identified. These are listed as follows:

**Metagene 1;** 35027\_at Cluster Incl. X14830:Human mRNA for muscle acetylcholine receptor beta-;  
 34935\_at Cluster Incl. AL021026:dJ127D3.3 (Flavin-containing Monooxygenase 2) /c; 37808\_at  
 Cluster Incl. AL049989:Homo sapiens mRNA; cDNA DKFZp564F052 (from clone; 39244\_at  
 Cluster Incl. M28211:Homo sapiens GTP-binding protein (RAB4) mRNA, comp; 39280\_at Cluster  
 15 Incl. U80744:Homo sapiens CTG4a mRNA, complete cds /cds=(387,81; 37604\_at Cluster Incl.  
 U44111:Human histamine N-methyltransferase (HNMT) gene /c; 32191\_at Cluster Incl.  
 D13969:Human mRNA for Mel-18 protein, complete cds /cds=(; 37364\_at Cluster Incl.  
 U72511:Human B-cell receptor associated protein (hBAP) mR; 37705\_at Cluster Incl.  
 U14575:Human (ard-1) mRNA, complete cds /cds=(935,1318) /; 38108\_at Cluster Incl.  
 20 AF020543:Homo sapiens palmitoyl-protein thioesterase-2 (P; 41579\_s\_at Cluster Incl.  
 AI952267:wx50d11.x1 Homo sapiens cDNA, 3 end /clone=IM; 1624\_at Stimulatory Gdp/Gtp  
 Exchange Protein For C-Ki-Ras P21 And Smg P21 ; 673\_at J04031 /FEATURE=  
 /DEFINITION=HUMMDMCSF Human methylenetetrahydrofolate de.

- Metagene 2;** 39322\_at Cluster Incl. AL109693:Homo sapiens mRNA full length insert cDNA clone  
 25 ; 34209\_at Cluster Incl. D38169:Homo sapiens mRNA for inositol 1,4,5-trisphosphate; 37241\_at  
 Cluster Incl. AB020690:Homo sapiens mRNA for KIAA0883 protein, complete; 38832\_r\_at Cluster  
 Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(25; 32587\_at Cluster Incl.  
 U07802:Human Tis11d gene, complete cds /cds=(291,1739) /g.

- Metagene 3;** 33586\_at Cluster Incl. AF070620:Homo sapiens clone 24694 mRNA sequence  
 30 /cds=UNKN; 37468\_at Cluster Incl. AF058925:Homo sapiens Jak2 kinase mRNA, complete cds  
 /cds; 38228\_g\_at Cluster Incl. AB006909:Homo sapiens mRNA for A-type microphthalmia as;  
 39295\_s\_at Cluster Incl. AF049884:Homo sapiens Arg/Abl-interacting protein ArgBP; 41431\_at  
 Cluster Incl. AB023153:Homo sapiens mRNA for KIAA0936 protein, complete; 41625\_at Cluster  
 Incl. AB011165:Homo sapiens mRNA for KIAA0593 protein, partial ; 34668\_at Cluster Incl.  
 35 D88152:Homo sapiens mRNA for acetyl-coenzyme A transport; 35139\_at Cluster Incl.  
 AL049341:Homo sapiens mRNA; cDNA DKFZp566A163 (from clone; 37951\_at Cluster Incl.  
 AF035119:Homo sapiens deleted in liver cancer-1 (DLC-1) m; 41727\_at Cluster Incl.  
 AB023224:Homo sapiens mRNA for KIAA1007 protein, partial ; 34792\_at Cluster Incl.  
 AL049954:Homo sapiens mRNA; cDNA DKFZp564A1523 (from clon; 35764\_at Cluster Incl.



- Y15164:Homo sapiens mRNA for protein encoded by exorf5 (7; 37356\_r\_at Cluster Incl.  
D86326:Homo sapiens mRNA for p115, complete cds /cds=(1; 39474\_s\_at Cluster Incl.  
AF045800:Homo sapiens gremlin mRNA, complete cds /cds=(; 41498\_at Cluster Incl.  
AB020718:Homo sapiens mRNA for KIAA0911 protein, complete.
- 5 **Metagene 4;** 36322\_at Cluster Incl. AB012668:Homo sapiens hFuc-T VII gene for selectin-ligand;  
38853\_at Cluster Incl. X81892:H.sapiens mRNA for HE6 Tm7 receptor /cds=(72,3116); 40403\_at  
Cluster Incl. Z97171:Homo sapiens GLC1A (trabecular meshwork induced gl; 32025\_at Cluster Incl.  
Y11306:Homo sapiens mRNA for hTCF-4 /cds=(307,2097) /gb=Y; 33288\_i\_at Cluster Incl.  
D88827:Homo sapiens mRNA for zinc finger protein FPM315; 37183\_at Cluster Incl.
- 10 M81883:Human glutamate decarboxylase (GAD67) mRNA, comple; 39001\_at Cluster Incl.  
AF047470:Homo sapiens malate dehydrogenase precursor (MDH; 35849\_at Cluster Incl.  
AB011157:Homo sapiens mRNA for KIAA0585 protein, partial ; 38804\_at Cluster Incl.  
AF053641:Homo sapiens brain cellular apoptosis susceptibi; 1120\_at J05459 /FEATURE=mRNA  
/DEFINITION=HUMGSTM3A Human glutathione transferase; 1121\_g\_at J05459
- 15 /FEATURE=mRNA /DEFINITION=HUMGSTM3A Human glutathione transferase; 1101\_at L77864  
/FEATURE= /DEFINITION=HUMFE65 Homo sapiens stat-like protein (Fe6.  
**Metagene 5;** 31386\_at Cluster Incl. M20812:Human kappa-immunoglobulin germline pseudogene  
(co; 31396\_r\_at Cluster Incl. AB012851:Homo sapiens mRNA for Musashi, complete cds /c;  
31410\_at Cluster Incl. AF023614:Homo sapiens transmembrane activator and CAML in; 31590\_g\_at
- 20 Cluster Incl. AL031983:dJ271M21.2 (hs6M1-12 (7 transmembrane receptor; 31594\_at Cluster Incl.  
Y16788:Homo sapiens hHa3-I gene, complete CDS /cds=(0,121; 31626\_i\_at Cluster Incl.  
AF047485:Homo sapiens amine oxidase pseudogene mRNA, sp; 31681\_at Cluster Incl.  
X57282:H.sapiens mRNA for soluble erythropoietin receptor; 32000\_g\_at Cluster Incl.  
AI344681:qp09h03.x1 Homo sapiens cDNA, 3 end /clone=IM; 32407\_f\_at Cluster Incl.
- 25 U92818:Homo sapiens c33.28 unnamed HERV-H protein mRNA.; 32498\_at Cluster Incl.  
L35318:Human rearranged metabotropic glutamate receptor t; 33016\_at Cluster Incl.  
AI052224:oz21a02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34066\_at Cluster Incl.  
AJ012590:Homo sapiens mRNA for glucose 1-dehydrogenase /c; 34067\_at Cluster Incl.  
AL022314:dJ1170K4.2 (novel Trypsin family protein with cl; 34089\_at Cluster Incl.
- 30 AB028953:Homo sapiens mRNA for KIAA1030 protein, partial ; 34161\_at Cluster Incl.  
U39573:Human salivary peroxidase mRNA, complete cds /cds=; 34573\_at Cluster Incl.  
U14187:Human receptor tyrosine kinase ligand LERK-3 (EPLG; 35534\_at Cluster Incl.  
AB011086:Homo sapiens mRNA for KIAA0514 protein, complete; 36332\_at Cluster Incl.  
U40391:Human serotonin N-acetyltransferase gene, complete; 32866\_at Cluster Incl.
- 35 AB011177:Homo sapiens mRNA for KIAA0605 protein, complete; 34463\_at Cluster Incl.  
M55983:Human DNase I mRNA, complete cds /cds=(159,1007) /; 34508\_r\_at Cluster Incl.  
AI971726:wr07a08.x1 Homo sapiens cDNA, 3 end /clone=IM; 34894\_r\_at Cluster Incl.  
AC003965:Homo sapiens chromosome 16, cosmid clone 325D7; 35939\_s\_at Cluster Incl.  
L20433:Human octamer binding transcription factor 1 (OT; 36222\_at Cluster Incl. AJ012008:Homo

- sapiens genes encoding RNCC protein, DDAH p; 36276\_at Cluster Incl. X67734:H.sapiens mRNA for transient axonal glycoprotein (; 36285\_at Cluster Incl. U07364:Human inwardly rectifying potassium channel mRNA, ; 36737\_at Cluster Incl. U59057:Human beta-A4 crystallin (CRYBA4) mRNA, complete c; 37429\_g\_at Cluster Incl. A1140857:qa83c11.s1 Homo sapiens cDNA, 3 end
- 5 /clone=IM; 37490\_at Cluster Incl. L27213:Homo sapiens anion exchange protein mRNA, complete; 38851\_at Cluster Incl. M63394:Human 3 nucleotide sequence mRNA /cds=UNKNOWN /gb=; 38903\_at Cluster Incl. AF099731:Homo sapiens connexin 31.1 (GJB5) gene, complete; 38936\_at Cluster Incl. M16652:Human pancreatic elastase IIA mRNA, complete cds /; 39308\_r\_at Cluster Incl. X81637:H.sapiens clathrin light chain b gene /cds=UNKNO; 39965\_at Cluster Incl.
- 10 A1570572:tm78c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40668\_s\_at Cluster Incl. U34624:Human T cell surface glycoprotein CD-6 mRNA, com; 41118\_at Cluster Incl. A1921843:wp07a11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41458\_at Cluster Incl. AB007936:Homo sapiens mRNA for KIAA0467 protein, partial ; 32100\_r\_at Cluster Incl. U06088:Human N-acetylgalactosamine 6-sulphatase (GALNS); 32699\_s\_at Cluster Incl.
- 15 X64116:H.sapiens PVR gene for poliovirus receptor (exon; 32701\_at Cluster Incl. U51269:Human armadillo repeat protein mRNA, complete cds ; 33779\_at Cluster Incl. AF060538:Homo sapiens vesicle associated membrane protein; 36004\_at Cluster Incl. AF074382:Homo sapiens Ikb kinase gamma subunit (IKK-gamma; 38622\_at Cluster Incl. W28953:54b7 Homo sapiens cDNA /gb=W28953 /gi=1308901 /ug=; 38707\_r\_at Cluster Incl. S75174:E2F-4=transcription factor
- 20 [human, Nalm6 and HeL; 34864\_at Cluster Incl. AF070638:Homo sapiens clone 24448 unknown mRNA, partial c; 36114\_r\_at Cluster Incl. M19309:Human slow skeletal muscle troponin T mRNA, clon; 36663\_at Cluster Incl. AL021155:dJ934G17.2.1 (Atrial Natriuretic Factor ANF prec; 38447\_at Cluster Incl. U08438:Human beta-adrenergic receptor kinase (ADRBK1) gen; 39137\_at Cluster Incl. X80878:H.sapiens R kappa B mRNA /cds=(130,4104) /gb=X8087; 39817\_s\_at Cluster Incl.
- 25 AF040105:Homo sapiens RCL (Rcl) mRNA, complete cds /cds; 39832\_at Cluster Incl. AL096723:Homo sapiens mRNA; cDNA DKFZp564H2023 (from clon; 39855\_at Cluster Incl. AC005787:Homo sapiens chromosome 19, cosmid R33374 /cds=(; 39872\_at Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99) ; 39920\_r\_at Cluster Incl. AF095154:Homo sapiens C1q-related factor mRNA, complete; 41359\_at Cluster Incl. Z98265:Homo
- 30 sapiens mRNA for plakophilin 3 /cds=(74,2467); 41525\_at Cluster Incl. N25429:yx76b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 32557\_at Cluster Incl. A1762438:wg57a07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 2079\_s\_at M13970 /FEATURE=mRNA /DEFINITION=HUMGFI21 Human insulin-like growth fa; 2046\_at M21536 /FEATURE= /DEFINITION=HUMERG12 Human
- 35 JAK family tyrosine protei; 1925\_at Z36714 /FEATURE=mRNA /DEFINITION=HSCYCLF H.sapiens mRNA for cyclin F ; 1894\_f\_at Neurofibromatosis 2 Tumor Suppressor ; 1827\_s\_at M13929 /FEATURE=mRNA /DEFINITION=HUMMYCPOA Human c-myc-P64 mRNA, initi; 1494\_f\_at M33318 /FEATURE=mRNA /DEFINITION=HUMCP1IA3A Human cytochrome P450IIA3 ; 1432\_s\_at D16105 /FEATURE= /DEFINITION=HUMLTCLP2 Human mRNA for

- leukocyte tyrosi; 1244\_at U18671 /FEATURE=mRNA /DEFINITION=HSU18671 Human Stat2 gene, complete cds; 1220\_g\_at X15949 /FEATURE=cds /DEFINITION=HSIRF2 Human mRNA for interferon regul; 1167\_s\_at D86331 /FEATURE= /DEFINITION=D86331 Human MT2-MMP gene for matrix meta; 1122\_f\_at K03183 /FEATURE=cds /DEFINITION=HUMCGBBA3 Human
- 5 chorionic gonadotropin; 883\_s\_at M54915 /FEATURE= /DEFINITION=HUMPIM1LE Human h-pim-1 protein (h-pim-1) ; 789\_at X52541 /FEATURE=cds /DEFINITION=HSEGR1 Human mRNA for early growth respon; 799\_at X80343 /FEATURE=cds /DEFINITION=HSP35R H.sapiens p35 mRNA for regulatory ; 493\_at U29171 /FEATURE= /DEFINITION=HSU29171 Human casein kinase I delta mRNA, c; 421\_at X66397 /FEATURE=cds /DEFINITION=HSTPRM H.sapiens tpr
- 10 mRNA ; 160020\_at Z48481 /FEATURE=cds /DEFINITION=HSMMPM1 H.sapiens mRNA for membrane-ty.
- Metagene 6;** 38550\_at Cluster Incl. AB021638:Homo sapiens X11L2 mRNA for X11-like protein 2, ; 36108\_at Cluster Incl. M16276:Human MHC class II HLA-DR2-Dw12 mRNA DQw1-beta, co; 37722\_s\_at Cluster Incl. U26266:Human deoxyhypusine synthase mRNA, complete cds ; 1015\_s\_at
- 15 U62293 /FEATURE=mRNA /DEFINITION=HSU62293 Human LIM-kinase1 and altern; 290\_s\_at L32831 /FEATURE=exon /DEFINITION=HUMGPCRD Homo sapiens G protein-couple.
- Metagene 7;** 31691\_g\_at Cluster Incl. U08997:Human glutamate dehydrogenase gene, complete cds; 34069\_s\_at Cluster Incl. S79325:SYT...SSX1 {translocation breakpoint} [human, sy; 32903\_at Cluster Incl. L11695:Human activin receptor-like kinase (ALK-5) mRNA, c; 34925\_at Cluster Incl.
- 20 AB003062:Homo sapiens MYPT2 mRNA, complete cds /cds=(163,; 38207\_at Cluster Incl. AW006742:wr28g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38230\_at Cluster Incl. U81984:Human endothelial PAS domain protein 1 (EPAS1) mRN; 39225\_at Cluster Incl. Y09443:H.sapiens mRNA for alkyl-dihydroxyacetonephosphate; 41373\_s\_at Cluster Incl. W27148:23g6 Homo sapiens cDNA /gb=W27148 /gi=1306727 /u; 31827\_s\_at Cluster Incl.
- 25 AF027516:Homo sapiens trans-golgi network glycoprotein ; 34217\_at Cluster Incl. AB015132:Homo sapiens UKLF mRNA for ubiquitous Kruppel li; 34240\_s\_at Cluster Incl. AL049786:Novel human gene mapping to chromosome 13 /cds=; 34683\_at Cluster Incl. U63289:Human RNA-binding protein CUG-BP/hNab50 (NAB50) mR; 37601\_at Cluster Incl. AJ001417:Homo sapiens mRNA for extraneuronal monoamine tr; 38614\_s\_at Cluster Incl.
- 30 U77413:Human O-linked GlcNAc transferase mRNA, complete; 40792\_s\_at Cluster Incl. AF091395:Homo sapiens Trio isoform mRNA, complete cds /; 32765\_f\_at Cluster Incl. W28330:45d4 Homo sapiens cDNA /gb=W28330 /gi=1308278 /u; 33417\_at Cluster Incl. D31886:Human mRNA for KIAA0066 gene, partial cds /cds=(0,; 33855\_at Cluster Incl. M96995:Homo sapiens epidermal growth factor receptor-bind; 36962\_at Cluster Incl. U24105:Homo
- 35 sapiens coatomer protein (COPA) mRNA, complet; 39523\_at Cluster Incl. AF038897:Homo sapiens syntaxin 16 mRNA, complete cds /cds; 39531\_at Cluster Incl. L06237:Human microtubule-associated protein 1B (MAP1B) ge; 40581\_at Cluster Incl. U42390:Homo sapiens Trio mRNA, complete cds /cds=(66,8651; 40606\_at Cluster Incl. U88629:Human RNA polymerase II elongation factor ELL2, co; 41287\_s\_at Cluster Incl. W28510:48f3 Homo sapiens cDNA /gb=W28510

- /gi=1308521 /u; 2048\_s\_at M26747 /FEATURE= /DEFINITION=HUMCERBA Human c-erbA mRNA, complete cds ; 1983\_at X68452 /FEATURE=cds /DEFINITION=HSCYCD2 H.sapiens mRNA for cyclin D2 ; 1843\_at Ret Transforming Gene ; 1818\_at Ras-Like Protein Tc10 ; 1793\_at M80629 /FEATURE= /DEFINITION=HUMCHED Human cdc2-related protein kinase ( ; 1556\_at
- 5 U23946 /FEATURE= /DEFINITION=HSU23946 Human putative tumor suppressor (L; 1189\_at X85753 /FEATURE= /DEFINITION=HSCDK8 Homo sapiens mRNA for CDK8 protein k; 976\_s\_at Z11695 /FEATURE=cds /DEFINITION=HS40KDAP H.sapiens 40 kDa protein kinas; 777\_at D13988 /FEATURE= /DEFINITION=HUMRABGDI Human rab GDI mRNA, complete cds ; 623\_s\_at M28213 /FEATURE= /DEFINITION=HUMRAB2A Homo sapiens GTP-binding protein
- 10 ; 591\_s\_at M33684 /FEATURE=cds /DEFINITION=HUMPPP1A5 Human (clone lambda-16-1) no; 531\_at U16307 /FEATURE= /DEFINITION=HSU16307 Human glioma pathogenesis-related p; 148\_at U88629 /FEATURE=cds /DEFINITION=HSU88629 Human RNA polymerase II elongati.
- Metagene 8;** 31350\_at Cluster Incl. AC004597:Homo sapiens chromosome 19, cosmid F20722 /cds=( ; 35571\_at Cluster Incl. AF055917:Homo sapiens protease-activated receptor 4 mRNA,;
- 15 35884\_at Cluster Incl. Y07829:Homo sapiens RFB30 gene for RING finger protein /c; 40042\_r\_at Cluster Incl. U82381:Human proline dehydrogenase/proline oxidase (PRO; 31889\_at Cluster Incl. U06452:Human melanoma antigen recognized by T-cells (MART; 32106\_at Cluster Incl. L28101:Homo sapiens kallistatin (PI4) gene, exons 1-4, co; 35993\_s\_at Cluster Incl. A1698103:we20h11.x1 Homo sapiens cDNA, 3 end /clone=IM; 37977\_at Cluster Incl.
- 20 A1138834:qe04b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34872\_at Cluster Incl. W26547:32h10 Homo sapiens cDNA /gb=W26547 /gi=1307390 /ug; 39187\_at Cluster Incl. AF001450:untitled /cds=(0,1568) /gb=AF001450 /gi=2245523 ; 41340\_at Cluster Incl. AA827795:od08a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 695\_at Tenascin .
- Metagene 9;** 36427\_at Cluster Incl. W27129:22g8 Homo sapiens cDNA /gb=W27129 /gi=1306663
- 25 /ug=; 37106\_at Cluster Incl. D89928:Homo sapiens HKL1 mRNA, complete cds /cds=(152,196; 38864\_at Cluster Incl. W26851:17b12 Homo sapiens cDNA /gb=W26851 /gi=1306214 /ug; 39949\_at Cluster Incl. AJ224328:Homo sapiens mRNA for MOCS1A & MOCS1B proteins, ; 40665\_at Cluster Incl. M83772:Human flavin-containing monooxygenase form II (FMO; 41372\_at Cluster Incl. AB020638:Homo sapiens mRNA for KIAA0831 protein, complete; 31794\_at Cluster
- 30 Incl. D38524:Human mRNA for 5-nucleotidase /cds=(83,1768) /gb=D; 32039\_at Cluster Incl. U81504:Homo sapiens beta-3A-adaptin subunit of the AP-3 c; 33260\_at Cluster Incl. L13857:Human guanine nucleotide exchange factor mRNA, com; 33710\_at Cluster Incl. U72515:Human C3f mRNA, complete cds /cds=(117,1262) /gb=U; 34201\_at Cluster Incl. Y13350:Homo sapiens mRNA for DnaJ protein /cds=(0,975) /g; 35153\_at Cluster Incl.
- 35 AF058696:Homo sapiens cell cycle regulatory protein p95 ( ; 35184\_at Cluster Incl. AB011118:Homo sapiens mRNA for KIAA0546 protein, partial ; 35618\_at Cluster Incl. D29677:Human mRNA for KIAA0054 gene, complete cds /cds=(1; 35681\_r\_at Cluster Incl. AB011141:Homo sapiens mRNA for KIAA0569 protein, comple; 36048\_at Cluster Incl. AB015342:Homo sapiens HRIHFB2436 mRNA, partial cds /cds=( ; 36057\_at Cluster Incl.

- AB011084:Homo sapiens mRNA for KIAA0512 protein, complete; 36080\_at Cluster Incl.
- AB002332:Human mRNA for KIAA0334 gene, complete cds /cds=; 36474\_at Cluster Incl.
- AB018319:Homo sapiens mRNA for KIAA0776 protein, partial ; 36521\_at Cluster Incl.
- AB023213:Homo sapiens mRNA for KIAA0996 protein, complete; 36527\_at Cluster Incl.
- 5 AL050405:Novel human gene mapping to chromosome X /cds=(39; 36818\_at Cluster Incl.
- AF052100:Homo sapiens clone 23645 mRNA sequence /cds=UNKN; 36849\_at Cluster Incl.
- U90920:Human PTPL1-associated RhoGAP mRNA, complete cds /; 38252\_s\_at Cluster Incl.
- U84007:Human glycogen debranching enzyme isoform 1 (AGL; 38253\_at Cluster Incl.
- U84011:Human glycogen debranching enzyme isoform 6 (AGL) ; 38270\_at Cluster Incl.
- 10 AF005043:Homo sapiens poly(ADP-ribose) glycohydrolase (hP; 38626\_at Cluster Incl.
- AB007859:Homo sapiens KIAA0399 mRNA, partial cds /cds=(0; 39379\_at Cluster Incl.
- AL049397:Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone; 39686\_g\_at Cluster Incl.
- AL050282:Homo sapiens mRNA; cDNA DKFZp586H2219 (from clone; 39706\_at Cluster Incl.
- AB014536:Homo sapiens mRNA for KIAA0636 protein, complete; 39776\_at Cluster Incl.
- 15 AB014523:Homo sapiens mRNA for KIAA0623 protein, complete; 39785\_at Cluster Incl.
- D42054:Human mRNA for KIAA0092 gene, complete cds /cds=(5; 40066\_at Cluster Incl.
- AF046024:Homo sapiens UBA3 (UBA3) mRNA, complete cds /cds; 40129\_at Cluster Incl.
- U47077:Human DNA-dependent protein kinase catalytic subunit; 40404\_s\_at Cluster Incl.
- U18291:Human CDC16Hs mRNA, complete cds /cds=(24,1883) ; 40810\_at Cluster Incl.
- 20 U66615:Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA; 40844\_at Cluster Incl.
- D63875:Human mRNA for KIAA0155 gene, complete cds /cds=(8; 41202\_s\_at Cluster Incl.
- AF000152:Homo sapiens OS-4 protein (OS-4) mRNA, complete; 33365\_at Cluster Incl.
- AB023162:Homo sapiens mRNA for KIAA0945 protein, complete; 33870\_at Cluster Incl.
- AB029005:Homo sapiens mRNA for KIAA1082 protein, partial ; 33899\_at Cluster Incl.
- 25 U34252:Human gamma-aminobutyraldehyde dehydrogenase mRNA; 34312\_at Cluster Incl.
- AI040324:oy33a12.x1 Homo sapiens cDNA, 3' end /clone=IMAG; 34324\_at Cluster Incl.
- AF068227:Homo sapiens putative transmembrane protein (CLN; 34327\_at Cluster Incl.
- Z46606:H.sapiens HLTF gene for helicase-like transcriptio; 34825\_at Cluster Incl.
- AL031775:dJ30M3.3 (novel protein similar to C. elegans Y6; 35289\_at Cluster Incl.
- 30 AJ011679:Homo sapiens mRNA for Rab6 GTPase activating protein; 35845\_at Cluster Incl.
- AJ131245:Homo sapiens mRNA for Sec24 protein (Sec24B isoform; 36588\_at Cluster Incl.
- AB018353:Homo sapiens mRNA for KIAA0810 protein, partial ; 36596\_r\_at Cluster Incl.
- S68805:L-arginine-glycine amidinotransferase [human, kidney; 36628\_at Cluster Incl. L42542:Human RLIP76 protein mRNA, complete cds /cds=(223; 37031\_at Cluster Incl. D80005:Human mRNA for
- 35 KIAA0183 gene, partial cds /cds=(0; 37673\_at Cluster Incl. X96586:H.sapiens mRNA for FAN protein /cds=(12,2765) /gb=; 38010\_at Cluster Incl. AF002697:Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 ; 38436\_at Cluster Incl. D87440:Human mRNA for KIAA0252 gene, partial cds /cds=(0; 38470\_i\_at Cluster Incl. D86981:Human mRNA for KIAA0228 gene, partial cds /cds=; 38727\_at Cluster Incl. M23161:Human transposon-like element mRNA /cds=UNKNOWN

- /g; 38763\_at Cluster Incl. L29254:Human (clone P1-5) L-iditol-2 dehydrogenase gene /; 38843\_at Cluster Incl. AL079310:Novel human gene mapping to chromosome 22 /cds=(5; 39823\_at Cluster Incl. U06631:Human (H326) mRNA, complete cds /cds=(176,1969) /g; 40258\_at Cluster Incl. M55265:Human casein kinase II alpha subunit mRNA, complet; 33113\_at Cluster Incl.
- 5 U65093:Human msg1-related gene 1 (mrg1) mRNA, complete cd; 2003\_s\_at U28946 /FEATURE= /DEFINITION=HSU28946 Human G/T mismatch binding prote; 1675\_at M23379 /FEATURE= /DEFINITION=HUMGAPA Human GTPase-activating protein ras; 1213\_at U88666 /FEATURE= /DEFINITION=HSU88666 Homo sapiens serine kinase SRPK2 m.
- Metagene** 10; 31669\_s\_at Cluster Incl. AF039307:Homo sapiens homeobox A11 (HOXA11) gene, compl; 31908\_at Cluster Incl. U94354:Human lunatic fringe mRNA, partial cds /cds=(0,775; 33034\_at Cluster Incl. Y17108:Homo sapiens mRNA for rhomboid-related protein, co; 33640\_at Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /cds; 35514\_at Cluster Incl. AA916905:oh85a09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33952\_at Cluster Incl. U71601:Human zinc finger protein zfp47 (zfp47) mRNA, parti; 34005\_at Cluster Incl. X73079:Homo sapiens encoding Polymeric immunoglobulin rec; 34963\_at Cluster Incl. AA557228:nl75c09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35387\_r\_at Cluster Incl. S71129:acetylcholinesterase {I4-E5 doman} [human, tumor; 35492\_at Cluster Incl. AC004523:Homo sapiens chromosome 19, cosmid F22329 /cds=(; 38229\_at Cluster Incl. X90579:H.sapiens DNA for cyp related pseudogene /cds=UNKN; 38512\_r\_at Cluster Incl. D26158:Homo sapiens mRNA for PLE21 protein, complete
- 15 cd; 38528\_at Cluster Incl. U19822:Human acetyl-CoA carboxylase mRNA, complete cds /c; 38566\_at Cluster Incl. X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type ; 38607\_at Cluster Incl. AF027204:Homo sapiens putative tetraspan transmembrane pr; 39242\_at Cluster Incl. X96783:H.sapiens Syt V gene (genomic and cDNA sequence) /; 39660\_at Cluster Incl. AI309115:qo71a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40003\_at Cluster Incl.
- 25 U36221:Human pancreatic zymogen granule membrane protein ; 40288\_r\_at Cluster Incl. AA471042:ne23b10.s1 Homo sapiens cDNA, 3 end /clone=IM; 40337\_at Cluster Incl. M35531:Human GDP-L-fucose-beta-D-galactoside 2-alpha-l-fu; 41036\_at Cluster Incl. AL022314:dJ1170K4.1 (novel protein similar to KIAA0176 an; 41374\_at Cluster Incl. AB016869:Homo sapiens mRNA for p70 ribosomal S6 kinase be; 41694\_at Cluster Incl.
- 30 M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M; 33778\_at Cluster Incl. AL096779:Novel human gene mapping to chromosome 2213.3 si; 35988\_i\_at Cluster Incl. AI417075:tg78e09.x1 Homo sapiens cDNA, 3 end /clone=IM; 36473\_at Cluster Incl. AB023220:Homo sapiens mRNA for KIAA1003 protein, complete; 37210\_at Cluster Incl. S78296:neurofilament-66 [human, fetal brain, mRNA, 3197 n; 37551\_at Cluster Incl.
- 35 D86966:Human mRNA for KIAA0211 gene, complete cds /cds=(5; 39803\_s\_at Cluster Incl. U84570:Human A2 mRNA, complete cds /cds=(239,883) /gb=U; 40094\_r\_at Cluster Incl. X80026:H.sapiens B-cam mRNA /cds=(6,1772) /gb=X80026 /g; 40842\_at Cluster Incl. M60784:Human U1 snRNP-specific protein A gene /cds=(137,9; 39455\_r\_at Cluster Incl. AJ002607:Homo sapiens HOX11L1 gene, exon 1 and joined C; 39489\_g\_at Cluster Incl.

- W27720:39e11 Homo sapiens cDNA /gb=W27720 /gi=1307866 /; 39917\_at Cluster Incl.  
 AI961040:wq58f01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41792\_at Cluster Incl.  
 L78207:Homo sapiens sulfonylurea receptor (SUR1) mRNA, co; 2028\_s\_at M96577 /FEATURE=  
 /DEFINITION=HUME2F Homo sapiens (E2F-1) pRB-binding p; 1559\_at U24153 /FEATURE=  
 5 /DEFINITION=HSU24153 Human p21-activated protein kinase; 1280\_i\_at Serine/Threonine Kinase  
 ; 1169\_at D88799 /FEATURE= /DEFINITION=D88799 Homo sapiens mRNA for cadherin, part;  
 970\_r\_at X98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin ;  
 934\_at L11702 /FEATURE= /DEFINITION=HUMPHOSDPD Human phospholipase D mRNA,  
 compl; 726\_f\_at Chorionic Somatomammotropin Hormone Cs-5 ; 729\_i\_at Mucin 3, Intestinal ;  
 10 730\_r\_at Mucin 3, Intestinal ; 519\_g\_at U07132 /FEATURE= /DEFINITION=HSU07132 Human  
 steroid hormone receptor Ne; 255\_s\_at M13981 /FEATURE= /DEFINITION=HUMINHA Human  
 inhibin A-subunit mRNA, comp.  
**Metagene 11**; 32395\_r\_at Cluster Incl. X55954:Human mRNA for HL23 ribosomal protein  
 homologue ; 38922\_at Cluster Incl. AF097738:Homo sapiens non-receptor tyrosine kinase (TNK1) ;  
 15 39591\_s\_at Cluster Incl. Z36531:H.sapiens mRNA for fibrinogen-like protein (pT49; 39593\_at  
 Cluster Incl. AI432401:tg73b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41102\_at Cluster  
 Incl. U66359:Human T54 protein (T54) mRNA, complete cds /cds=(6; 31852\_at Cluster Incl.  
 AL050390:Homo sapiens mRNA; cDNA DKFZp564O043 (from clone; 33218\_at Cluster Incl.  
 M11730:Human tyrosine kinase-type receptor (HER2) mRNA, c; 37692\_at Cluster Incl.  
 20 AI557240:PT2.1\_15\_C11.r Homo sapiens cDNA, 3 end /clone\_ ; 40269\_at Cluster Incl.  
 U51990:Human hPrp18 mRNA, complete cds /cds=(72,1100) /gb; 32602\_at Cluster Incl.  
 X63465:H.sapiens hGDS mRNA for smg GDS /cds=(0,1676) /gb=; 213\_at M97675 /FEATURE=  
 /DEFINITION=HUMROR1A Human transmembrane receptor (ror1).  
**Metagene 12**; 32635\_at Cluster Incl. AB029036:Homo sapiens mRNA for KIAA1113 protein,  
 partial ; 38640\_at Cluster Incl. AI582831:tn36c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 25 40471\_at Cluster Incl. Y09048:H.sapiens PxF gene /cds=(10,909) /gb=Y09048 /gi=25; 40822\_at  
 Cluster Incl. L41067:Homo sapiens NF-AT4c mRNA, complete cds /cds=(210; 33364\_at Cluster  
 Incl. U51694:HSU51694 Homo sapiens cDNA /gb=U51694 /gi=1255286 ; 36978\_at Cluster Incl.  
 D38521:Human mRNA for KIAA0077 gene, partial cds /cds=(0; 39546\_s\_at Cluster Incl.  
 30 AA191426:zp83g09.s1 Homo sapiens cDNA, 3 end /clone=IM; 40273\_at Cluster Incl.  
 AA485440:zx90g03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40895\_g\_at Cluster Incl.  
 AI393342:tg44c04.x1 Homo sapiens cDNA, 3 end /clone=IM; 41506\_at Cluster Incl.  
 AF032437:Homo sapiens mitogen activated protein kinase ac.  
**Metagene 13**; 31427\_at Cluster Incl. U43604:Human unidentified mRNA, partial sequence  
 35 /cds=UNK; 35547\_at Cluster Incl. AF058056:Homo sapiens monocarboxylate transporter 2 (hMCT;  
 33562\_g\_at Cluster Incl. X80031:Homo sapiens COL4A3 mRNA /cds=(161,5173) /gb=X80;  
 35436\_at Cluster Incl. L06147:Human (clone SY11) golgin-95 mRNA, complete cds /c; 35439\_at  
 Cluster Incl. D26121:Human mRNA for ZFM1 protein alternatively spliced ; 35933\_f\_at Cluster  
 Incl. D38498:Human PMS5 mRNA (yeast mismatch repair gene PMS1; 35958\_at Cluster Incl.

- AL050379:Homo sapiens mRNA; cDNA DKFZp586F1922 (from clon; 37491\_at Cluster Incl.  
D90359:Human CCG1 mRNA /cds=(51,5669) /gb=D90359 /gi=5593; 38176\_at Cluster Incl.  
AF017656:Homo sapiens G protein beta 5 subunit mRNA, comp; 39969\_at Cluster Incl.  
AA255502:zr85b06.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 40343\_at Cluster Incl.
- 5 AJ005814:Homo sapiens mRNA for hoxA7 protein /cds=(106,79; 41005\_at Cluster Incl.  
L36531:Homo sapiens integrin alpha 8 subunit mRNA, 3 end; 41091\_at Cluster Incl.  
U05237:Human fetal Alz-50-reactive clone 1 (FAC1) mRNA, c; 41466\_s\_at Cluster Incl.  
L04282:Human CACCC box-binding protein mRNA, complete c; 32129\_at Cluster Incl.  
AL079314:Homo sapiens mRNA full length insert cDNA clone ; 32734\_at Cluster Incl.
- 10 L76703:Homo sapiens protein phosphatase 2A B56-epsilon (P; 35725\_at Cluster Incl. D89618:Homo  
sapiens mRNA for karyopherin alhph 3, complet; 35985\_at Cluster Incl. AB023137:Homo sapiens  
mRNA for KIAA0920 protein, complete; 38639\_at Cluster Incl. AF040963:Homo sapiens Mad4  
homolog (Mad4) mRNA, complete ; 39419\_at Cluster Incl. AB011088:Homo sapiens mRNA for  
KIAA0516 protein, partial ; 40463\_at Cluster Incl. U70322:Human transportin (TRN) mRNA,  
15 complete cds /cds=(9; 40464\_g\_at Cluster Incl. U70322:Human transportin (TRN) mRNA, complete  
cds /cds=; 40478\_at Cluster Incl. AL021396:Human DNA sequence from clone 971N18 on  
chromoso; 32159\_at Cluster Incl. L00049:Human cellular c-Ki-ras2 proto-oncogene, 5 flank a;  
32815\_at Cluster Incl. AI687419:tp95h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33381\_at  
Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) m; 35295\_g\_at Cluster  
20 Incl. M25077:Human SS-A/Ro ribonucleoprotein autoantigen 60 k; 38420\_at Cluster Incl.  
Y14690:Homo sapiens mRNA for procollagen alpha 2(V) /cds=; 40260\_g\_at Cluster Incl.  
AL009266:H. sapiens cDNA similar to C. elegans RNA bind; 40589\_at Cluster Incl. U40572:Human  
beta2-syntrophin (SNT B2) mRNA, complete cds; 40990\_at Cluster Incl. AF065389:Homo sapiens  
tetraspan NET-4 mRNA, complete cds ; 41591\_at Cluster Incl. AI652978:wb42a05.x1 Homo sapiens  
25 cDNA, 3 end /clone=IMAG; 1937\_at Retinoblastoma 1 ; 1603\_g\_at L33881 /FEATURE=  
/DEFINITION=HUMPKCI Human protein kinase C iota isofo; 1537\_at X00588 /FEATURE=cds  
/DEFINITION=HSEGFPRE Human mRNA for precursor of epi; 1258\_s\_at L76568  
/FEATURE=exon#5 /DEFINITION=HUMERCC4G Homo sapiens excision and; 1124\_at L04731  
/FEATURE= /DEFINITION=HUMTRLALL1 Homo sapiens translocation T(4:1; 933\_f\_at L11672  
30 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finge; 342\_at D12485  
/FEATURE= /DEFINITION=HUMNPP Human mRNA for nucleotide pyrophospha; 274\_at L04282  
/FEATURE= /DEFINITION=HUMTB Human CACCC box-binding protein mRNA, ; 199\_s\_at  
U33052 /FEATURE= /DEFINITION=HSU33052 Human lipid-activated, protein ki.  
**Metagene** 14; 34104\_i\_at Cluster Incl. AI147237:qb36f02.x1 Homo sapiens cDNA, 3 end  
35 /clone=IM; 37527\_at Cluster Incl. Z36715:H.sapiens mRNA for Net transcription factor /cds=(;  
31833\_at Cluster Incl. U78575:Human 68 kDa type I phosphatidylinositol-4-phospha; 34747\_at  
Cluster Incl. X83535:H.sapiens mRNA for membrane-type matrix metallopro; 36675\_r\_at Cluster  
Incl. J03191:Human profilin mRNA, complete cds /cds=(127,549); 36977\_at Cluster Incl.  
U39412:Homo sapiens alpha SNAP mRNA, complete cds /cds=(6; 38757\_at Cluster Incl.



- U41745:Human PDGF associated protein mRNA, complete cds /; 39182\_at Cluster Incl.  
 U87947:Human hematopoietic neural membrane protein (HNMP-; 39183\_at Cluster Incl.  
 X66363:H.sapiens mRNA PCTAIRE-1 for serine/threonine prot; 39835\_at Cluster Incl.  
 U93181:Homo sapiens nuclear dual-specificity phosphatase ; 41551\_at Cluster Incl.
- 5 AW044624:wy78c04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 471\_f\_at U47634 /FEATURE=  
 /DEFINITION=HSU47634 Human beta-tubulin class III isot; 429\_f\_at X00734 /FEATURE=cds  
 /DEFINITION=HSREP10 Human beta-tubulin gene (5-beta.  
**Metagene** 15; 31597\_r\_at Cluster Incl. L36055:Human 4E-binding protein 1 mRNA, complete cds  
 /c; 36728\_at Cluster Incl. M76446:Human alpha-A1-adrenergic receptor mRNA, complete ;  
 10 36983\_f\_at Cluster Incl. X00442:Human mRNA for haptoglobin alpha(2FS)-beta precu; 204\_at  
 M74297 /FEATURE= /DEFINITION=HUMHOX14 Human homeobox 1.4 protein mRNA, co.  
**Metagene** 16; 33660\_at Cluster Incl. U14966:Human ribosomal protein L5 mRNA, complete cds  
 /cds; 34604\_at Cluster Incl. L05568:Human Na<sup>+</sup>/Cl<sup>-</sup> dependent serotonin transporter mRNA;  
 32345\_at Cluster Incl. AL109696:Homo sapiens mRNA full length insert cDNA clone ; 37159\_at  
 15 Cluster Incl. U79259:Human clone 23945 mRNA, complete cds /cds=(636,140; 37446\_at Cluster  
 Incl. AB007903:Homo sapiens KIAA0443 mRNA, complete cds /cds=(6; 37839\_at Cluster Incl.  
 AL109700:Homo sapiens mRNA full length insert cDNA clone ; 39939\_at Cluster Incl.  
 D21337:Human mRNA for collagen /cds=(234,5270) /gb=D21337; 41013\_at Cluster Incl.  
 AL080114:Homo sapiens mRNA; cDNA DKFZp586M2022 (from clon; 41043\_at Cluster Incl.
- 20 AB006867:Homo sapiens mRNA for hSOX20 protein, complete c; 41478\_at Cluster Incl.  
 AL033538:Human DNA sequence from clone 477H23 on chromoso; 32674\_at Cluster Incl.  
 D83032:Homo sapiens mRNA for nuclear protein, NP220, comp; 33255\_at Cluster Incl.  
 M97856:Homo sapiens histone-binding protein mRNA, complet; 35142\_at Cluster Incl.  
 AF070617:Homo sapiens clone 24812 mRNA sequence /cds=UNKN; 36049\_at Cluster Incl.
- 25 W27899:39c4 Homo sapiens cDNA /gb=W27899 /gi=1307847 /ug=; 36890\_at Cluster Incl.  
 AF001691:Homo sapiens 195 kDa cornified envelope precursor; 38681\_at Cluster Incl.  
 U62962:Human Int-6 mRNA, complete cds /cds=(22,1359) /gb=; 38982\_at Cluster Incl.  
 W28865:53g9 Homo sapiens cDNA /gb=W28865 /gi=1308876 /ug=; 39765\_at Cluster Incl.  
 AB002318:Human mRNA for KIAA0320 gene, partial cds /cds=(; 40069\_at Cluster Incl.
- 30 AF051850:Homo sapiens supervillin mRNA, complete cds /cds; 40828\_at Cluster Incl.  
 D63476:Human mRNA for KIAA0142 gene, complete cds /cds=(4; 41142\_at Cluster Incl.  
 U62961:Human succinyl CoA-3-oxoacid CoA transferase precu; 33819\_at Cluster Incl..  
 X13794:H.sapiens lactate dehydrogenase B gene exon 1 and ; 33910\_at Cluster Incl.  
 AL049338:Homo sapiens mRNA; cDNA DKFZp564P116 (from clone; 33911\_at Cluster Incl.
- 35 AI765053:wh56e11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34323\_at Cluster Incl.  
 AF084260:Homo sapiens signalosome subunit 2 (SGN2) mRNA, ; 35778\_at Cluster Incl.  
 AB011103:Homo sapiens mRNA for KIAA0531 protein, complete; 38816\_at Cluster Incl.  
 AF095791:Homo sapiens TACC2 protein (TACC2) mRNA, partial; 39556\_at Cluster Incl.  
 M96803:Human general beta-spectrin (SPTBN1) mRNA, complet; 41503\_at Cluster Incl.

- AB020661:Homo sapiens mRNA for KIAA0854 protein, complete; 32521\_at Cluster Incl.  
 AF056087:Homo sapiens secreted frizzled related protein m; 1882\_g\_at Oncogene Aml1-Evi-1,  
 Fusion Activated ; 496\_s\_at U32324 /FEATURE= /DEFINITION=HSU32324 Human interleukin-11  
 receptor alp; 346\_s\_at D13814 /FEATURE= /DEFINITION=HUMAGRT1B Homo sapiens mRNA  
 5 for angiotensi.
- Metagene 17;** 38981\_at Cluster Incl. AA203354:zx58b07.r1 Homo sapiens cDNA, 5 end  
 /clone=IMAG; 39020\_at Cluster Incl. U82938:Human CD27BP (Siva) mRNA, complete cds  
 /cds=(252,8; 33829\_at Cluster Incl. Y12670:Homo sapiens mRNA for leptin receptor gene-related;  
 35331\_at Cluster Incl. U97067:Homo sapiens alpha-catenin-like protein mRNA, comp; 35346\_at  
 10 Cluster Incl. AB007856:Homo sapiens KIAA0396 mRNA, partial cds /cds=(0,.
- Metagene 18;** 36367\_at Cluster Incl. U79247:Human clone 23599 mRNA sequence  
 /cds=UNKNOWN /gb=U; 33941\_at Cluster Incl. AB009675:Homo sapiens mRNA for  
 MDC/ADAM11, complete cds /; 34512\_at Cluster Incl. J03853:Human kidney alpha-2-adrenergic  
 receptor mRNA, com; 35457\_at Cluster Incl. U20325:Human cocaine and amphetamine regulated  
 15 transcript; 35673\_at Cluster Incl. U02082:Human guanine nucleotide regulatory protein (tim1);  
 36459\_at Cluster Incl. AB020686:Homo sapiens mRNA for KIAA0879 protein, complete; 39750\_at  
 Cluster Incl. W61005:zd29a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 32853\_at Cluster  
 Incl. AB018262:Homo sapiens mRNA for KIAA0719 protein, complete; 33857\_at Cluster Incl.  
 N25122:yx19d10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 34384\_at Cluster Incl.
- 20 AF022853:untitled /cds=(0,4202) /gb=AF022853 /gi=2585771 ; 39878\_at Cluster Incl.  
 AI524125:th09d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40193\_at Cluster Incl.  
 X51956:Human ENO2 gene for neuron specific (gamma) enolas; 33137\_at Cluster Incl.  
 Y13622:Homo sapiens mRNA for latent transforming growth f.
- Metagene 19;** 39993\_at Cluster Incl. D11466:Homo sapiens mRNA for PIG-A protein, complete cds  
 25 ; 39763\_at Cluster Incl. M36803:Human hemopexin gene /cds=(28,1416) /gb=M36803 /gi; 34791\_at  
 Cluster Incl. X52882:Human t-complex polypeptide 1 gene /cds=(21,1691) ; 39860\_at Cluster Incl.  
 U05040:Human FUSE binding protein mRNA, complete cds /cds.
- Metagene 20;** 33587\_f\_at Cluster Incl. AI369146:qy74f11.x1 Homo sapiens cDNA, 3 end  
 /clone=IM; 36423\_at Cluster Incl. W47047:zc38g10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-  
 30 ; 38613\_at Cluster Incl. U61837:Homo sapiens putative cyclin G1 interacting protei; 38754\_at  
 Cluster Incl. AI557295:PT2.1\_16\_D02.r Homo sapiens cDNA, 3 end /clone\_ ; 40897\_at Cluster Incl.  
 M26061:Human cGMP phosphodiesterase alpha subunit (CGPR-A; 954\_s\_at Protein Phosphatase 1,  
 Alpha Catalytic Subunit ; 824\_at U90313 /FEATURE= /DEFINITION=HSU90313 Human  
 glutathione-S-transferase hom; 703\_at Immunoglobulin Heavy Chain, Vdjrc Regions .
- 35 **Metagene 21;** 34538\_at Cluster Incl. AL109682:Homo sapiens mRNA full length insert cDNA clone  
 ; 35441\_at Cluster Incl. AF058922:Homo sapiens GLE1 (GLE1) mRNA, complete cds /cds;  
 37071\_at Cluster Incl. AF042498:Homo sapiens rod photoreceptor CNG-channel beta ; 38193\_at  
 Cluster Incl. X96754:H.sapiens gene encoding kappa light chain constant; 38942\_r\_at Cluster Incl.  
 W28610:49b12 Homo sapiens cDNA /gb=W28610 /gi=1308558 /; 35978\_at Cluster Incl.

- AF009242:Homo sapiens proline-rich Gla protein 1 (PRGP1) ; 33416\_at Cluster Incl.  
 A1332820:qp96e06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34846\_at Cluster Incl.  
 AF112472:Homo sapiens calcium/calmodulin-dependent protei; 36178\_at Cluster Incl.  
 U23143:Human mitochondrial serine hydroxymethyltransferas; 37372\_at Cluster Incl.
- 5 M81780:Homo sapiens acid sphingomyelinase (SMPD1) gene, c; 38735\_at Cluster Incl.  
 AB011085:Homo sapiens mRNA for KIAA0513 protein, complete; 40173\_at Cluster Incl.  
 N32617:yw95f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 1967\_f\_at U18334  
 /FEATURE=cds /DEFINITION=HSUNOSIIC1 Human nitric oxide synthase; 1292\_at L11329  
 /FEATURE= /DEFINITION=HUMPAC1 Homo sapiens protein tyrosine phosp; 792\_s\_at X52611
- 10 /FEATURE=cds /DEFINITION=HSAP2 Human mRNA for transcription fact; 558\_at M98776  
 /FEATURE=mRNA /DEFINITION=HUMKRT1X Human keratin 1 gene, complete .  
**Metagene 22;** 31911\_at Cluster Incl. AF000989:Homo sapiens thymosin beta 4 Y isoform (TB4Y)  
 mR; 34586\_s\_at Cluster Incl. U51003:Human DLX-2 (Dlx2) mRNA, complete cds /cds=UNKNO;  
 35905\_s\_at Cluster Incl. U34995:Human normal keratinocyte subtraction library m; 40336\_at
- 15 Cluster Incl. J03826:Human adrenodoxin reductase mRNA, complete cds /cd; 40342\_at Cluster Incl.  
 U66077:Human DAZ mRNA, 3UTR /cds=UNKNOWN /gb=U66077 /gi=1; 40376\_at Cluster Incl.  
 X83573:Homo sapiens ARSE gene, complete CDS /cds=(67,1836; 32080\_at Cluster Incl.  
 L11669:Human tetracycline transporter-like protein mRNA, ; 35693\_at Cluster Incl.  
 AF070616:Homo sapiens clone 24772 BDP-1 protein mRNA, par; 36865\_at Cluster Incl.
- 20 AB018302:Homo sapiens mRNA for KIAA0759 protein, partial ; 37912\_at Cluster Incl.  
 X80200:H.sapiens MLN62 mRNA /cds=(85,1497) /gb=X80200 /gi; 38290\_at Cluster Incl.  
 AF037195:Homo sapiens regulator of G protein signaling RG; 39801\_at Cluster Incl.  
 AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3); 37047\_at Cluster Incl.  
 AF002020:Homo sapiens Niemann-Pick C disease protein (NPC; 38069\_at Cluster Incl.
- 25 Z67743:H.sapiens mRNA for CLC-7 chloride channel protein ; 38813\_at Cluster Incl.  
 X75621:Homo sapiens TSC2 mRNA for tuberin /cds=(18,5441) ; 41586\_at Cluster Incl.  
 AF075292:Homo sapiens fibroblast growth factor 18 (FGF18); 1790\_s\_at Cell Division Cycle  
 Protein 2-Related Protein Kinase (Pisslre) ; 720\_at D87673 /FEATURE= /DEFINITION=D87673  
 Homo sapiens mRNA for heat shock tran; 505\_at U43077 /FEATURE= /DEFINITION=HSU43077
- 30 Human CDC37 homolog mRNA, complete ; 100\_g\_at Y08200 /FEATURE=  
 /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab gerany.  
**Metagene 23;** 38174\_at Cluster Incl. X99688:H.sapiens mRNA from TYL gene /cds=(1806,3743)  
 /gb=; 38508\_s\_at Cluster Incl. U89337:Human HLA class III region containing cAMP respo;  
 31902\_at Cluster Incl. AF093774:Homo sapiens type 2 iodothyronine deiodinase mRN; 40405\_at
- 35 Cluster Incl. X70991:H.sapiens MADER mRNA /cds=(0,1427) /gb=X70991 /gi=; 1337\_s\_at X06614  
 /FEATURE=cds /DEFINITION=HSRRA Human mRNA for receptor of retin; 684\_at K02215  
 /FEATURE=mRNA#1 /DEFINITION=HUMANG Human angiotensinogen mRNA, com.  
**Metagene 24;** 31472\_s\_at Cluster Incl. AF098641:Homo sapiens CD44 isoform RC (CD44) mRNA,  
 comp; 37714\_at Cluster Incl. M25667:Human neuronal growth protein 43 (GAP-43) mRNA, co;

- 2036\_s\_at M59040 /FEATURE= /DEFINITION=HUMCD44B Human cell adhesion molecule (CD;  
1126\_s\_at L05424 /FEATURE=cds#5 /DEFINITION=HUMSCG19 Human cell surface glycopro.
- Metagene 25;** 31533\_s\_at Cluster Incl. AF048713:Homo sapiens Kv4.3 potassium channel long spli;  
31739\_at Cluster Incl. AA977513:on60e11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 39430\_at  
5 Cluster Incl. AF082557:Homo sapiens TRF1-interacting ankyrin-related AD; 36200\_at Cluster Incl.  
X69838:H.sapiens mRNA for G9a /cds=(47,3052) /gb=X69838 /; 36640\_at Cluster Incl.  
X66141:H.sapiens mRNA for cardiac ventricular myosin high; 37001\_at Cluster Incl.  
M23254:Human Ca2-activated neutral protease large subunit.
- Metagene 26;** 35442\_at Cluster Incl. AB007958:Homo sapiens mRNA, chromosome 1 specific  
10 transcr; 40401\_at Cluster Incl. AL050069:Homo sapiens mRNA; cDNA DKFZp566A0946 (from  
clon; 31885\_at Cluster Incl. M64572:Human protein tyrosine phosphatase mRNA, complete ;  
36532\_at Cluster Incl. AF039945:Homo sapiens synaptojanin 2B mRNA, partial cds /; 36873\_at  
Cluster Incl. D16532:Human gene for very low density lipoprotein recept; 40454\_at Cluster Incl.  
X87241:H.sapiens mRNA for hFat protein /cds=(186,13958) /; 32184\_at Cluster Incl.
- 15 X61118:Human TTG-2 mRNA for a cysteine rich protein with ; 34795\_at Cluster Incl.  
U84573:Homo sapiens lysyl hydroxylase isoform 2 (PLOD2) m; 36204\_at Cluster Incl.  
Y00815:Human mRNA for LCA-homolog. LAR protein (leukocyte; 37350\_at Cluster Incl.  
AL031177:dJ889N15.2.1 (26S Proteasome subunit p28 (Ankyri; 1458\_at M64572 /FEATURE=  
/DEFINITION=HUMCAP Human protein tyrosine phosphatase m; 837\_s\_at U43944 /FEATURE=  
20 /DEFINITION=HSU43944 Human breast cancer cytosolic NAD.
- Metagene 27;** 35595\_at Cluster Incl. AI557374:PT2.1\_6\_C10.r Homo sapiens cDNA, 3 end  
/clone\_e; 33985\_s\_at Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u;  
33986\_r\_at Cluster Incl. W28616:49b9 Homo sapiens cDNA /gb=W28616 /gi=1308564 /u; 35468\_at  
Cluster Incl. AL050381:Homo sapiens mRNA; cDNA DKFZp586B2023 (from clon; 37869\_at  
25 Cluster Incl. AB029004:Homo sapiens mRNA for KIAA1081 protein, partial ; 39962\_at Cluster Incl.  
U59305:Human ser-thr protein kinase PK428 mRNA, complete ; 34279\_at Cluster Incl.  
AL050141:Homo sapiens mRNA; cDNA DKFZp586O031 (from clone; 38610\_s\_at Cluster Incl.  
X14487:Human gene for acidic (type I) cyokeratin 10 /c; 38701\_at Cluster Incl. AJ000519:Homo  
sapiens mRNA for ubiquitin-conjugating enzy; 40137\_at Cluster Incl. M31724:Human  
30 phosphotyrosyl-protein phosphatase (PTP-1B) ; 40150\_at Cluster Incl. AA205857:zq50e04.r1 Homo  
sapiens cDNA, 5 end /clone=IMAG; 41233\_at Cluster Incl. AB014888:Homo sapiens mRNA for  
MRJ, complete cds /cds=(10; 34891\_at Cluster Incl. AI540958:PEC1.2\_15\_H01.r Homo sapiens  
cDNA, 5 end /clone; 36209\_at Cluster Incl. S78771:NAT=CpG island-associated gene [human,  
mRNA, 1741 ; 36611\_at Cluster Incl. U25849:Human red cell-type low molecular weight acid phos;  
35 36637\_at Cluster Incl. L19605:Homo sapiens 56K autoantigen annexin XI gene mRNA,; 36982\_at  
Cluster Incl. U30888:Human tRNA-guanine transglycosylase mRNA, complete; 39540\_at Cluster  
Incl. AF000561:Homo sapiens TTF-I interacting peptide 21 mRNA, ; 40535\_i\_at Cluster Incl.  
AI254524:qv48f07.x1 Homo sapiens cDNA, 3 end /clone=IM; 40536\_f\_at Cluster Incl.  
AI254524:qv48f07.x1 Homo sapiens cDNA, 3 end /clone=IM; 40959\_at Cluster Incl.

- AB011171:Homo sapiens mRNA for KIAA0599 protein, partial ; 41276\_at Cluster Incl.  
W27641:37d11 Homo sapiens cDNA /gb=W27641 /gi=1307715 /ug; 41537\_r\_at Cluster Incl.  
L31881:Human nuclear factor I-X mRNA, complete cds /cds; 32509\_at Cluster Incl.  
AI307607:tb15h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33172\_at Cluster Incl.
- 5 T75292:yc89b05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 1612\_s\_at X56681  
/FEATURE=mRNA /DEFINITION=HSJUNDR Human junD mRNA ; 1594\_at J05448  
/FEATURE= /DEFINITION=HUMRPOLAA Human RNA polymerase subunit hRPB; 1578\_g\_at  
M23263 /FEATURE= /DEFINITION=HUMARB Human androgen receptor mRNA, comp;  
1460\_g\_at M68941 /FEATURE=mRNA /DEFINITION=HUMPTYPH Human protein-tyrosine  
10 phosph; 693\_g\_at Adenylyl Cyclase-Associated Protein 2 ; 588\_at M31724 /FEATURE=mRNA  
/DEFINITION=HUMPTPBX Human phosphotyrosyl-protein ph; 237\_s\_at M60483  
/FEATURE=mRNA /DEFINITION=HUMPP2AA Human protein phosphatase 2A .  
**Metagene** 28; 31353\_f\_at Cluster Incl. X94553:H.sapiens HFKH4 mRNA for fork head like protein  
; 31399\_at Cluster Incl. AF101441:Homo sapiens bone morphogenetic protein 10 (BMP1; 34093\_at  
15 Cluster Incl. AI829701:wf09d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34154\_at Cluster  
Incl. U62437:Human nicotinic acetylcholine receptor beta2 subun; 34172\_s\_at Cluster Incl.  
M99578:Human lymphocyte surface protein exons 1-5, comp; 32274\_r\_at Cluster Incl.  
AF052148:Homo sapiens clone 24507 mRNA sequence /cds=UN; 32874\_at Cluster Incl.  
M65214:Human (HeLa) helix-loop-helix protein HE47 (E2A) m; 32907\_at Cluster Incl.
- 20 L41147:Homo sapiens 5-HT6 serotonin receptor mRNA, comple; 35911\_r\_at Cluster Incl.  
AJ003147:Homo sapiens complete genomic sequence between; 37095\_r\_at Cluster Incl.  
M84562:Human formyl peptide receptor-like receptor (FPR; 37414\_at Cluster Incl.  
AF037066:Homo sapiens ORCTL2S hypothetical protein (ORCTL; 37442\_at Cluster Incl.  
AL050378:Homo sapiens mRNA; cDNA DKFZp586I1420 (from clon; 39960\_at Cluster Incl.
- 25 AF091086:Homo sapiens clone 640 unknown mRNA, complete se; 40650\_r\_at Cluster Incl.  
X72304:H.sapiens mRNA for corticotrophin releasing fact; 41383\_at Cluster Incl. AJ001403:Homo  
sapiens mRNA for MUC5AC protein (placental); 31804\_f\_at Cluster Incl. X78283:H.sapiens mRNA  
for aryl sulfotransferase (ST1A3); 34221\_at Cluster Incl. D83778:Human mRNA for KIAA0194  
gene, partial cds /cds=(0; 36547\_r\_at Cluster Incl. AA521233:aa79a12.s1 Homo sapiens cDNA, 3  
30 end /clone=IM; 37633\_s\_at Cluster Incl. J04129:Human placental protein 14 (PP14) mRNA,  
complete; 38356\_at Cluster Incl. M19481:Human follistatin gene /cds=(0,953) /gb=M19481 /gi;  
40499\_r\_at Cluster Incl. AF040708:Homo sapiens candidate tumor suppressor gene 2; 32756\_at  
Cluster Incl. AF030249:Homo sapiens putative dienoyl-CoA isomerase (ECH; 33361\_at Cluster Incl.  
AF052149:Homo sapiens clone 24733 mRNA sequence /cds=UNKN; 33826\_at Cluster Incl.
- 35 AL120500:DKFZp761M078\_s1 Homo sapiens cDNA, 3 end /clone; 36173\_r\_at Cluster Incl.  
AF002163:Homo sapiens delta-adaptin mRNA, complete cds ; 38056\_at Cluster Incl.  
D83779:Human mRNA for KIAA0195 gene, complete cds /cds=(2; 38107\_at Cluster Incl.  
U40998:Human retinal protein (HRG4) mRNA, complete cds /c; 38414\_at Cluster Incl.  
U05340:Human p55CDC mRNA, complete cds /cds=(110,1609) /g; 38478\_at Cluster Incl.

- U08377:Human homolog of Drosophila splicing regulator sup; 38741\_at Cluster Incl.
- U70728:Human cytohesin-2 mRNA, complete cds /cds=(158,136; 39919\_at Cluster Incl.
- AI423340:tf36c07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40594\_r\_at Cluster Incl.
- Z22533:H.sapiens ALK-1 mRNA /cds=(282,1793) /gb=Z22533 ; 41255\_at Cluster Incl.
- 5 W28848:52g4 Homo sapiens cDNA /gb=W28848 /gi=1308814 /ug=; 41484\_r\_at Cluster Incl.
- X56681:Human junD mRNA /cds=(174,1217) /gb=X56681 /gi=3; 2091\_at H23429 /FEATURE=  
/DEFINITION=H23429 ym52d12.s1 Soares infant brain 1NIB ; 1998\_i\_at U19599 /FEATURE=  
/DEFINITION=HSU19599 Human (BAX delta) mRNA, complete; 1553\_r\_at U22028  
/FEATURE=expanded\_cds /DEFINITION=HSU22028 Human cytochrome P45; 1346\_at S72043
- 10 /FEATURE=mRNA /DEFINITION=S72043 GIF=growth inhibitory factor [hu; 1277\_at D89016  
/FEATURE= /DEFINITION=D89016 Homo sapiens mRNA for Neuroblastoma; 1131\_at L11285  
/FEATURE= /DEFINITION=HUMMEK2NF Homosapiens ERK activator kinase ; 854\_at S76617  
/FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B; 838\_s\_at U45328  
/FEATURE= /DEFINITION=HSU45328 Human ubiquitin-conjugating enzym; 721\_g\_at D87673
- 15 /FEATURE= /DEFINITION=D87673 Homo sapiens mRNA for heat shock tr; 656\_at L08488  
/FEATURE= /DEFINITION=HUMINOS Human inositol polyphosphate 1-phosp; 240\_at M64231  
/FEATURE=mRNA /DEFINITION=HUMSPERSYN Human spermidine synthase gen.
- Metagene** 29; 31698\_at Cluster Incl. Y08223:H.sapiens MFH-1 gene /cds=(0,1505) /gb=Y08223  
/gi=; 32400\_at Cluster Incl. D14539:Human mRNA for LTG19 /cds=(164,1843) /gb=D14539 /g;  
20 34478\_at Cluster Incl. X79780:H.sapiens YPT3 mRNA /cds=(6,662) /gb=X79780 /gi=76; 35426\_at  
Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 /cds=(0; 35434\_at Cluster  
Incl. L16794:Human transcription factor (MEF2) mRNA, complete c; 35438\_at Cluster Incl.  
X87852:H.sapiens mRNA for SEX gene /cds=(184,5799) /gb=X8; 36733\_at Cluster Incl.  
AI093511:qb08e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41420\_at Cluster Incl.
- 25 AF055033:Homo sapiens clone 24645 insulin-like growth fac; 33806\_at Cluster Incl.  
AF052106:Homo sapiens clone 23781 mRNA sequence /cds=UNKN; 34722\_at Cluster Incl.  
U44385:Human tissue inhibitor of metalloproteinases-2 (TI; 35155\_at Cluster Incl. AC005306:Homo  
sapiens chromosome 19, cosmid R27216 /cds=(; 35242\_at Cluster Incl. X66362:H.sapiens mRNA  
PCTAIRE-3 for serine/threonine prot; 38722\_at Cluster Incl. X15880:Human mRNA for collagen VI
- 30 alpha-1 C-terminal glob; 40873\_at Cluster Incl. D86963:Human mRNA for KIAA0208 gene,  
complete cds /cds=(1; 32209\_at Cluster Incl. AF052151:Homo sapiens clone 24574 mRNA sequence  
/cds=UNKN; 36180\_s\_at Cluster Incl. X75346:H.sapiens mRNA for MAP kinase activated protein ;  
40592\_at Cluster Incl. L13329:Homo sapiens iduronate-2-sulfatase (IDS) gene /cds; 40972\_at  
Cluster Incl. M77198:Human rac protein kinase beta mRNA, complete cds /; 32556\_at Cluster Incl.
- 35 X64044:H.sapiens mmRNA for large subunit of splicing fact; 2076\_s\_at L37361 /FEATURE=  
/DEFINITION=HUMEFL3 Homo sapiens (clone hELK-L) ELK r; 1678\_g\_at M65062 /FEATURE=  
/DEFINITION=HUMIGFBP6 Human insulin-like growth facto; 1601\_s\_at L27559  
/FEATURE=mRNA /DEFINITION=HUMIGFBP04 Human insulin-like growth ; 1330\_at U78876  
/FEATURE= /DEFINITION=HSU78876 Human MEK kinase 3 mRNA, complete ; 918\_at Atp-

- Binding Cassette Protein ; 845\_at U16031 /FEATURE= /DEFINITION=HSU16031 Human transcription factor IL-4 Sta; 625\_at L78833 /FEATURE=cds#4 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vatI gen; 612\_s\_at M19650 /FEATURE= /DEFINITION=HUMCNPDEA Human 2,3 -cyclic nucleotide 3 ; 569\_g\_at M80335 /FEATURE= /DEFINITION=HUMPKACATO
- 5 Homo sapiens protein kinase A c; 242\_at M64571 /FEATURE=mRNA /DEFINITION=HUMMAP4 Human microtubule-associated pro.
- Metagene** 30; 34459\_at Cluster Incl. U50529:Human BRCA2 region, mRNA sequence CG016 /cds=UNKNO; 37794\_at Cluster Incl. AF035281:Homo sapiens clone 23903 mRNA sequence /cds=UNKN; 34256\_at Cluster Incl. AB018356:Homo sapiens mRNA for GM3 synthase, complete
- 10 cds; 34743\_at Cluster Incl. D63481:Human mRNA for KIAA0147 gene, partial cds /cds=(0,; 32800\_at Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, parti; 39896\_at Cluster Incl. AB011149:Homo sapiens mRNA for KIAA0577 protein, complete; 40195\_at Cluster Incl. X14850:Human H2A.X mRNA encoding histone H2A.X /cds=(73,5; 1933\_g\_at U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug resistanc.
- 15 **Metagene** 31; 34644\_at Cluster Incl. AB021288:Homo sapiens mRNA for beta 2-microglobulin, comp; 37497\_at Cluster Incl. L16499:Human orphan homeobox protein (PRH) mRNA, complete; 41405\_at Cluster Incl. AF026692:Homo sapiens frizzled related protein frpHE mRNA; 32675\_at Cluster Incl. D21878:Human mRNA for BST-1, complete cds /cds=(127,1083); 33236\_at Cluster Incl. AF060228:Homo sapiens retinoic acid receptor responder 3 ; 36569\_at Cluster Incl.
- 20 X64559:H.sapiens mRNA for tetranectin /cds=(93,701) /gb=X; 36927\_at Cluster Incl. AB000115:Homo sapiens mRNA expressed in osteoblast, compl; 37641\_at Cluster Incl. D28915:Human gene for hepatitis C-associated microtubular; 37975\_at Cluster Incl. X04011:Human mRNA of X-CGD gene involved in chronic granu; 39409\_at Cluster Incl. M14058:Human complement C1r mRNA, complete cds /cds=(63,2; 39424\_at Cluster Incl. U70321:Human
- 25 herpesvirus entry mediator mRNA, complete cd; 40153\_at Cluster Incl. X57522:H.sapiens RING4 cDNA /cds=(30,2456) /gb=X57522 /gi; 40496\_at Cluster Incl. J04080:Human complement component C1r mRNA, complete cds ; 40766\_at Cluster Incl. U24578:Human RP1 and complement C4B precursor (C4B) genes; 32814\_at Cluster Incl. M24594:Human interferon-inducible 56 Kd protein mRNA, com; 33338\_at Cluster Incl. M97936:Human transcription factor ISGF-3 mRNA
- 30 sequence /c; 33453\_at Cluster Incl. AI400326:tg89c03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35311\_at Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulate; 35367\_at Cluster Incl. AB006780:Homo sapiens mRNA for galectin-3, complete cds /; 35822\_at Cluster Incl. L15702:Human complement factor B mRNA, complete cds /cds=; 36600\_at Cluster Incl. L07633:Homo sapiens (clone 1950.2) interferon-gamma IEF S; 36672\_at Cluster Incl.
- 35 L13977:Human prolylcarboxypeptidase mRNA, complete cds /c; 37014\_at Cluster Incl. M33882:Human p78 protein mRNA, complete cds /cds=(345,233; 38052\_at Cluster Incl. M14539:Human factor XIII subunit a mRNA, 3 end /cds=(0,2; 915\_at M24594 /FEATURE=mRNA /DEFINITION=HUMII56KD Human interferon-inducible 56 .
- Metagene** 32; 33543\_s\_at Cluster Incl. U77718:Human desmosome associated protein pinin mRNA,

- c; 38510\_at Cluster Incl. AL049435:Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone; 39291\_at Cluster Incl. X73874:H.sapiens PHKA 1 mRNA /cds=(161,3832) /gb=X73874 /; 40353\_at Cluster Incl. AL049962:Homo sapiens mRNA; cDNA DKFZp564P0823 (from clone; 34191\_at Cluster Incl. AB002445:Homo sapiens mRNA from chromosome 5q21-22, clone; 35199\_at Cluster
- 5 Incl. AB023199:Homo sapiens mRNA for KIAA0982 protein, complete; 35252\_at Cluster Incl. AB011100:Homo sapiens mRNA for KIAA0528 protein, complete; 35695\_at Cluster Incl. U67615:Human beige protein homolog (chs) mRNA, complete c; 35722\_at Cluster Incl. AL080198:Homo sapiens mRNA; cDNA DKFZp434D222 (from clone; 37928\_at Cluster Incl. AA621555:af53a04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38001\_at Cluster Incl.
- 10 L04569:Homo sapiens (clone hHT-1) L-type voltage-dependen; 39035\_at Cluster Incl. AF006010:Human progesterone induced protein (DD5) mRNA, comp; 39354\_at Cluster Incl. D14662:Human mRNA for KIAA0106 gene, complete cds /cds=(4; 39444\_at Cluster Incl. AF054284:Homo sapiens spliceosomal protein SAP 155 mRNA, ; 39699\_at Cluster Incl. D28476:Human mRNA for KIAA0045 gene, complete cds /cds=(1; 40063\_at Cluster Incl.
- 15 U22897:Homo sapiens nuclear domain 10 protein (ndp52) mRNA; 40102\_at Cluster Incl. AB018315:Homo sapiens mRNA for KIAA0772 protein, complete; 40832\_s\_at Cluster Incl. AL050126:Homo sapiens mRNA; cDNA DKFZp586G011 (from clo; 40839\_at Cluster Incl. AL080177:Homo sapiens mRNA; cDNA DKFZp434K151 (from clone; 40868\_at Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41147\_at Cluster Incl.
- 20 AF038186:Homo sapiens clone 23914 mRNA sequence /cds=UNKN; 32798\_at Cluster Incl. AF043105:Homo sapiens glutathione S-transferase mu 3 (GST; 32835\_at Cluster Incl. AA725102:ai08h05.s1 Homo sapiens cDNA, 3 end /clone=1342; 33447\_at Cluster Incl. X54304:Human mRNA for myosin regulatory light chain /cds=; 34394\_at Cluster Incl. AB018327:Homo sapiens mRNA for KIAA0784 protein, partial ; 34397\_at Cluster Incl.
- 25 AF069250:Homo sapiens okadaic acid-inducible phosphoprote; 34785\_at Cluster Incl. AB028948:Homo sapiens mRNA for KIAA1025 protein, partial ; 34786\_at Cluster Incl. AB018285:Homo sapiens mRNA for KIAA0742 protein, partial ; 34797\_at Cluster Incl. AF014402:Homo sapiens type-2 phosphatidic acid phosphatas; 35317\_at Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial ; 35802\_at Cluster Incl.
- 30 AB023231:Homo sapiens mRNA for KIAA1014 protein, partial ; 37007\_at Cluster Incl. U49188:Human placenta (Diff33) mRNA, complete cds /cds=(1; 38070\_at Cluster Incl. AL080234:Homo sapiens mRNA; cDNA DKFZp586L081 (from clone; 38405\_at Cluster Incl. U25165:Human fragile X mental retardation protein 1 homol; 39897\_at Cluster Incl. N36997:yy39g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 41333\_at Cluster Incl.
- 35 D26069:Human mRNA for KIAA0041 gene, partial cds /cds=(0; 41488\_at Cluster Incl. AC002394:Human Chromosome 16 BAC clone CIT987SK-A-211C6 /; 32597\_at Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488; 1913\_at U47414 /FEATURE= /DEFINITION=HSU47414 Human cyclin G2 mRNA, complete cds; 1420\_s\_at D30655 /FEATURE= /DEFINITION=HUMELF4AII Homo sapiens mRNA for eukaryot; 603\_at M29960



- /FEATURE=mRNA /DEFINITION=HUMTR211 Human steroid receptor (TR2-11); 176\_at U37352  
 /FEATURE= /DEFINITION=HSU37352 Human protein phosphatase 2A B alph.
- Metagene 33;** 36403\_s\_at Cluster Incl. AI434146:ti36g07.x1 Homo sapiens cDNA, 3 end  
 /clone=IM; 37411\_at Cluster Incl. D30758:Human mRNA for KIAA0050 gene, complete cds
- 5 /cds=(1; 38362\_at Cluster Incl. W27545:32c4 Homo sapiens cDNA /gb=W27545 /gi=1307349 /ug=.
- Metagene 34;** 33085\_at Cluster Incl. U64863:Human hPD-1 (hPD-1) mRNA, complete cds  
 /cds=(68,93; 32919\_at Cluster Incl. AC004010:Human BAC clone GS099H08 /cds=(0,1568)  
 /gb=AC004; 36226\_r\_at Cluster Incl. W27611:35b9 Homo sapiens cDNA /gb=W27611 /gi=1307559  
 /u; 32741\_at Cluster Incl. X77723:H.sapiens mRNA for unknown protein of uterine endo;
- 10 39466\_s\_at Cluster Incl. W27995:43e12 Homo sapiens cDNA /gb=W27995 /gi=1308150 /.
- Metagene 35;** 32284\_at Cluster Incl. AF012130:Homo sapiens brachyury variant A (TBX1) mRNA,  
 co; 41736\_g\_at Cluster Incl. AI808958:wf67a09.x1 Homo sapiens cDNA, 3 end /clone=IM;  
 37681\_i\_at Cluster Incl. AB018266:Homo sapiens mRNA for KIAA0723 protein, comple; 39849\_at  
 Cluster Incl. AF043473:Homo sapiens delayed-rectifier K<sup>+</sup> channel alpha .
- 15 **Metagene 36;** 34149\_at Cluster Incl. W28558:48f7 Homo sapiens cDNA /gb=W28558 /gi=1308524  
 /ug=; 34460\_at Cluster Incl. AB014512:Homo sapiens mRNA for KIAA0612 protein, partial ;  
 37772\_at Cluster Incl. AB020711:Homo sapiens mRNA for KIAA0904 protein, partial ; 41026\_f\_at  
 Cluster Incl. U05255:Human glycophorin HeP2 mRNA, partial cds /cds=(0; 33220\_at Cluster Incl.  
 Z11773:Homo sapiens mRNA for SRE-ZBP /cds=(0,1226) /gb=Z1; 33221\_at Cluster Incl.
- 20 U80735:Homo sapiens CAGF28 mRNA, partial cds /cds=(0,2235; 36923\_at Cluster Incl.  
 M98045:Homo sapiens folylpolyglutamate synthetase mRNA, c; 32240\_at Cluster Incl.  
 D31889:Human mRNA for KIAA0072 gene, partial cds /cds=(0; 640\_at L48211 /FEATURE=cds  
 /DEFINITION=HUMAIR Homo Sapiens angiotensin II recept.
- Metagene 37;** 41080\_at Cluster Incl. AI218431:qh24d10.x1 Homo sapiens cDNA, 3 end
- 25 /clone=IMAG; 31860\_at Cluster Incl. X51804:Human PMI gene for a putative receptor protein /cd;  
 32137\_at Cluster Incl. AF029778:Homo sapiens Jagged2 (JAG2) mRNA, complete cds /; 34833\_at  
 Cluster Incl. AL050157:Homo sapiens mRNA; cDNA DKFZp586O0120 (from clon; 41535\_at  
 Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor prot.
- Metagene 38;** 31600\_s\_at Cluster Incl. D38435:Homo sapiens hPMS3 mRNA, partial cds
- 30 /cds=(0,772; 39664\_at Cluster Incl. U28413:Human Cockayne syndrome complementation group A  
 CS; 36088\_at Cluster Incl. AJ006291:Homo sapiens mRNA for leucine rich protein /cds=; 37177\_at  
 Cluster Incl. Y00636:Human mRNA for lymphocyte function associated anti; 37610\_at Cluster Incl.  
 AI765280:wi73a08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38275\_at Cluster Incl.  
 AF054996:Homo sapiens clone 23783 mRNA sequence /cds=UNKN; 39056\_at Cluster Incl.
- 35 X53793:H.sapiens ADE2H1 mRNA showing homologies to SAICAR; 39357\_at Cluster Incl.  
 U72514:Human C2f mRNA, complete cds /cds=(0,720) /gb=U725; 39416\_at Cluster Incl.  
 U90913:Human clone 23665 mRNA sequence /cds=UNKNOWN /gb=U; 40122\_at Cluster Incl.  
 AF037448:Homo sapiens RRM RNA binding protein Gry-rbp (GR; 40789\_at Cluster Incl.  
 U54645:Human adenylate kinase 2B (adk2b) gene, complete c; 41741\_at Cluster Incl.

- U28686:Human putative RNA binding protein RNPL mRNA, comp; 32198\_at Cluster Incl.  
W28979:54e8 Homo sapiens cDNA /gb=W28979 /gi=1308927 /ug=; 34798\_at Cluster Incl.  
Z35491:H.sapiens mRNA for novel glucocorticoid receptor-a; 35353\_at Cluster Incl.  
D11094:Human mRNA for MSS1, complete cds /cds=(66,1367) /; 36193\_at Cluster Incl.
- 5 U52522:Human arfaptin 2, putative target protein of ADP-r; 36652\_at Cluster Incl. J03824:Human uroporphyrinogen III synthase mRNA, complete; 37044\_at Cluster Incl. D49490:Homo sapiens mRNA for protein disulfide isomerase-; 37713\_at Cluster Incl. L07548:Human aminoacylase-1 (ACY1) mRNA, complete cds /cd; 38811\_at Cluster Incl. D82348:Homo sapiens mRNA for 5-aminoimidazole-4-carboxami; 32579\_at Cluster Incl. U29175:Human transcriptional activator
- 10 (BRG1) mRNA, compl; 32584\_at Cluster Incl. D38047:Human mRNA for 26S proteasome subunit p31, complet; 32586\_at Cluster Incl. D86971:Human mRNA for KIAA0217 gene, partial cds /cds=(0,; 1394\_at L25080 /FEATURE= /DEFINITION=HUMRHOAA Homo sapiens GTP-binding protein (.  
**Metagene 39;** 34011\_at Cluster Incl. D83699:Human brain 3UTR of mRNA for neuronal death
- 15 protei; 32691\_s\_at Cluster Incl. D86096:Human DNA for prostaglandin E receptor EP3 subty; 34704\_r\_at Cluster Incl. AA151971:zo30b03.r1 Homo sapiens cDNA, 5 end /clone=IM; 36139\_at Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from clon; 37382\_at Cluster Incl. N25117:yx19c09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39870\_at Cluster Incl. AI377866:te63h04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40212\_at Cluster Incl.
- 20 AI123553:qa49h04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41845\_at Cluster Incl. W29036:55d12 Homo sapiens cDNA /gb=W29036 /gi=1308993 /ug; 1619\_g\_at D21241 /FEATURE=exon#1#3 /DEFINITION=HUMCP4B Human cytochrome P-450 ar; 1567\_at S77812 /FEATURE= /DEFINITION=S77812 flt=vascular endothelial growth fact.  
**Metagene 40;** 31337\_at Cluster Incl. AF036329:Homo sapiens gonadotropin-releasing hormone
- 25 prec; 35511\_at Cluster Incl. AB014559:Homo sapiens mRNA for KIAA0659 protein, partial ; 35484\_at Cluster Incl. U95737:Human Chromosome 16 BAC clone CIT987SK-A-388D4 /cd; 36303\_f\_at Cluster Incl. U35376:Human repressor transcriptional factor (ZNF85) m; 35646\_at Cluster Incl. Z35093:H.sapiens mRNA for SURF-1 /cds=(14,916) /gb=Z35093; 40416\_at Cluster Incl. U04847:Human Ini1 mRNA, complete cds /cds=(69,1226) /gb=U; 40435\_at Cluster Incl.
- 30 J03592:Human ADP/ATP translocase mRNA, 3 end, clone pHAT; 41212\_r\_at Cluster Incl. D26068:Human mRNA for KIAA0038 gene, partial cds /cds=(; 32828\_at Cluster Incl. AF026548:Homo sapiens branched chain alpha-ketoacid dehyd; 33889\_s\_at Cluster Incl. D79985:Human mRNA for KIAA0163 gene, complete cds /cds=; 35343\_at Cluster Incl. M37400:Human cytosolic aspartate aminotransferase mRNA, c; 37723\_at Cluster Incl.
- 35 U47414:Human cyclin G2 mRNA, complete cds /cds=(135,1169); 38081\_at Cluster Incl. J03459:Human leukotriene A-4 hydrolase mRNA, complete cds; 38381\_at Cluster Incl. U32315:Human syntaxin 3 mRNA, complete cds /cds=(38,907) ; 39534\_at Cluster Incl. L77564:Homo sapiens DGS-G mRNA, 3 end /cds=UNKNOWN /gb=L.  
**Metagene 41;** 34931\_at Cluster Incl. AB023157:Homo sapiens mRNA for KIAA0940 protein,

- complete; 37146\_at Cluster Incl. AB007864:Homo sapiens KIAA0404 mRNA, partial cds /cds=(0,; 39637\_at Cluster Incl. U14528:Human sulfate transporter (DTD) mRNA, complete cds; 32069\_at Cluster Incl. AB014515:Homo sapiens mRNA for KIAA0615 protein, complete; 32721\_at Cluster Incl. AA151922:zo30d07.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 34199\_at Cluster Incl.
- 5 AJ131244:Homo sapiens mRNA for Sec24 protein (Sec24A isof; 34737\_at Cluster Incl. AF058718:Homo sapiens putative 13 S Golgi transport compl; 35709\_at Cluster Incl. AF038172:Homo sapiens clone 23923 mRNA sequence /cds=UNKN; 36857\_at Cluster Incl. AF084513:Homo sapiens DNA repair exonuclease (REC1) mRNA,; 36926\_at Cluster Incl. X80692:H.sapiens ERK3 mRNA /cds=(478,2643) /gb=X80692 /gi; 38271\_at Cluster Incl.
- 10 AB006626:Homo sapiens mRNA for KIAA0288 gene, complete cd; 38667\_at Cluster Incl. AA189161:zq45g01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40146\_at Cluster Incl. AL080212:Homo sapiens mRNA; cDNA DKFZp586H0723 (from clon; 41174\_at Cluster Incl. AF012086:Homo sapiens Ran binding protein 2 (RanBP2alpha); 32217\_at Cluster Incl. AF052105:Homo sapiens clone 23965 mRNA sequence /cds=UNKN; 32222\_at Cluster Incl.
- 15 AA152202:zl06a03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33342\_at Cluster Incl. AF039029:Homo sapiens snurportin1 mRNA, complete cds /cds; 33830\_at Cluster Incl. AW026535:wv14f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33896\_at Cluster Incl. U01877:Human p300 protein mRNA, complete cds /cds=(1199,8; 34411\_at Cluster Incl. Y10387:H.sapiens mRNA for PAPS synthetase /cds=(36,1910) ; 35303\_at Cluster Incl.
- 20 U96876:Homo sapiens insulin induced protein 1 (INSIG1) ge; 35838\_at Cluster Incl. U90919:Human clones 23667 and 23775 zinc finger protein m; 35847\_at Cluster Incl. AB028980:Homo sapiens mRNA for KIAA1057 protein, partial ; 37306\_at Cluster Incl. D38549:Human mRNA for KIAA0068 gene, partial cds /cds=(0,; 37735\_at Cluster Incl. U31383:Human G protein gamma-10 subunit mRNA, complete cd; 37737\_at Cluster Incl.
- 25 D25547:Homo sapiens mRNA for PIMT isozyme I, complete cds; 38395\_at Cluster Incl. X61100:Human mRNA for mitochondrial 75 kDa iron sulphur p; 39923\_at Cluster Incl. AI935420:wo84c08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40167\_s\_at Cluster Incl. AF038187:Homo sapiens clone 23714 mRNA sequence /cds=UN; 40612\_at Cluster Incl. AB029040:Homo sapiens mRNA for KIAA1117 protein, partial ; 41790\_at Cluster Incl.
- 30 AL031230:dJ73M23.2 (NAD+-dependent succinic semialdehyde ; 2063\_at L20046 /FEATURE= /DEFINITION=HUMERCC5A Human ERCC5 excision repair prote; 1070\_at M76766 /FEATURE= /DEFINITION=HUMTFIIB Human transcription factor (TFIIB); 706\_at Glucocorticoid Receptor, Beta ; 631\_g\_at L39874 /FEATURE=expanded\_cds /DEFINITION=HUMDODDA Homo sapiens deoxycyt.
- 35 **Metagene 42;** 32954\_at Cluster Incl. U79263:Human clone 23760 mRNA, partial cds /cds=(0,1021) ; 31903\_at Cluster Incl. AB014593:Homo sapiens mRNA for KIAA0693 protein, partial ; 35140\_at Cluster Incl. R59697:yh11b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 36506\_at Cluster Incl. AJ131693:Homo sapiens mRNA for AKAP450 protein /cds=(222,; 38676\_at Cluster Incl. AA059408:zl96e07.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 32150\_at Cluster Incl.

- X82834:H.sapiens mRNA for golgin /cds=(207,6764) /gb=X828; 34387\_at Cluster Incl.  
 D86960:Human mRNA for KIAA0205 gene, complete cds /cds=(2; 36099\_at Cluster Incl.  
 M69040:Human SF2p33 mRNA, complete cds /cds=(124,870) /gb; 36975\_at Cluster Incl.  
 W26659:34d2 Homo sapiens cDNA /gb=W26659 /gi=1307502 /ug=; 37693\_at Cluster Incl.
- 5 L40393:Homo sapiens (clone S171) mRNA, complete cds /cds=; 38473\_at Cluster Incl.  
 M63180:Human threonyl-tRNA synthetase mRNA, complete cds ; 32563\_at Cluster Incl.  
 U51478:Human sodium/potassium-transporting ATPase beta-3 ; 1480\_at L12723 /FEATURE=  
 /DEFINITION=HUMHSP70H Human heat shock protein 70 (hsp7; 1446\_at D00760 /FEATURE=  
 /DEFINITION=HUMPSC3 Human mRNA for proteasome subunit H; 449\_at U66469 /FEATURE=  
 10 /DEFINITION=HSU66469 Human cell growth regulator CGR19 m; 350\_at D28118 /FEATURE=  
 /DEFINITION=HUMDB1 Human mRNA for DB1, complete cds ; 193\_at U21858 /FEATURE=  
 /DEFINITION=HSU21858 Human transcriptional activation fa.
- Metagene 43;** 33091\_at Cluster Incl. AF005220:Homo sapiens transcription factor HOXD13  
 (Hoxd13; 35918\_at Cluster Incl. AB020522:Homo sapiens DLEC1 (deleted in lung and esophage;  
 15 41064\_at Cluster Incl. AL049296:Homo sapiens mRNA; cDNA DKFZp564P013 (from clone;  
 40047\_at Cluster Incl. AF077599:Homo sapiens hypothetical SBBI03 protein mRNA, c; 35328\_at  
 Cluster Incl. AF055023:Homo sapiens clone 24723 mRNA sequence /cds=UNKN; 39543\_at Cluster  
 Incl. AI077476:oz49b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1464\_at S73149  
 /FEATURE=mRNA /DEFINITION=S73149 insulin-like growth factor II {i; 917\_g\_at L18983  
 20 /FEATURE=mRNA /DEFINITION=HUMTYROPHO Homo sapiens tyrosine phosp; 477\_at  
 U51127 /FEATURE= /DEFINITION=HSU51127 Human interferon regulatory factor .
- Metagene 44;** 34649\_at Cluster Incl. M14219:Human chondroitin/dermatan sulfate proteoglycan (P;  
 32324\_at Cluster Incl. X57346:H.sapiens mRNA for HS1 protein /cds=(372,1112) /gb; 38233\_at  
 Cluster Incl. AF093265:Homo sapiens homer-3 mRNA, complete cds /cds=(90; 41662\_at Cluster  
 25 Incl. AL050272:Homo sapiens mRNA; cDNA DKFZp566B183 (from clone; 37611\_at Cluster Incl.  
 AB008822:Homo sapiens gene for osteoclastogenesis inhibit; 37948\_at Cluster Incl. J05682:Human  
 subunit C of V-ATPase (vat C) mRNA, 3 end /; 39733\_at Cluster Incl. AF055001:Homo sapiens  
 clone 24560 unknown mRNA, complete ; 34818\_at Cluster Incl. X96381:H.sapiens erm gene, exon  
 2,3,4,5 (and joined CDS) ; 34857\_at Cluster Incl. Z24724:H.sapiens polyA site DNA  
 30 /cds=UNKNOWN /gb=Z24724 /; 35799\_at Cluster Incl. AL080081:Homo sapiens mRNA; cDNA  
 DKFZp564F1862 (from clon; 38111\_at Cluster Incl. X15998:H.sapiens mRNA for the chondroitin  
 sulphate proteo; 38112\_g\_at Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate  
 prot; 41352\_at Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6.  
**Metagene 45;** 33623\_g\_at Cluster Incl. Z26308:H.sapiens isoform 1 gene for L-type calcium chan;  
 35 34139\_at Cluster Incl. AL049651:Human DNA sequence from clone 753D10 on chromoso;  
 34146\_at Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, part; 34241\_at  
 Cluster Incl. L34357:Homo sapiens GATA-4 mRNA, complete cds /cds=(240,1; 39554\_at Cluster  
 Incl. AI186701:qe82d12.x1 Homo sapiens cDNA, 3 end /clone=IMAG.  
**Metagene 46;** 38148\_at Cluster Incl. D83702:Homo sapiens mRNA for photolyase, complete cds

- /cd; 39219\_at Cluster Incl. U20240:Human C/EBP gamma mRNA, complete cds /cds=(250,702; 41027\_at Cluster Incl. AF078096:Homo sapiens forkhead/winged helix-like transcri; 31897\_at Cluster Incl. U53445:Human ovarian cancer downregulated myosin heavy ch; 33730\_at Cluster Incl. AF095448:Homo sapiens putative G protein-coupled receptor; 36536\_at Cluster Incl.
- 5 AF070614:Homo sapiens clone 24732 unknown mRNA, partial c; 38704\_at Cluster Incl. AB007934:Homo sapiens mRNA for KIAA0465 protein, partial ; 39329\_at Cluster Incl. X15804:Human mRNA for alpha-actinin /cds=(198,2876) /gb=X; 39748\_at Cluster Incl. AL050021:Homo sapiens mRNA; cDNA DKFZp564D016 (from clone; 40785\_g\_at Cluster Incl. Z69030:H.sapiens mRNA for gamma 1 isoform of 61kDa regu; 41137\_at Cluster Incl.
- 10 AB007972:Homo sapiens mRNA, chromosome 1 specific transcr; 34800\_at Cluster Incl. AL039458:DKFZp434N0910\_s1 Homo sapiens cDNA, 3 end /clon; 36143\_at Cluster Incl. U13737:Human cysteine protease CPP32 isoform alpha mRNA, ; 37679\_at Cluster Incl. Y10313:Homo sapiens mRNA IFRD1 (PC4) interferon-related d; 41523\_at Cluster Incl. U59878:Human low-Mr GTP-binding protein (RAB32) mRNA, par; 1638\_at U11732 /FEATURE=
- 15 /DEFINITION=HSU11732 Human ets-like gene (tel) mRNA, co; 1529\_at U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence ; 670\_s\_at L05515 /FEATURE= /DEFINITION=HUMCREBPA Homo sapiens cAMP response eleme; 232\_at M55210 /FEATURE=mRNA#1 /DEFINITION=HUMLB2A26 Human laminin B2 chain gene, .  
**Metagene** 47; 34474\_at Cluster Incl. W28429:49c1 Homo sapiens cDNA /gb=W28429 /gi=1308584
- 20 /ug=; 32107\_at Cluster Incl. AL050173:Homo sapiens mRNA; cDNA DKFZp586F0422 (from clon; 33275\_at Cluster Incl. AB016194:Homo sapiens elk1 oncogene, complete cds /cds=(3; 35992\_at Cluster Incl. AF087036:Homo sapiens musculin mRNA, partial cds /cds=(0; 38618\_at Cluster Incl. AC002073:Human PAC clone DJ515N1 from 22q11.2-q22 /cds=(0; 38651\_at Cluster Incl. U60061:Human FEZ2 mRNA, partial cds /cds=(0,461) /gb=U600; 40422\_at Cluster Incl.
- 25 X16302:Human mRNA for insulin-like growth factor binding ; 33925\_at Cluster Incl. X99076:H.sapiens NRG1 gene, exons 2,3 & 4 (joined CDS) /c; 35828\_at Cluster Incl. D42123:Homo sapiens mRNA for ESP1/CRP2, complete cds /cds; 36950\_at Cluster Incl. X90872:H.sapiens mRNA for gp25L2 protein /cds=(91,735) /g; 40560\_at Cluster Incl. U28049:Human TBX2 (TXB2) mRNA, complete cds /cds=(47,2155; 1741\_s\_at S37730
- 30 /FEATURE=cds /DEFINITION=S37712S4 insulin-like growth factor bi; 996\_at X59065 /FEATURE=exon /DEFINITION=HSFGFEX3 H.sapiens FGF gene, exon 3 ; 941\_at D29012 /FEATURE= /DEFINITION=HUMPSY Human mRNA for proteasome subunit Y, ; 885\_g\_at M59911 /FEATURE= /DEFINITION=HUMINTA3A Human integrin alpha-3 chain mRN. .  
**Metagene** 48; 34128\_at Cluster Incl. AB020337:Homo sapiens mRNA for UDP-Gal-GlcNAc
- 35 beta1,3-gal; 34197\_at Cluster Incl. X80907:H.sapiens mRNA for p85 beta subunit of phosphatidy; 35179\_at Cluster Incl. AB009598:Homo sapiens mRNA for glucuronyltransferase I, c; 36897\_at Cluster Incl. D25217:Human mRNA for KIAA0027 gene, partial cds /cds=(0; 40521\_at Cluster Incl. AL050259:Homo sapiens mRNA; cDNA DKFZp547D0710 (from clon; 39542\_at Cluster Incl. AF059611:Homo sapiens nuclear matrix protein NRP/B (NRPB); 40614\_at Cluster Incl.

- X75342:H.sapiens SHB mRNA /cds=(310,2100) /gb=X75342 /gi=; 1726\_at Dna Polymerase, Epsilon, Catalytic Subunit ; 1724\_at S75174 /FEATURE= /DEFINITION=S75174 E2F-4=transcription factor [human, N; 1271\_g\_at L19067 /FEATURE= /DEFINITION=HUMNFKB65A Human NF-kappa-B transcription; 1202\_g\_at D14889 /FEATURE= /DEFINITION=HUMSGBP
- 5 Human mRNA for small GTP-binding .
- Metagene 49;** 1803\_at X05360 /FEATURE=cds /DEFINITION=HSCDC2 Human CDC2 gene involved in cell ; 434\_at X03473 /FEATURE=cds /DEFINITION=HSHIS10G Human gene for histone H1(0) .
- Metagene 50;** 31389\_at Cluster Incl. U46752:Human phosphotyrosine independent ligand p62B B-cc; 33033\_at Cluster Incl. W26326:29a10 Homo sapiens cDNA /gb=W26326 /gi=1307088 /ug; 34589\_f\_at Cluster Incl. AC002366:Human Xp22 BAC CT-285I15 (from CalTech/Research; 36275\_at Cluster Incl. AB002438:Homo sapiens mRNA from chromosome 5q21-22, clone; 38541\_at Cluster Incl. M12792:Human steroid 21-hydroxylase [P-450(C21)] A pseudo; 31793\_at Cluster Incl. AL036554:DKFZp564J2262\_r1 Homo sapiens cDNA, 5 end /clone; 37204\_at Cluster
- 15 Incl. X67055:H.sapiens mRNA for inter-alpha-trypsin inhibitor h; 37950\_at Cluster Incl. X74496:H.sapiens mRNA for prolyl oligopeptidase /cds=(0,2; 37972\_at Cluster Incl. U75744:Homo sapiens DNase gamma mRNA, complete cds /cds=(; 34333\_at Cluster Incl. AL021707:Human DNA sequence from clone 508I15 on chromoso; 2000\_at U26455 /FEATURE= /DEFINITION=HSU26455 Human phosphatidylinositol 3-kinas; 1370\_at M29696 /FEATURE=
- 20 /DEFINITION=HUMIL7AA Human interleukin-7 receptor (IL-7; 1325\_at U59423 /FEATURE= /DEFINITION=HSU59423 Human Smad1 mRNA, complete cds ; 733\_at Mucin .
- Metagene 51;** 31492\_at Cluster Incl. AB019392:Homo sapiens mRNA of muscle specific gene M9, co; 32454\_at Cluster Incl. AL080215:Homo sapiens mRNA; cDNA DKFZp586J0323 (from clone; 38211\_at Cluster Incl. AL050276:Homo sapiens mRNA; cDNA DKFZp566F123 (from clone;
- 25 39682\_at Cluster Incl. X87159:H.sapiens mRNA for beta subunit of epithelial amil; 41606\_at Cluster Incl. AJ005940:Homo sapiens mRNA for GTP-binding protein /cds=(; 41644\_at Cluster Incl. AB018333:Homo sapiens mRNA for KIAA0790 protein, partial ; 32713\_at Cluster Incl. U51587:Homo sapiens Golgi complex autoantigen golgin-97 m; 33795\_at Cluster Incl. AB006630:Homo sapiens mRNA for KIAA0292 gene, partial cds; 34703\_f\_at Cluster Incl.
- 30 AA151971:zo30b03.r1 Homo sapiens cDNA, 5 end /clone=IM; 39412\_at Cluster Incl. U09825:Human acid finger protein mRNA, complete cds /cds=(; 40428\_i\_at Cluster Incl. AW043812:wy81b07.x1 Homo sapiens cDNA, 3 end /clone=IM; 40765\_at Cluster Incl. D87438:Human mRNA for KIAA0251 gene, partial cds /cds=(0,; 41161\_at Cluster Incl. AB015051:Homo sapiens mRNA for Daxx, complete cds /cds=(1; 32261\_at Cluster Incl.
- 35 AF072810:Homo sapiens transcription factor WSTF mRNA, com; 33371\_s\_at Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, c; 34839\_at Cluster Incl. AB029027:Homo sapiens mRNA for KIAA1104 protein, complete; 34841\_at Cluster Incl. AC002544:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-; 34849\_at Cluster Incl. X91257:H.sapiens mRNA for seryl-tRNA synthetase /cds=(75,; 36186\_at Cluster Incl.

- L37368:Human (clone E5.1) RNA-binding protein mRNA, compl; 32588\_s\_at Cluster Incl.  
 X78992:H.sapiens ERF-2 mRNA /cds=(66,1544) /gb=X78992 /.
- Metagene 52;** 41451\_s\_at Cluster Incl. W28498:50e2 Homo sapiens cDNA /gb=W28498  
 /gi=1308653 /u; 41640\_at Cluster Incl. AL031427:dJ167A19.1 (novel protein) /cds=(122,1042)  
 5 /gb=A; 38000\_at Cluster Incl. S72370:pyruvate carboxylase [human, kidney, mRNA, 4017 nt;  
 38292\_at Cluster Incl. AF093264:Homo sapiens homer-2b mRNA, complete cds /cds=(0; 39752\_at  
 Cluster Incl. AF040704:Homo sapiens putative tumor suppressor protein (; 40124\_at Cluster Incl.  
 Y18418:Homo sapiens mRNA for erythrocyte cytosolic protei; 32151\_at Cluster Incl.  
 X82260:H.sapiens mRNA for RanGTPase activating protein 1 ; 41850\_s\_at Cluster Incl.
- 10 U63825:Human hepatitis delta antigen interacting protei.  
**Metagene 53;** 31684\_at Cluster Incl. M62896:Human lipocortin (LIP) 2 pseudogene mRNA,  
 complete; 36267\_at Cluster Incl. X77909:H.sapiens IKBL mRNA /cds=(68,1213) /gb=X77909 /gi=;  
 40328\_at Cluster Incl. X99268:H.sapiens mRNA for B-HLH DNA binding protein /cds=; 41699\_f\_at  
 Cluster Incl. AL080149:Homo sapiens mRNA; cDNA DKFZp434B094 (from clo; 33292\_at Cluster  
 15 Incl. AL008583:dJ327J16.1 (human ortholog of mouse outer arm Dy; 36507\_at Cluster Incl.  
 D30612:Homo sapiens mRNA for repressor protein, partial c; 38251\_at Cluster Incl.  
 AI127424:qb75b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39369\_at Cluster Incl.  
 AB023152:Homo sapiens mRNA for KIAA0935 protein, partial ; 32202\_at Cluster Incl.  
 U67322:Human HBV associated factor (XAP4) mRNA, complete ; 37700\_at Cluster Incl.
- 20 X92106:H.sapiens mRNA for bleomycin hydrolase /cds=(78,14; 38812\_at Cluster Incl.  
 X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5; 39133\_at Cluster Incl.  
 AI525379:PT1.1\_06\_H01.r Homo sapiens cDNA, 5 end /clone\_ ; 39846\_at Cluster Incl.  
 AF071748:Homo sapiens cathepsin F (CATSF) mRNA, complete ; 39861\_at Cluster Incl.  
 M98343:Homo sapiens amplexin (EMS1) mRNA, complete cds /c; 40253\_at Cluster Incl.
- 25 AJ011123:Homo sapiens mRNA for phosphatidylinositol 4-kin; 41251\_at Cluster Incl.  
 L40410:Homo sapiens thyroid receptor interactor (TRIP3) m; 41530\_at Cluster Incl. D16294:Human  
 mRNA for mitochondrial 3-oxoacyl-CoA thiolas; 32527\_at Cluster Incl. AJ381790:te41h10.x1  
 Homo sapiens cDNA, 3 end /clone=IMAG; 1746\_s\_at Tumor Necrosis Factor Receptor 2 Associated  
 Protein Trap3 ; 1257\_s\_at L42379 /FEATURE=mRNA /DEFINITION=HUMBPGF Homo sapiens  
 30 bone-derived gro; 484\_at U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor  
 coactivator-; 197\_at U29656 /FEATURE= /DEFINITION=HSU29656 Human DR-nm23 mRNA,  
 complete cds ; 198\_g\_at U29656 /FEATURE= /DEFINITION=HSU29656 Human DR-nm23  
 mRNA, complete cds .
- Metagene 54;** 31548\_at Cluster Incl. L13291:Human ADP-ribosylarginine hydrolase mRNA,  
 35 complete; 31690\_at Cluster Incl. U08997:Human glutamate dehydrogenase gene, complete cds /;  
 31927\_s\_at Cluster Incl. D86062:Human mRNA for KNP-Ib, complete cds /cds=(18,731;  
 34170\_s\_at Cluster Incl. U56813:Human polycystwin mRNA, partial cds /cds=(0,1826; 36414\_s\_at  
 Cluster Incl. AF032119:Homo sapiens hCASK (CASK) mRNA, complete cds /; 35886\_at Cluster  
 Incl. AL049758:dJ437M21.3 (novel Src homology domain 3 containi; 37528\_at Cluster Incl.

- U03109:Human aspartyl beta-hydroxylase mRNA, complete cds; 37886\_at Cluster Incl.
- AB015332:Homo sapiens HRIHFB2018 mRNA, partial cds /cds=(; 40737\_at Cluster Incl.
- U13913:Human large-conductance calcium-activated potassiu; 41650\_at Cluster Incl. U63810:Homo sapiens WD40 protein Ciao 1 mRNA, complete cd; 34680\_s\_at Cluster Incl. D14663:Human mRNA
- 5 for KIAA0107 gene, complete cds /cds=; 36470\_s\_at Cluster Incl. U84551:Human dystrobrevin (DTN) gene /cds=(1,2232) /gb=; 39364\_s\_at Cluster Incl. Y18207:Homo sapiens mRNA for protein phosphatase 1 (PPP; 40101\_g\_at Cluster Incl. U72206:Human guanine nucleotide regulatory factor (LFP4; 32146\_s\_at Cluster Incl. L07261:Human alpha adducin mRNA, partial cds including ; 33393\_at Cluster Incl. AJ237946:Homo sapiens mRNA for DEAD Box Protein 5 /cds=(0; 40524\_at
- 10 Cluster Incl. X79510:H.sapiens mRNA for protein-tyrosine-phosphatase D1; 40545\_at Cluster Incl. AB018566:Homo sapiens gene for Proline synthetase associa; 2037\_s\_at M60725 /FEATURE= /DEFINITION=HUMP70S6KB Human p70 ribosomal S6 kinase ; 2018\_at M65188 /FEATURE= /DEFINITION=HUMCX43 Human connexin 43 (GJA1, Cx43) mRNA; 1981\_s\_at X60287 /FEATURE=cds /DEFINITION=HSMAXM H.sapiens max mRNA ; 1986\_at X74594
- 15 /FEATURE=cds /DEFINITION=HSRB2P130 H.sapiens mRNA for Rb2/p130 pr; 1912\_s\_at M74088 /FEATURE= /DEFINITION=HUMFAPAPC Human APC gene mRNA, complete c; 1837\_at Ras-Like Protein Tc21 ; 1838\_g\_at Ras-Like Protein Tc21 ; 1581\_s\_at M27504 /FEATURE= /DEFINITION=HUMTOPIIX Homo sapiens topoisomerase type; 1382\_at M63488 /FEATURE= /DEFINITION=HUMRPA70KD Human replication protein A 70kD; 1320\_at X79510
- 20 /FEATURE=cds /DEFINITION=HSPTPD1 H.sapiens mRNA for protein-tyros; 969\_s\_at X98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin ; 944\_s\_at D49354 /FEATURE= /DEFINITION=HUMHSP70A Human mRNA for enhancer protein ; 704\_at Nuclear Factor 1, A Type ; 476\_s\_at U50079 /FEATURE= /DEFINITION=HSU50079 Human histone deacetylase HD1 mRN; 455\_at U66618 /FEATURE= /DEFINITION=HSU66618 Human SWI/SNF
- 25 complex 60 KDa subuni; 305\_g\_at Guanine Nucleotide Exchange Factor 2 ; 226\_at M33336 /FEATURE= /DEFINITION=HUMCAMPPK Human cAMP-dependent protein kinas.
- Metagene** 55; 38152\_at Cluster Incl. AI632589:wb10h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39612\_at Cluster Incl. AL050061:Homo sapiens mRNA; cDNA DKFZp566J123 (from clone; 39621\_at Cluster Incl. AB007928:Homo sapiens mRNA for KIAA0459 protein, partial
- 30 ; 33698\_at Cluster Incl. AB028975:Homo sapiens mRNA for KIAA1052 protein, complete; 35651\_at Cluster Incl. AF002715:Homo sapiens MAP kinase kinase kinase (MTK1) mRN; 35683\_at Cluster Incl. AB020659:Homo sapiens mRNA for KIAA0852 protein, complete; 35994\_at Cluster Incl. AC002398:Human DNA from chromosome 19-specific cosmid F25; 38273\_at Cluster Incl. AJ006268:Homo sapiens mRNA for putative ATPase, partial /; 38679\_g\_at Cluster Incl.
- 35 AA733050:zg79b05.s1 Homo sapiens cDNA, 3 end /clone=39; 39381\_at Cluster Incl. AF055030:Homo sapiens clone 24538 mRNA sequence /cds=UNKN; 40846\_g\_at Cluster Incl. U10324:Human nuclear factor NF90 mRNA, complete cds /cd; 41146\_at Cluster Incl. J03473:Human poly(ADP-ribose) synthetase mRNA, complete c; 37750\_at Cluster Incl. AF049140:Homo sapiens MMS2 (MMS2) mRNA, complete cds /cds; 38384\_at Cluster Incl.



- X54199:Human mRNA for GARS-AIRS-GART /cds=UNKNOWN /gb=X54; 38728\_at Cluster Incl.  
D86978:Human mRNA for KIAA0225 gene, partial cds /cds=(0,; 38732\_at Cluster Incl.  
X91788:H.sapiens mRNA for Icln protein /cds=(88,801) /gb=; 1698\_g\_at U71087 /FEATURE=  
/DEFINITION=HSU71087 Human MAP kinase kinase MEK5b mR; 1287\_at J03473  
5 /FEATURE=mRNA /DEFINITION=HUMRISDAD Human poly(ADP-ribose) synthe.  
**Metagene** 56; 31375\_at Cluster Incl. W28546:48c8 Homo sapiens cDNA /gb=W28546 /gi=1308494  
/ug=; 31701\_r\_at Cluster Incl. X83412:H.sapiens B1 mRNA for mucin /cds=(0,515) /gb=X83;  
31977\_at Cluster Incl. M92432:Homo sapiens retinal guanylyl cyclase (retGC) mRNA; 34545\_at  
Cluster Incl. AF070587:Homo sapiens clone 24741 mRNA sequence /cds=UNKN; 36375\_at Cluster  
10 Incl. X74614:H.sapiens ODF2 (allele 2) gene for outer dense fib; 33539\_at Cluster Incl.  
W28567:51c2 Homo sapiens cDNA /gb=W28567 /gi=1308722 /ug=; 36230\_at Cluster Incl.  
AI624038:ts25h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40298\_at Cluster Incl.  
AB014603:Homo sapiens mRNA for KIAA0703 protein, complete; 40714\_at Cluster Incl.  
S82198:caldecrin=serum calcium-decreasing factor [human, ; 41095\_at Cluster Incl.  
15 X52221:H.sapiens ERCC2 gene, exons 1 & 2 (partial) /cds=U; 32029\_at Cluster Incl.  
AF017995:Homo sapiens 3-phosphoinositide dependent protei; 32677\_at Cluster Incl.  
AF000979:Homo sapiens testis-specific Basic Protein Y 1 (; 34291\_at Cluster Incl. U07424:Human  
putative tRNA synthetase-like protein mRNA, ; 36051\_s\_at Cluster Incl. X58199:Human mRNA for  
beta adducin /cds=(322,2502) /gb=; 36829\_at Cluster Incl. AF022991:Homo sapiens Rigui (RIGUI)  
20 mRNA, complete cds /c; 37898\_r\_at Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3  
end /clone=IM; 37905\_r\_at Cluster Incl. X66436:H.sapiens hsr1 mRNA (partial) /cds=UNKNOWN  
/gb=X; 37925\_r\_at Cluster Incl. AJ245434:Homo sapiens mRNA for G3a protein (G3a gene, l;  
39766\_r\_at Cluster Incl. AI744294:tr08h04.x1 Homo sapiens cDNA, 3 end /clone=IM; 40160\_at  
Cluster Incl. AL080109:Homo sapiens mRNA; cDNA DKFZp586G1822 (from clon; 32220\_at  
25 Cluster Incl. D63874:Human mRNA for HMG-1, complete cds /cds=(76,723) /; 33828\_at Cluster  
Incl. AF035262:Homo sapiens BAF57 (BAF57) gene, complete cds /c; 34837\_at Cluster Incl.  
AB002374:Human mRNA for KIAA0376 gene, partial cds /cds=(; 35852\_at Cluster Incl.  
AB014558:Homo sapiens mRNA for KIAA0658 protein, partial ; 37379\_at Cluster Incl.  
X81789:H.sapiens mRNA for splicing factor SF3a60 /cds=(56; 39167\_r\_at Cluster Incl.  
30 D83174:Human mRNA for collagen binding protein 2, compl; 39508\_at Cluster Incl.  
AI201607:qb81b03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40265\_s\_at Cluster Incl.  
AI401287:tg92b04.x1 Homo sapiens cDNA, 3 end /clone=IM; 41258\_at Cluster Incl.  
N29665:yw73e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 41532\_at Cluster Incl.  
Y09723:H.sapiens mRNA for Miz-1 protein /cds=(126,2537) /; 41561\_s\_at Cluster Incl.  
35 AI651368:wb05d07.x1 Homo sapiens cDNA, 3 end /clone=IM; 41825\_at Cluster Incl. W26652:34c6  
Homo sapiens cDNA /gb=W26652 /gi=1307495 /ug=; 32540\_at Cluster Incl. AI762547:wh92e05.x1  
Homo sapiens cDNA, 3 end /clone=IMAG; 1524\_at U46194 /FEATURE=  
/DEFINITION=HSU46194 Human renal cell carcinoma antigen; 1047\_s\_at U37055  
/FEATURE=mRNA /DEFINITION=HSU37055 Human hepatocyte growth fact; 358\_at AF000545

- /FEATURE=cds /DEFINITION=HSAF000545 Homo sapiens putative purine; 315\_at D45132  
 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens mRNA for zinc-finger D.  
**Metagene 57**; 32016\_at Cluster Incl. AL050256:Novel human gene mapping to chromosome 22  
 /cds=(1; 35054\_at Cluster Incl. AF035278:Homo sapiens clone 23676 mRNA sequence  
 5 /cds=UNKN; 33471\_g\_at Cluster Incl. AF052177:Homo sapiens clone 24510 mRNA sequence  
 /cds=UN; 38880\_at Cluster Incl. AB011168:Homo sapiens mRNA for KIAA0596 protein, partial ;  
 39232\_at Cluster Incl. U09284:Human PINCH protein mRNA, complete cds /cds=(119,1;  
 40290\_f\_at Cluster Incl. L13972:Homo sapiens beta-galactoside alpha-2,3-sialyltr; 40291\_r\_at  
 Cluster Incl. L13972:Homo sapiens beta-galactoside alpha-2,3-sialyltr; 41113\_at Cluster Incl.  
 10 AI871396:wl81f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 31858\_at Cluster Incl.  
 X07315:Human gene for PP15 (placental protein 15) /cds=(9; 33303\_at Cluster Incl.  
 N21470:yx57e11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 33329\_at Cluster Incl.  
 X92857:H.sapiens mRNA for NFI/CAAT-binding transcription ; 35160\_at Cluster Incl.  
 AF064491:Homo sapiens LIM homeobox protein cofactor (CLIM; 36841\_at Cluster Incl.  
 15 AA811338:ob81g05.s1 Homo sapiens cDNA /clone=IMAGE-133781; 40149\_at Cluster Incl.  
 AL049924:Homo sapiens mRNA; cDNA DKFZp547G1110 (from clon; 32811\_at Cluster Incl.  
 X98507:H.sapiens mRNA for myosin-I beta /cds=(65,3151) /g; 35812\_at Cluster Incl.  
 AJ133769:Homo sapiens mRNA for nuclear transport receptor; 36210\_g\_at Cluster Incl.  
 S78771:NAT=CpG island-associated gene [human, mRNA, 174; 39202\_at Cluster Incl.  
 20 W26403:29b4 Homo sapiens cDNA /gb=W26403 /gi=1307102 /ug=; 41344\_s\_at Cluster Incl.  
 M96684:H.sapiens Pur (pur-alpha) mRNA, complete cds /cd; 1316\_at X55005 /FEATURE=mRNA  
 /DEFINITION=HSCERBAR Homo sapiens mRNA for thyroid ; 1089\_i\_at M64936 /FEATURE=  
 /DEFINITION=HUMRIRT Homo sapiens retinoic acid-induci; 551\_at U01877 /FEATURE=  
 /DEFINITION=HSU01877 Human p300 protein mRNA, complete c; 440\_at X12492  
 25 /FEATURE=cds /DEFINITION=HSCTF1 Human mRNA for CAAT-box binding tr.  
**Metagene 58**; 35961\_at Cluster Incl. AL049390:Homo sapiens mRNA; cDNA DKFZp586O1318  
 (from clon; 36227\_at Cluster Incl. AF043129:untitled /cds=(0,1379) /gb=AF043129 /gi=3978161 ;  
 36280\_at Cluster Incl. U26174:Human pre-granzyme 3 mRNA, complete cds /cds=(40,8; 37416\_at  
 Cluster Incl. Z35227:H.sapiens TTF mRNA for small G protein /cds=(579,1; 37479\_at Cluster Incl.  
 30 M54992:Human B cell differentiation antigen mRNA, complet; 40364\_at Cluster Incl.  
 U83460:Human high-affinity copper uptake protein (hCTR1) ; 40699\_at Cluster Incl.  
 M12824:Human T-cell differentiation antigen Leu-2/T8 mRNA; 40738\_at Cluster Incl.  
 M16336:Human T-cell surface antigen CD2 (T11) mRNA, compl; 35698\_at Cluster Incl.  
 Y00318:Human mRNA for complement control protein factor I; 36878\_f\_at Cluster Incl.  
 35 M60028:Human MHC class II HLA-DQ-beta (DQB1,DQw9), comp; 41764\_at Cluster Incl.  
 AA976838:oq35c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 34342\_s\_at Cluster Incl.  
 AF052124:Homo sapiens clone 23810 osteopontin mRNA, com; 34362\_at Cluster Incl.  
 M55531:Human glucose transport-like 5 (GLUT5) mRNA, compl; 35260\_at Cluster Incl.  
 AB020674:Homo sapiens mRNA for KIAA0867 protein, complete; 33168\_at Cluster Incl.

- H24861:yl42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 2092\_s\_at J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA, complete; 1403\_s\_at M21121 /FEATURE= /DEFINITION=HUMTCSM Human T cell-specific protein (RA; 964\_at X95715 /FEATURE=cds /DEFINITION=HSARAPROT H.sapiens mRNA for anthracyclin; 608\_at M12529
- 5 /FEATURE=mRNA /DEFINITION=HUMAPOE Human apolipoprotein E mRNA, com.  
**Metagene 59;** 37793\_r\_at Cluster Incl. AF034956:Homo sapiens RAD51D mRNA, complete cds /cds=(1; 39304\_g\_at Cluster Incl. Y14153:Homo sapiens mRNA for beta-transducin repeat con; 41624\_r\_at Cluster Incl. AA932443:oo75b11.s1 Homo sapiens cDNA, 3 end /clone=IM; 35686\_s\_at Cluster Incl. Z24459:H.sapiens MTCP1 gene, exons 2A to 7 (and joined ; 36000\_at Cluster Incl.
- 10 X98054:H.sapiens mRNA for G13 protein /cds=(33,2144) /gb=; 36516\_at Cluster Incl. AL080143:Homo sapiens mRNA; cDNA DKFZp434N043 (from clone; 38307\_at Cluster Incl. AB011179:Homo sapiens mRNA for KIAA0607 protein, partial ; 40058\_s\_at Cluster Incl. AI341656:qq95e10.x1 Homo sapiens cDNA, 3 end /clone=IM; 40466\_at Cluster Incl. Z74792:H.sapiens mRNA for CCAAT transcription binding fac; 40490\_at Cluster Incl.
- 15 U41387:Human Gu protein mRNA, partial cds /cds=(0,2405) /; 36168\_at Cluster Incl. X66945:H.sapiens N-sam mRNA for fibroblast growth factor ; 38027\_at Cluster Incl. X53742:H.sapiens mRNA for fibulin-1 B /cds=(10,1815) /gb=; 41597\_s\_at Cluster Incl. AF047442:Homo sapiens vesicle trafficking protein sec22; 1910\_s\_at M14745 /FEATURE=cds /DEFINITION=HUMBCL2C Human bcl-2 mRNA .
- 20 **Metagene 60;** 39683\_at Cluster Incl. U35340:Human beta B1-crystallin mRNA, complete cds /cds=(; 35715\_at Cluster Incl. AL080071:Homo sapiens mRNA; cDNA DKFZp564M082 (from clone; 36916\_at Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2; 37216\_at Cluster Incl. AB023180:Homo sapiens mRNA for KIAA0963 protein, complete; 38333\_at Cluster Incl. Y11731:H.sapiens mRNA for DNA glycosylase /cds=(338,1375); 38996\_at Cluster
- 25 Incl. U15655:Human ets domain protein ERF mRNA, complete cds /c; 35851\_g\_at Cluster Incl. AI950382:wp10g06.x1 Homo sapiens cDNA, 3 end /clone=IM; 815\_at U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok (D; 754\_s\_at D87002 /FEATURE=cds#1 /DEFINITION=D87002 Homo sapiens immunoglobulin la; 544\_at S76638 /FEATURE= /DEFINITION=S76638 p50-NF-kappa B homolog [human, periph; 136\_at U65402
- 30 /FEATURE=cds /DEFINITION=HSU65402 Human seven transmembrane G-coup.  
**Metagene 61;** 41004\_at Cluster Incl. U43431:Human DNA topoisomerase III mRNA, complete cds /cd; 38675\_at Cluster Incl. AI087268:oz77e01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37767\_at Cluster Incl. L12392:Homo sapiens Huntingtons Disease (HD) mRNA, comple; 40547\_at Cluster Incl. AI688516:wc90b03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 543\_g\_at S74445
- 35 /FEATURE= /DEFINITION=S74445 cellular retinoic acid-binding prot.  
**Metagene 62;** 39082\_at Cluster Incl. Y00097:Human mRNA for protein p68 /cds=(100,2121) /gb=Y00; 32230\_at Cluster Incl. U39067:Homo sapiens translation initiation factor eIF3 p3; 40951\_at Cluster Incl. AL049250:Homo sapiens mRNA; cDNA DKFZp564D113 (from clone; 41800\_s\_at Cluster Incl. U46571:Human tetratricopeptide repeat protein (tpr2) mR; 960\_g\_at

- Guanine Nucleotide-Binding Protein G25k ; 223\_at S81003 /FEATURE= /DEFINITION=S81003 L-UBC=ubiquitin conjugating enzyme [h.
- Metagene 63;** 32991\_f\_at Cluster Incl. M86933:Human amelogenin (AMELY) mRNA, complete cds /cds; 38154\_at Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence
- 5 /cds=UNKN; 40020\_at Cluster Incl. AB011536:Homo sapiens mRNA for MEGF2, partial cds /cds=(0; 33249\_at Cluster Incl. M16801:Human mineralocorticoid receptor mRNA (hMR), compl; 37588\_s\_at Cluster Incl. U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 comple; 39050\_at Cluster Incl. AF026029:Homo sapiens poly(A) binding protein II (PABP2) ; 33908\_at Cluster Incl. X04366:Human mRNA for calcium activated neutral protease ; 38480\_s\_at Cluster Incl.
- 10 U66867:Human ubiquitin conjugating enzyme 9 (hUBC9) mRNA; 39190\_s\_at Cluster Incl. AC002126:Homo sapiens DNA from chromosome 19-cosmids R3; 40542\_at Cluster Incl. AI793265:oo49c07.y5 Homo sapiens cDNA, 5 end /clone=IMAG; 633\_s\_at L40386 /FEATURE=mRNA /DEFINITION=HUMDP2M Human DP-2 mRNA, complete cds ; 252\_at L42324 /FEATURE=cds /DEFINITION=HUMFRCG Homo sapiens (clone GPCR W) G pro.
- 15 **Metagene 64;** 38860\_at Cluster Incl. U66346:Homo sapiens cAMP phosphodiesterase (PDE4C) mRNA, ; 39582\_at Cluster Incl. AL050166:Homo sapiens mRNA; cDNA DKFZp586D1122 (from clon; 35164\_at Cluster Incl. AF084481:Homo sapiens transmembrane protein (WFS1) mRNA, ; 35710\_s\_at Cluster Incl. U95006:Human D9 splice variant A mRNA, complete cds /cd; 36523\_at Cluster Incl. L06133:Human putative Cu<sup>++</sup>-transporting P-type ATPase mRNA; 38627\_at Cluster
- 20 Incl. M95585:Human hepatic leukemia factor (HLF) mRNA, complete; 39441\_at Cluster Incl. Y11395:H.sapiens mRNA for p40 /cds=(104,1303) /gb=Y11395 ; 40052\_at Cluster Incl. X82206:H.sapiens mRNA for alpha-centractin /cds=(66,1196); 40447\_at Cluster Incl. D87436:Human mRNA for KIAA0249 gene, complete cds /cds=(2; 40816\_at Cluster Incl. L07758:Human IEF SSP 9502 mRNA, complete cds /cds=(87,159; 34338\_at Cluster Incl.
- 25 D49738:Human cytoskeleton associated protein (CG22) mRNA,; 34348\_at Cluster Incl. U78095:Homo sapiens placental bikunin mRNA, complete cds ; 35318\_at Cluster Incl. AB007944:Homo sapiens mRNA for KIAA0475 protein, complete; 36667\_at Cluster Incl. U47025:Human fetal brain glycogen phosphorylase B mRNA, c; 37293\_at Cluster Incl. D43948:Human mRNA for KIAA0097 gene, complete cds /cds=(4; 37362\_at Cluster Incl.
- 30 X54871:H.sapiens mRNA for ras-related protein Rab5b /cds=; 38842\_at Cluster Incl. AB023206:Homo sapiens mRNA for KIAA0989 protein, partial ; 743\_at D50370 /FEATURE= /DEFINITION=D50370 Homo sapiens mRNA for nucleosome asse.
- Metagene 65;** 32378\_at Cluster Incl. M26252:Human TCB gene encoding cytosolic thyroid hormone-; 38945\_at Cluster Incl. X78710:H.sapiens MTF-1 mRNA for metal-regulatory transcri; 40332\_at Cluster Incl. AF109134:Homo sapiens 7-60 mRNA, complete cds /cds=(205,2; 34707\_at Cluster Incl. U91543:Homo sapiens zinc-finger helicase (hZFH) mRNA, com; 38998\_g\_at Cluster Incl. X96924:H.sapiens gene encoding mitochondrial citrate tr; 39722\_at Cluster Incl. AF044209:Homo sapiens nuclear receptor co-repressor N-CoR; 40143\_at Cluster Incl. D50930:Human mRNA for KIAA0140 gene, complete cds /cds=(2; 40147\_at Cluster Incl.

- U18009:Human chromosome 17q21 mRNA clone LF113 /cds=(0,93; 40514\_at Cluster Incl.  
 AF091085:Homo sapiens clone 638 unknown mRNA, complete se; 40791\_at Cluster Incl.  
 X63564:H.sapiens mRNA for RNA polymerase II largest subun; 41724\_at Cluster Incl.  
 X81817:H.sapiens BAP31 mRNA /cds=(73,813) /gb=X81817 /gi=; 34874\_at Cluster Incl.
- 5 AJ004832:Homo sapiens mRNA for neuropathy target esterase; 38483\_at Cluster Incl.  
 AJ011916:Homo sapiens mRNA for hypothetical protein /cds=; 38789\_at Cluster Incl.  
 L12711:Homo sapiens transketolase (tk) mRNA, complete cds; 38790\_at Cluster Incl. L25879:Homo sapiens p53/HEH epoxide hydrolase (EPHX) mRNA; 39112\_at Cluster Incl. Y07661:H.sapiens USF2 gene /cds=(0,1040) /gb=Y07661 /gi=1; 39155\_at Cluster Incl. D67025:Homo sapiens mRNA
- 10 for proteasome subunit p58, comp; 39825\_at Cluster Incl. L77567:Homo sapiens mitochondrial citrate transport prote; 39833\_at Cluster Incl. R54564:yg81b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 1268\_at M58028 /FEATURE=mRNA /DEFINITION=HUMUBIQAA Human ubiquitin-activating en; 1170\_at Colony-Stimulating Factor 1, Macrophage, Alt. Splice 3 ; 605\_at L78833 /FEATURE=exon#36 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vat1 g.
- 15 **Metagene** 66; 35531\_at Cluster Incl. AB007933:Homo sapiens mRNA for KIAA0464 protein, complete; 37136\_at Cluster Incl. AB000520:Homo sapiens mRNA for APS, complete cds /cds=(12; 33733\_at Cluster Incl. AF093771:Homo sapiens mitoxantrone resistance protein 1 m; 34260\_at Cluster Incl. AB014583:Homo sapiens mRNA for KIAA0683 protein, complete; 38641\_at Cluster Incl. AJ133115:Homo sapiens mRNA for TSC-22-like protein /cds=(; 39332\_at Cluster Incl.
- 20 AF035316:Homo sapiens clone 23678 mRNA, partial cds /cds=; 40444\_s\_at Cluster Incl. AB002382:Human mRNA for KIAA0384 gene, complete cds /cd; 36583\_at Cluster Incl. U53225:Human sorting nexin 1 (SNX1) mRNA, complete cds /c; 37005\_at Cluster Incl. D28124:Human mRNA for unknown product, complete cds /cds=; 37400\_at Cluster Incl. J03068:Human DNF1552 (lung) mRNA, complete cds /cds=(292,; 37744\_r\_at Cluster Incl.
- 25 U60062:Human FEZ1-T mRNA, alternatively spliced form, c; 38398\_at Cluster Incl. AB002356:Human mRNA for KIAA0358 gene, complete cds /cds=; 1587\_at M38258 /FEATURE= /DEFINITION=HUMRARGA Human retinoic acid receptor gamma; 1401\_g\_at M13207 /FEATURE=expanded\_cds /DEFINITION=HUMCSFGMA Human granulocyte-m; 1019\_g\_at U81787 /FEATURE= /DEFINITION=HSU81787 Human Wnt10B mRNA, complete cds ; 858\_at
- 30 S90469 /FEATURE= /DEFINITION=S90469 cytochrome P450 reductase [human, pla; 679\_at J04990 /FEATURE=cds /DEFINITION=HUMCAPG Human cathepsin G gene, complete ; 495\_at U31628 /FEATURE= /DEFINITION=HSU31628 Human interleukin-15 receptor alpha.
- Metagene** 67; 34491\_at Cluster Incl. AJ225089:Homo sapiens mRNA for 2-5 oligoadenylate synthe; 35633\_at Cluster Incl. D87457:Human mRNA for KIAA0281 gene, complete cds /cds=(1; 37545\_at
- 35 Cluster Incl. W22110:64F11 Homo sapiens cDNA /clone=(not-directional) /; 37630\_at Cluster Incl. AL049176:Human DNA sequence from clone 141H5 on chromosom; 36680\_at Cluster Incl. M24895:Homo sapiens alpha-amylase mRNA, complete cds /cds; 37695\_at Cluster Incl. D79983:Human mRNA for KIAA0161 gene, complete cds /cds=(3; 1708\_at U07620 /FEATURE= /DEFINITION=HSU07620 Human MAP kinase mRNA, complete cd; 1389\_at J03779

- /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblast; 753\_at D86425 /FEATURE= /DEFINITION=D86425 Homo sapiens mRNA for osteonidogen, c; 160029\_at X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase.
- Metagene 68;** 41087\_at Cluster Incl. AC004774:Homo sapiens BAC clone RG300E22 from 7q21-q31.1 ; 37560\_at Cluster Incl. AL050143:Homo sapiens mRNA; cDNA DKFZp586B2420 (from clon; 32154\_at Cluster Incl. M36711:Human sequence-specific DNA-binding protein (AP-2); 1177\_at Dna-Binding Protein Ap-2, Alt. Splice 3 ; 235\_at M59488 /FEATURE=mRNA /DEFINITION=HUMS100B3 Human S100 protein beta-subuni.
- Metagene 69;** 31504\_at Cluster Incl. M64098:Human high density lipoprotein binding protein (HB; 39258\_at Cluster Incl. AI627877:ty20b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41670\_at Cluster Incl. R38263:yc92c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 34255\_at Cluster Incl. AF059202:Homo sapiens ACAT related gene product 1 mRNA, c; 35979\_at Cluster Incl. AF081287:Homo sapiens serine phosphatase FCP1a (FCP1) mRN; 38612\_at Cluster Incl. M69023:Human globin gene /cds=UNKNOWN /gb=M69023 /gi=1831; 39003\_at Cluster Incl. Z50022:H.sapiens mRNA for surface glycoprotein /cds=(93,6; 39064\_at Cluster Incl. L38928:Homo sapiens 5,10-methenyltetrahydrofolate synthet; 40087\_at Cluster Incl. AF020202:Homo sapiens Munc13 mRNA, complete cds /cds=(224; 40090\_at Cluster Incl. AI797997:wh80b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40134\_at Cluster Incl. AF047436:Homo sapiens F1Fo-ATPase synthase f subunit mRNA; 40882\_at Cluster Incl. Y09616:H.sapiens mRNA for putative carboxylesterase /cds=; 41223\_at Cluster Incl. M22760:Homo sapiens nuclear-encoded mitochondrial cytochr; 33424\_at Cluster Incl. Y00281:Human mRNA for ribophorin I /cds=(137,1960) /gb=Y0; 35322\_at Cluster Incl. D50922:Human mRNA for KIAA0132 gene, complete cds /cds=(1; 36189\_at Cluster Incl. U10323:Human nuclear factor NF45 mRNA, complete cds /cds=; 36951\_at Cluster Incl. U39400:Human NOF1 mRNA, complete cds /cds=(13,513) /gb=U3; 37361\_at Cluster Incl. AF010187:Homo sapiens FGF-1 intracellular binding protein; 37730\_at Cluster Incl. U22055:Human 100 kDa coactivator mRNA, complete cds /cds=; 37751\_at Cluster Incl. D87444:Human mRNA for KIAA0255 gene, complete cds /cds=(3.
- Metagene 70;** 31532\_at Cluster Incl. U43292:Human MDS1B (MDS1) mRNA, complete cds /cds=(307,81; 33683\_at Cluster Incl. D50525:Human mRNA for TI-227H /cds=UNKNOWN /gb=D50525 /gi; 41046\_s\_at Cluster Incl. X95808:H.sapiens mRNA for protein encoded by a candidat; 41604\_at Cluster Incl. U79297:Human clone 23589 mRNA sequence /cds=UNKNOWN /gb=U; 32623\_at Cluster Incl. AJ225028:Homo sapiens mRNA for GABA-B R1a receptor /cds=(; 34276\_at Cluster Incl. AB023197:Homo sapiens mRNA for KIAA0980 protein, partial ; 37592\_at Cluster Incl. J05401:Human sarcomeric mitochondrial creatine kinase (Mt; 38664\_at Cluster Incl. AB009285:Homo sapiens BCNT mRNA, complete cds /cds=(109,1; 40057\_at Cluster Incl. U94777:Human muscle glycogen phosphorylase (PYGM) gene, 5; 40779\_at Cluster Incl. U59919:Human Smg GDS-associated protein SMAP mRNA, comple; 33880\_at Cluster Incl. D89053:Homo sapiens mRNA for Acyl-CoA synthetase 3, compl; 33881\_at Cluster Incl. AA977580:on61b02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 37683\_at Cluster Incl.

- D80012:Human mRNA for KIAA0190 gene, partial cds /cds=(0,; 39123\_s\_at Cluster Incl.  
 X89066:H.sapiens mRNA for TRPC1 protein /cds=(137,2416); 1229\_at U78556 /FEATURE=  
 /DEFINITION=HSU78556 Human cisplatin resistance associa.
- Metagene 71;** 32468\_f\_at Cluster Incl. D90278:Human CGM1b mRNA for CD66d /cds=(61,594)  
 5 /gb=D90; 32265\_at Cluster Incl. D85245:Homo sapiens mRNA for TR3beta, complete cds /cds=(;  
 39596\_at Cluster Incl. U05012:Human receptor tyrosine kinase TrkC (NTRK3) mRNA, ; 33740\_at  
 Cluster Incl. AF023268:Homo sapiens clk2 kinase (CLK2), propin1, cotel1,; 38658\_at Cluster Incl.  
 X81636:H.sapiens clathrin light chain a gene /cds=UNKNOWN; 39164\_at Cluster Incl.  
 AF099149:Homo sapiens TRIAD1 type I mRNA, complete cds /c; 1059\_at S76475 /FEATURE=  
 10 /DEFINITION=S76475 trkC [human, brain, mRNA, 2715 nt] ; 1060\_g\_at S76475 /FEATURE=  
 /DEFINITION=S76475 trkC [human, brain, mRNA, 2715 nt].
- Metagene 72;** 32901\_s\_at Cluster Incl. AC005192:Homo sapiens BAC clone RG163K11 from 7q31  
 /cds; 32134\_at Cluster Incl. AL050162:Homo sapiens mRNA; cDNA DKFZp586B2022 (from clon;  
 33240\_at Cluster Incl. AB029018:Homo sapiens mRNA for KIAA1095 protein, partial ; 36535\_at  
 15 Cluster Incl. U04209:Human associated microfibrillar protein mRNA, comp; 36814\_at Cluster Incl.  
 AB029032:Homo sapiens mRNA for KIAA1109 protein, partial ; 38690\_at Cluster Incl.  
 AL080097:Homo sapiens mRNA; cDNA DKFZp564P0462 (from clon; 39072\_at Cluster Incl.  
 L07648:Human MXII mRNA, complete cds /cds=(208,894) /gb=L; 39790\_at Cluster Incl.  
 M23115:Homo sapiens calcium-ATPase (HK2) mRNA, complete c; 39797\_at Cluster Incl.  
 20 AB002347:Human mRNA for KIAA0349 gene, partial cds /cds=(; 40140\_at Cluster Incl.  
 D76444:Homo sapiens hkf-1 mRNA, complete cds /cds=(922,29; 41191\_at Cluster Incl.  
 AB023209:Homo sapiens mRNA for KIAA0992 protein, partial ; 32780\_at Cluster Incl.  
 AB018271:Homo sapiens mRNA for KIAA0728 protein, partial ; 32827\_at Cluster Incl.  
 AI365215;qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32847\_at Cluster Incl.  
 25 U48959:Homo sapiens myosin light chain kinase (MLCK) mRNA; 33378\_at Cluster Incl.  
 AB019494:Homo sapiens IDN3 mRNA, partial cds /cds=(706,75; 33442\_at Cluster Incl.  
 AB002365:Human mRNA for KIAA0367 gene, partial cds /cds=(; 33865\_at Cluster Incl.  
 AA127624:zk89b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 35255\_at Cluster Incl.  
 AF098799:Homo sapiens RanBP7/importin 7 mRNA, complete cd; 35279\_at Cluster Incl.  
 30 U33821:Human tax1-binding protein TXBP151 mRNA, complete ; 36620\_at Cluster Incl.  
 X02317:Human mRNA for Cu/Zn superoxide dismutase (SOD) /c; 36627\_at Cluster Incl.  
 X86693:H.sapiens mRNA for hevin like protein /cds=(322,23; 37698\_at Cluster Incl.  
 X97335:H.sapiens mRNA for kinase A anchor protein /cds=(1; 38047\_at Cluster Incl. D84109:Homo  
 sapiens mRNA for RBP-MS/type 3, complete cds ; 38120\_at Cluster Incl. U50928:Human autosomal  
 35 dominant polycystic kidney disease; 38375\_at Cluster Incl. AF112219:Homo sapiens esterase D  
 mRNA, complete cds /cds=; 38443\_at Cluster Incl. U79291:Human clone 23721 mRNA sequence  
 /cds=UNKNOWN /gb=U; 38768\_at Cluster Incl. X96752:H.sapiens mRNA for L-3-hydroxyacyl-  
 CoA dehydrogenase; 39163\_at Cluster Incl. W27233:24b7 Homo sapiens cDNA /gb=W27233  
 /gi=1306749 /ug=; 39838\_at Cluster Incl. AB014522:Homo sapiens mRNA for KIAA0622 protein,

- partial ; 39852\_at Cluster Incl. AB011182:Homo sapiens mRNA for KIAA0610 protein, partial ;  
 40610\_at Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAG; 41000\_at  
 Cluster Incl. U68723:Human checkpoint suppressor 1 mRNA, complete cds /; 41277\_at Cluster Incl.  
 AW021542:df25a06.y1 Homo sapiens cDNA, 5 end /clone=IMAG; 41289\_at Cluster Incl.
- 5 AA126505:zn86a09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41795\_at Cluster Incl.  
 X17576:Human melanoma mRNA for nck protein, showing homol; 41815\_at Cluster Incl.  
 AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone; 32542\_at Cluster Incl.  
 AF063002:Homo sapiens LIM protein SLIMMER mRNA, complete ; 1725\_s\_at Oncogene E6-Ap,  
 Papillomavirus ; 1327\_s\_at U67156 /FEATURE= /DEFINITION=HSU67156 Human mitogen-  
 10 activated kinase k; 1278\_at Tyrosine Kinase, Receptor Axl, Alt. Splice 2 ; 654\_at L07648  
 /FEATURE= /DEFINITION=HUMMX11A Human MX11 mRNA, complete cds ; 409\_at X56468  
 /FEATURE=mRNA /DEFINITION=HS1433 Human mRNA for 14.3.3 protein, a ; 171\_at U56833  
 /FEATURE= /DEFINITION=HSU56833 Human VHL binding protein-1 (VBP-1).  
**Metagene** 73; 34033\_s\_at Cluster Incl. AF025531:Homo sapiens leucocyte immunoglobulin-like  
 15 rec; 40019\_at Cluster Incl. M60830:Human EVI2B3P gene, exon and complete cds /cds=(21;  
 34660\_at Cluster Incl. AI142565:qb47d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37541\_at  
 Cluster Incl. U25956:Human P-selectin glycoprotein ligand (SELPLG) gene; 37598\_at Cluster Incl.  
 D79990:Human mRNA for KIAA0168 gene, complete cds /cds=(1; 38973\_at Cluster Incl.  
 AB028943:Homo sapiens mRNA for KIAA1020 protein, partial .
- 20 **Metagene** 74; 31627\_f\_at Cluster Incl. AF047485:Homo sapiens amine oxidase pseudogene mRNA,  
 sp; 31988\_at Cluster Incl. AF043468:Homo sapiens neurexophilin 3 (NPH3) mRNA, partia;  
 33014\_at Cluster Incl. AF059194:Homo sapiens basic-leucine zipper transcription ; 36369\_at Cluster  
 Incl. AF000421:Homo sapiens TTF-I interacting peptide 12 mRNA, ; 34533\_at Cluster Incl.  
 AF038192:Homo sapiens clone 23808 mRNA sequence /cds=UNKN; 36235\_at Cluster Incl.
- 25 W26334:26b1 Homo sapiens cDNA /gb=W26334 /gi=1306889 /ug=; 37111\_g\_at Cluster Incl.  
 AB012229:Homo sapiens gene for fructose-6-phosphate,2-k; 32063\_at Cluster Incl.  
 M86546:H.sapiens PBX1a and PBX1b mRNA, complete cds /cds=; 32098\_at Cluster Incl.  
 M20777:Homo sapiens, alpha-2 (VI) collagen /cds=UNKNOWN /; 32698\_at Cluster Incl.  
 X64116:H.sapiens PVR gene for poliovirus receptor (exon 1; 34725\_at Cluster Incl. M73077:Human  
 30 glucocorticoid receptor repression factor 1 ; 38002\_s\_at Cluster Incl. Z34822:H.sapiens (HLCC85)  
 mRNA for voltage-dependent L-; 40060\_r\_at Cluster Incl. AF061258:Homo sapiens LIM protein  
 mRNA, complete cds /c; 40100\_at Cluster Incl. U72206:Human guanine nucleotide regulatory factor  
 (LFP40); 34374\_g\_at Cluster Incl. Z97054:Human DNA sequence from PAC 339A18 on  
 chromosome; 37327\_at Cluster Incl. X00588:Human mRNA for precursor of epidermal growth  
 35 facto; 38844\_at Cluster Incl. L42451:Homo sapiens pyruvate dehydrogenase kinase isoenzy;  
 39522\_at Cluster Incl. D49817:Homo sapiens mRNA for 6-phosphofructo-2-kinase/fru; 40913\_at  
 Cluster Incl. W28589:48h12 Homo sapiens cDNA /gb=W28589 /gi=1308537 /ug; 41285\_at Cluster  
 Incl. X77567:H.sapiens mRNA for InsP3 5-phosphatase /cds=(99,13; 41350\_at Cluster Incl.  
 M20776:Homo sapiens, alpha-1 (VI) collagen /cds=UNKNOWN /; 41550\_at Cluster Incl.



- AF091071:Homo sapiens clone 192 Rer1 mRNA, complete cds /; 2040\_s\_at M14752 /FEATURE=  
/DEFINITION=HUMABLA Human c-abl gene, complete cds ; 1938\_at K03218 /FEATURE=cds  
/DEFINITION=HUMSRC11 Human c-src-1 proto-oncogene, e; 1896\_s\_at L05628 /FEATURE=  
/DEFINITION=HUMMRPX Human multidrug resistance-associ; 1901\_s\_at M12036
- 5 /FEATURE=cds /DEFINITION=HUMHER2B Human tyrosine kinase-type re; 1221\_at X54871  
/FEATURE=cds /DEFINITION=HSRAB5B H.sapiens mRNA for ras-related p; 1045\_s\_at U33838  
/FEATURE= /DEFINITION=HSU33838 Human NF-kappa-B p65delta3 mRNA,; 773\_at D10667  
/FEATURE= /DEFINITION=HUMMHCAAA Homo sapiens mRNA for smooth muscl; 774\_g\_at  
D10667 /FEATURE= /DEFINITION=HUMMHCAAA Homo sapiens mRNA for smooth mus.
- 10 **Metagene 75;** 36790\_at Cluster Incl. M19267:Human tropomyosin mRNA, complete cds  
/cds=(286,114; 38590\_r\_at Cluster Incl. M14630:Human prothymosin alpha mRNA, complete cds  
/cds=; 32700\_at Cluster Incl. M55543:Human guanylate binding protein isoform II (GBP-2);  
34720\_at Cluster Incl. U85193:Human nuclear factor I-B2 (NFIB2) mRNA, complete c; 36918\_at  
Cluster Incl. Y15723:Homo sapiens mRNA for soluble guanylyl cyclase /cd; 39000\_at Cluster Incl.
- 15 AF043324:Homo sapiens N-myristoyltransferase 1 mRNA, comp; 33890\_at Cluster Incl.  
AB008109:Homo sapiens mRNA for RGS5, complete cds /cds=(8; 34811\_at Cluster Incl.  
U09813:Human mitochondrial ATP synthase subunit 9, P3 gen; 32544\_s\_at Cluster Incl.  
L12535:Human RSU-1/RSP-1 mRNA, complete cds /cds=(827,1; 1772\_s\_at L00634 /FEATURE=  
/DEFINITION=HUMFPTA Human farnesyl-protein transferas.
- 20 **Metagene 76;** 37243\_at Cluster Incl. X66533:H.sapiens soluble guanylate cyclase small subunit ;  
39431\_at Cluster Incl. AJ132583:Homo sapiens mRNA for puromycin sensitive aminop; 38439\_at  
Cluster Incl. L24123:Homo sapiens NRF1 protein (NRF1) mRNA /cds=UNKNOWN; 41841\_at  
Cluster Incl. AF052138:Homo sapiens clone 23718 mRNA sequence /cds=UNKN; 1814\_at D50683  
/FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIIR al.
- 25 **Metagene 77;** 33090\_at Cluster Incl. AJ007292:Homo sapiens mRNA for ephrin-A2 /cds=(15,656)  
/g; 40029\_at Cluster Incl. AB011539:Homo sapiens mRNA for MEGF6, partial cds /cds=(0;  
35347\_at Cluster Incl. AF093119:Homo sapiens UPH1 (UPH1) mRNA, complete cds /cds;  
1109\_s\_at M19989 /FEATURE=cds /DEFINITION=HUMPDGFA7 Human platelet-derived growt.
- Metagene 78;** 31638\_at Cluster Incl. AC005329:Homo sapiens chromosome 19, cosmid R34382
- 30 /cds=(; 33386\_at Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome ;  
38458\_at Cluster Incl. L39945:Human cytochrome b5 (CYB5) gene /cds=(120,548) /gb; 1645\_at  
U43527 /FEATURE= /DEFINITION=HSU43527 Human malignant melanoma metastasi; 751\_at  
D85418 /FEATURE= /DEFINITION=D85418 Homo sapiens mRNA for phosphatidylo; 286\_at  
L19779 /FEATURE= /DEFINITION=HUMH2A2A Homo sapiens histone H2A.2 mRNA, co.
- 35 **Metagene 79;** 35512\_at Cluster Incl. AC005764:Homo sapiens chromosome 19, cosmid R31343  
/cds=(; 33545\_at Cluster Incl. M81758:Homo sapiens skeletal muscle voltage-dependent sod;  
39620\_at Cluster Incl. Z21966:H.sapiens mPOU homeobox protein mRNA /cds=(192,109; 41652\_at  
Cluster Incl. AL031228:dJ1033B10.12 (collagen, type XI, alpha 2 (COL11A; 33792\_at Cluster Incl.  
AF043498:Homo sapiens prostate stem cell antigen (PSCA) m; 38012\_at Cluster Incl.

- U03272:Human fibrillin-2 mRNA, complete cds /cds=(0,8735); 1153\_f\_at J00117  
/FEATURE=mRNA /DEFINITION=HUMCGB Human chorionic gonadotropin (; 697\_f\_at  
Luteinizing Hormone, Beta Subunit ; 701\_s\_at Insulin-Like Leydig Hormone .
- Metagene 80;** 36804\_at Cluster Incl. M34455:Human interferon-gamma-inducible indoleamine 2,3-  
5 d; 37467\_at Cluster Incl. K02882:Human germline IgD chain gene, C-region, C-delta-1; 34799\_at  
Cluster Incl. AF070643:Homo sapiens clone 24636 mRNA sequence /cds=UNKN; 36205\_at Cluster  
Incl. L04490:Homo sapiens (clone CC6) NADH-ubiquinone oxidoredu; 634\_at L41351  
/FEATURE=mRNA /DEFINITION=HUMPROS Homo sapiens prostatic mRNA, com.
- Metagene 81;** 31991\_at Cluster Incl. AL049430:Homo sapiens mRNA; cDNA DKFZp586H201  
10 (from clone; 33011\_at Cluster Incl. Y10148:H.sapiens mRNA for NTR2 receptor /cds=(36,1268) /g;  
34108\_g\_at Cluster Incl. AJ005577:Homo sapiens pfkfb2 gene, exons 1 to 15 /cds=(; 34131\_at  
Cluster Incl. AB026891:Homo sapiens mRNA for cystine/glutamate transpor; 34933\_at Cluster Incl.  
AJ238381:Homo sapiens pax9 gene, exons 1-2 and joined CDS; 36237\_at Cluster Incl.  
AB009698:Homo sapiens mRNA for hOAT1-2, complete cds /cds; 38161\_at Cluster Incl.
- 15 Y09022:H.sapiens mRNA for Not56-like protein /cds=(31,134; 40402\_at Cluster Incl.  
X91117:H.sapiens HG NET gene exon 1 /cds=(49,1902) /gb=X9; 41443\_at Cluster Incl.  
U63127:Human SEC7 homolog Tic (TIC) mRNA, complete cds /c; 32028\_at Cluster Incl.  
U85773:Human phosphomannomutase (PMM2) mRNA, complete cds; 32031\_at Cluster Incl.  
D78586:Human CAD mRNA for multifunctional protein CAD, co; 33224\_at Cluster Incl.
- 20 AB007965:Homo sapiens mRNA, chromosome 1 specific transcr; 33281\_at Cluster Incl.  
D63485:Human mRNA for KIAA0151 gene, complete cds /cds=(3; 38297\_at Cluster Incl.  
X98654:H.sapiens mRNA for DRES9 protein /cds=(189,3923) /; 38710\_at Cluster Incl.  
AL096714:Homo sapiens mRNA; cDNA DKFZp564E242 (from clone; 39010\_at Cluster Incl.  
AI658639:tu06g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39339\_at Cluster Incl.
- 25 AB018335:Homo sapiens mRNA for KIAA0792 protein, complete; 40414\_at Cluster Incl.  
X59303:Human G7a mRNA for valyl-tRNA synthetase /cds=(219; 33360\_at Cluster Incl.  
AB023221:Homo sapiens mRNA for KIAA1004 protein, partial ; 33842\_at Cluster Incl.  
AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds=(; 36670\_at Cluster Incl.  
L26339:Human autoantigen mRNA, complete cds /cds=(136,378; 40176\_at Cluster Incl.
- 30 J03407:Human rfp transforming protein mRNA, complete cds ; 40890\_at Cluster Incl.  
U46920:Human metaxin (MTX) gene, complete cds /cds=(0,953; 41804\_at Cluster Incl.  
W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 1294\_at L13852 /FEATURE=  
/DEFINITION=HUME1URP Homo sapiens ubiquitin-activating ; 1003\_s\_at X68149  
/FEATURE=cds /DEFINITION=HSBLR1A Homo sapiens BLR1 gene for Bur; 686\_s\_at K03498
- 35 /FEATURE=cds#1 /DEFINITION=HUMERVDP Human endogenous retrovirus ; 567\_s\_at M79463  
/FEATURE= /DEFINITION=HUMPML2 Human PML-2 mRNA, complete CDS .
- Metagene 82;** 33082\_at Cluster Incl. AF074015:Homo sapiens integrin subunit alpha 10 precursor;  
35592\_at Cluster Incl. AB029010:Homo sapiens mRNA for KIAA1087 protein, partial ; 36364\_at  
Cluster Incl. L32961:Human 4-aminobutyrate aminotransferase (GABAT) mRNA; 33464\_at Cluster

- Incl. AL109703:Homo sapiens mRNA full length insert cDNA clone ; 41406\_at Cluster Incl.  
 AL080172:Homo sapiens mRNA; cDNA DKFZp434G231 (from clone.  
**Metagene 83;** 31347\_at Cluster Incl. AF058075:Homo sapiens clone ASPBLL54 immunoglobulin  
 lambda; 31512\_at Cluster Incl. Z00010:H.sapiens germ line pseudogene for immunoglobulin ;  
 5 32904\_at Cluster Incl. M28393:Human perforin mRNA, complete cds /cds=(0,1667) /g; 32967\_at  
 Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) m; 35228\_at Cluster Incl.  
 Y08682:H.sapiens mRNA for carnitine palmitoyltransferase ; 32793\_at Cluster Incl. X00437:Human  
 mRNA for T-cell specific protein /cds=(37,97; 38096\_f\_at Cluster Incl. M83664:Human MHC class  
 II lymphocyte antigen (HLA-DP) b.
- 10 **Metagene 84;** 34988\_at Cluster Incl. AF052119:Homo sapiens clone 23622 mRNA sequence  
 /cds=UNKN; 35435\_s\_at Cluster Incl. AF001903:Human 3-hydroxyacyl-CoA dehydrogenase,  
 isoform; 41111\_at Cluster Incl. U68418:Human branched chain aminotransferase precursor (B;  
 41401\_at Cluster Incl. U57646:Homo sapiens cysteine and glycine-rich protein 2 (; 33301\_g\_at  
 Cluster Incl. AL031282:dJ283E3.3.1 (Cell Division Cycle 2-Like 2 (PIT; 33706\_at Cluster Incl.
- 15 AB006198:Homo sapiens mRNA for SART-1, complete cds /cds=; 39391\_at Cluster Incl.  
 AF052135:Homo sapiens clone 23625 mRNA sequence /cds=UNKN; 39427\_at Cluster Incl.  
 T79616:yd71e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 41145\_at Cluster Incl.  
 AB020721:Homo sapiens mRNA for KIAA0914 protein, complete; 36586\_at Cluster Incl.  
 U78521:Homo sapiens immunophilin homolog ARA9 mRNA, compl; 38078\_at Cluster Incl.
- 20 AF042166:Homo sapiens beta-filamin mRNA, complete cds /cd; 39552\_at Cluster Incl.  
 U92436:Human mutated in multiple advanced cancers protein; 41339\_at Cluster Incl.  
 AF043117:Homo sapiens ubiquitin-fusion degradation protei; 41524\_at Cluster Incl. L08488:Human  
 inositol polyphosphate 1-phosphatase mRNA, c; 1836\_at D50310 /FEATURE=  
 /DEFINITION=HUMCYI Human mRNA for cyclin I, complete cd; 1606\_at L36645
- 25 /FEATURE=mRNA /DEFINITION=HUMRPTKC Homo sapiens receptor protein-; 1348\_s\_at  
 S79219 /FEATURE= /DEFINITION=S79219 metastasis-associated gene [human; 1103\_at M11567  
 /FEATURE=mRNA /DEFINITION=HUMAGG Human angiogenin gene, complete .  
**Metagene 85;** 34995\_at Cluster Incl. L76380:Homo sapiens (clone HSNME29) CGRP type 1  
 receptor ; 38584\_at Cluster Incl. AF026939:Homo sapiens CIG49 (cig49) mRNA, complete cds /c;  
 30 38854\_at Cluster Incl. AB014535:Homo sapiens mRNA for KIAA0635 protein, complete; 39641\_at  
 Cluster Incl. X52486:Human mRNA for uracil-DNA glycosylase /cds=(79,105; 39945\_at Cluster  
 Incl. U09278:Human fibroblast activation protein mRNA, complete; 40398\_s\_at Cluster Incl.  
 AI743406:wg92g12.x1 Homo sapiens cDNA, 3 end /clone=IM; 40716\_at Cluster Incl.  
 AL049274:Homo sapiens mRNA; cDNA DKFZp564H203 (from clone; 41058\_g\_at Cluster Incl.
- 35 AI760162:wg58e09.x1 Homo sapiens cDNA, 3 end /clone=IM; 34748\_at Cluster Incl.  
 AB020653:Homo sapiens mRNA for KIAA0846 protein, complete; 32859\_at Cluster Incl.  
 M97935:Homo sapiens transcription factor ISGF-3 mRNA, com; 35362\_at Cluster Incl.  
 AB018342:Homo sapiens mRNA for KIAA0799 protein, partial ; 35766\_at Cluster Incl.  
 M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343); 36181\_at Cluster Incl.

- X82456:H.sapiens MLN50 mRNA /cds=(75,860) /gb=X82456 /gi=; 38432\_at Cluster Incl.  
 AA203213:zx57e04.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1451\_s\_at D13666 /FEATURE=  
 /DEFINITION=HUMOSF2OS Homo sapiens osf-2 mRNA for ost; 1379\_at M59371  
 /FEATURE=mRNA /DEFINITION=HUMECK Human protein tyrosine kinase mR; 718\_at D87258  
 5 /FEATURE= /DEFINITION=D87258 Homo sapiens mRNA for serin protease ; 719\_g\_at D87258  
 /FEATURE= /DEFINITION=D87258 Homo sapiens mRNA for serin proteas.  
**Metagene** 86; 41159\_at Cluster Incl. D21260:Human mRNA for KIAA0034 gene, complete cds  
 /cds=(1; 32156\_at Cluster Incl. AF044968:untitled /cds=(0,1351) /gb=AF044968 /gi=3941380 ;  
 39126\_at Cluster Incl. AL080101:Homo sapiens mRNA; cDNA DKFZp564L0472 (from clon;  
 10 1719\_at U61981 /FEATURE= /DEFINITION=HSU61981 Human putative mismatch repair/bin.  
**Metagene** 87; 32003\_at Cluster Incl. D49357:Human mRNA for S-adenosylmethionine synthetase,  
 co; 34171\_at Cluster Incl. AI867349:wi24g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 39262\_at Cluster Incl. U79266:Human clone 23627 mRNA, complete cds /cds=(184,104; 41065\_at  
 Cluster Incl. L40407:Homo sapiens thyroid receptor interactor (TRIP9) g; 37911\_at Cluster Incl.  
 15 U07158:Human syntaxin mRNA, complete cds /cds=(66,959) /g; 38647\_at Cluster Incl.  
 AJ131182:Homo sapiens mRNA for Epsilon COP /cds=(42,968) ; 38970\_s\_at Cluster Incl.  
 AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated fa; 39704\_s\_at Cluster Incl.  
 L17131:Human high mobility group protein (HMG-I(Y)) gen; 40164\_at Cluster Incl.  
 X69550:H.sapiens mRNA for rho GDP-dissociation Inhibitor ; 41176\_at Cluster Incl.  
 20 AF052162:Homo sapiens clone 24655 mRNA sequence /cds=UNKN; 33887\_at Cluster Incl.  
 D84064:Homo sapiens mRNA for Hrs, complete cds /cds=(60,2; 34780\_at Cluster Incl.  
 AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(; 36187\_at Cluster Incl.  
 X13973:Human mRNA for ribonuclease/angiogenin inhibitor (; 37690\_at Cluster Incl.  
 U61263:Human acetolactate synthase homolog mRNA, complete; 38791\_at Cluster Incl.  
 25 D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(1; 39134\_at Cluster Incl.  
 AJ006973:Homo sapiens mRNA for TOM1 protein /cds=(61,1539; 39812\_at Cluster Incl.  
 X79865:H.sapiens Mrp17 mRNA /cds=(137,733) /gb=X79865 /gi; 32559\_s\_at Cluster Incl.  
 AJ238096:Homo sapiens mRNA for Lsm4 protein /cds=(23,44; 33133\_at Cluster Incl.  
 U80184:Homo sapiens FLII gene, complete cds /cds=(35,3844; 33212\_at Cluster Incl.  
 30 AF006751:Homo sapiens ES/130 mRNA, complete cds /cds=(70; 1942\_s\_at U37022  
 /FEATURE=mRNA /DEFINITION=HSU37022 Human cyclin-dependent kinas; 1243\_at U18300  
 /FEATURE= /DEFINITION=HSU18300 Human damage-specific DNA binding ; 1100\_at L76191  
 /FEATURE=mRNA /DEFINITION=HUMI1R Homo sapiens interleukin-1 recep; 545\_g\_at S76638  
 /FEATURE= /DEFINITION=S76638 p50-NF-kappa B homolog [human, peri; 180\_at S82470  
 35 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhance; 151\_s\_at V00599  
 /FEATURE=mRNA /DEFINITION=HSTUB2 Human mRNA fragment encoding be.  
**Metagene** 88; 31402\_at Cluster Incl. AF103884:Homo sapiens minor histocompatibility antigen HB;  
 31601\_s\_at Cluster Incl. U36610:Human Y-chromosome RNA recognition motif protein;  
 31673\_s\_at Cluster Incl. X65784:H.sapiens CAR gene /cds=(0,428) /gb=X65784 /gi=4; 35563\_at

- Cluster Incl. AL022238:dJ1042K10.5 (novel protein) /cds=(0,627) /gb=AL0; 32362\_r\_at Cluster Incl. D87012:Human (lambda) DNA for immunoglobulin light chain ; 34966\_at Cluster Incl. AJ001699:Homo sapiens mRNA for Brachyury (T) protein /cds; 35917\_at Cluster Incl. W26631:34a8 Homo sapiens cDNA /gb=W26631 /gi=1307474 /ug=; 37130\_g\_at Cluster Incl.
- 5 AI936758:wp69b11.x1 Homo sapiens cDNA, 3 end /clone=IM; 37413\_at Cluster Incl. J05257:Homo sapiens (clones MDP4, MDP7) microsomal dipept; 37872\_at Cluster Incl. AF072468:Homo sapiens (JH8) mRNA, partial cds /cds=(0,125; 38239\_at Cluster Incl. AI312905:qp84d03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39639\_s\_at Cluster Incl. X07948:Human mRNA for transition protein 1 (TP1) /cds=(; 40006\_at Cluster Incl. U63090:Human Gal beta-1,3 GalNAc alpha-2,3 sialyltransfer; 40286\_r\_at Cluster Incl. AL050370:Homo sapiens mRNA; cDNA DKFZp566C0546 (from cl; 32047\_at Cluster Incl. U91985:Human DNA fragmentation factor-45 mRNA, complete c; 33231\_at Cluster Incl. AI761148:wh97h07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33727\_r\_at Cluster Incl. AB029011:Homo sapiens mRNA for KIAA1088 protein, partial; 33738\_r\_at Cluster Incl. AI871359:wl81b11.x1 Homo sapiens cDNA, 3 end /clone=IM; 34287\_at Cluster Incl.
- 15 AB023175:Homo sapiens mRNA for KIAA0958 protein, partial ; 40098\_at Cluster Incl. AF001434:Human Hpast (HPAST) mRNA, complete cds /cds=(255; 40819\_at Cluster Incl. AA161065:zl50h04.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41218\_at Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial ; 33432\_at Cluster Incl. AI547308:PN001\_AH\_B03.r Homo sapiens cDNA, 5 end /clone=; 37297\_at Cluster Incl.
- 20 AL049422:Homo sapiens mRNA; cDNA DKFZp586A191 (from clone; 38371\_at Cluster Incl. M64992:Human prosomal protein P30-33K (pros-30) mRNA, complete; 39820\_at Cluster Incl. AF001549:Human Chromosome 16 BAC clone CIT987SK-A-270G1 /; 41543\_at Cluster Incl. U34360:Human lymphoid nuclear protein (LAF-4) mRNA, complete; 382\_at X70218 /FEATURE= /DEFINITION=HSPPX Homo sapiens mRNA for protein phosphat.
- 25 **Metagene 89;** 41637\_at Cluster Incl. AF108145:Homo sapiens MYLE mRNA, complete cds /cds=(52,25; 35663\_at Cluster Incl. U29195:Human neuronal pentraxin II (NPTX2) gene /cds=(58,; 40877\_s\_at Cluster Incl. AF041080:Homo sapiens D15F37 pseudogene, S3 allele, mRNA. **Metagene 90;** 36711\_at Cluster Incl. AL021977:bK447C4.1 (novel MAFF (v-maf musculoaponeurotic ; 38167\_at Cluster Incl. AB020704:Homo sapiens mRNA for KIAA0897 protein, partial ; 40747\_at Cluster Incl. AB002309:Human mRNA for KIAA0311 gene, partial cds /cds=(; 35625\_at Cluster Incl. X94630:H.sapiens CD97 gene exon 1 (and joined CDS) /cds=(; 35989\_at Cluster Incl. AF007160:Homo sapiens unknown mRNA, partial cds /cds=(0,4; 37193\_at Cluster Incl. D78335:Human mRNA for 5-terminal region of UMK, complete ; 37576\_at Cluster Incl. U52969:Human PEP19 (PCP4) mRNA, complete cds /cds=(81,269; 39044\_s\_at Cluster Incl.
- 35 D73409:Homo sapiens mRNA for diacylglycerol kinase delta; 39330\_s\_at Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cd; 40855\_at Cluster Incl. AB028976:Homo sapiens mRNA for KIAA1053 protein, partial ; 32242\_at Cluster Incl. AL038340:DKFZp566K192\_s1 Homo sapiens cDNA, 3 end /clone; 32243\_g\_at Cluster Incl. AL038340:DKFZp566K192\_s1 Homo sapiens cDNA, 3 end /clone; 33900\_at Cluster Incl.

- U76702:Homo sapiens follistatin-related protein FLRG (FLR; 36175\_s\_at Cluster Incl.  
 AL023584:Human DNA sequence from clone 67K17 on chromos; 36671\_at Cluster Incl.  
 M27396:Human asparagine synthetase mRNA, complete cds /cd; 36956\_at Cluster Incl.  
 L20852:Human leukemia virus receptor 2 (GLVR2) mRNA, comp; 39105\_at Cluster Incl.
- 5 Z46389:Homo sapiens encoding vasodilator-stimulated phosp; 32506\_at Cluster Incl.  
 AB029031:Homo sapiens mRNA for KIAA1108 protein, partial ; 1137\_at L20852 /FEATURE=  
 /DEFINITION=HUMGLVR2X Human leukemia virus receptor 2 ( ; 790\_at X52599 /FEATURE=cds  
 /DEFINITION=HSBNGFAC Human mRNA for beta nerve growth; 791\_g\_at X52599  
 /FEATURE=cds /DEFINITION=HSBNGFAC Human mRNA for beta nerve grow.
- 10 **Metagene 91**; 33942\_s\_at Cluster Incl. AF004563:Homo sapiens hUNC18b alternatively-spliced  
 mRN; 38312\_at Cluster Incl. AL050002:Homo sapiens mRNA; cDNA DKFZp564O222 (from  
 clone; 39779\_at Cluster Incl. U38847:Human TAR RNA loop binding protein (TRP-185) mRNA;;  
 40434\_at Cluster Incl. U97519:Homo sapiens podocalyxin-like protein mRNA, comple; 41189\_at  
 Cluster Incl. Y09392:H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 prote; 37375\_at Cluster
- 15 Incl. AB014538:Homo sapiens mRNA for KIAA0638 protein, partial ; 38430\_at Cluster Incl.  
 AA128249:z129d09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 38826\_at Cluster Incl.  
 D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0; 1954\_at AF035121 /FEATURE=  
 /DEFINITION=AF035121 Homo sapiens KDR/flk-1 protein m; 599\_at M60721  
 /FEATURE=mRNA /DEFINITION=HUMHB24 Human homeobox gene, complete cd.
- 20 **Metagene 92**; 31955\_at Cluster Incl. X65923:H.sapiens fau mRNA /cds=(56,457) /gb=X65923  
 /gi=31; 34446\_at Cluster Incl. AL049701:Human gene from PAC 433G19, chromosome 1 /cds=(0;  
 40032\_at Cluster Incl. D50923:Human mRNA for KIAA0133 gene, complete cds /cds=(1; 40038\_at  
 Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 32042\_at Cluster  
 Incl. S72904:APK1 antigen=MAb KI recognized [human, ovarian car; 33242\_at Cluster Incl.
- 25 U92980:Homo sapiens clone DT1P1A10 mRNA, CAG repeat regio; 33315\_at Cluster Incl.  
 M29204:Human DNA-binding factor mRNA, complete cds /cds=( ; 35724\_at Cluster Incl.  
 Y07867:H.sapiens mRNA for Pirin, isolate 1 /cds=(204,1076; 36457\_at Cluster Incl. U10860:Human  
 guanosine 5-monophosphate synthase mRNA, com; 36553\_at Cluster Incl. AA669799:ag36c04.s1  
 Homo sapiens cDNA, 3 end /clone=IMAG; 37597\_s\_at Cluster Incl. AF055006:Homo sapiens clone
- 30 24666 sec6 homolog mRNA, pa; 38286\_at Cluster Incl. AB028994:Homo sapiens mRNA for  
 KIAA1071 protein, partial ; 38648\_at Cluster Incl. U80760:Homo sapiens CAGH1 alternate open  
 reading frame mR; 38709\_at Cluster Incl. D80009:Human mRNA for KIAA0187 gene, complete cds  
 /cds=(2; 39060\_at Cluster Incl. D38048:Human mRNA for proteasome subunit z, complete cds ;  
 39420\_at Cluster Incl. S62138:TLS/CHOP=hybrid gene {translocation breakpoint} [h; 40465\_at
- 35 Cluster Incl. AF026402:Homo sapiens U5 snRNP 100 kD protein mRNA, compl; 40515\_at Cluster  
 Incl. AF035280:Homo sapiens clone 23689 mRNA, complete cds /cds; 40854\_at Cluster Incl.  
 J04973:Human cytochrome bc-1 complex core protein II mRNA; 41122\_at Cluster Incl.  
 AB011173:Homo sapiens mRNA for KIAA0601 protein, partial ; 41155\_at Cluster Incl.  
 U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4; 41729\_at Cluster Incl.

- AJ009771:Homo sapiens mRNA for putative RING finger prote; 32213\_at Cluster Incl.  
 AA203527:zx56f09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 32744\_at Cluster Incl.  
 AI526078:DU3.2-7.G08.r Homo sapiens cDNA, 5 end /clone\_e; 32766\_at Cluster Incl.  
 Z83840:Human DNA sequence from clone 216E10 on chromosome; 32809\_at Cluster Incl.
- 5 AL118582:DKFZp761B0810\_r1 Homo sapiens cDNA, 5 end /clon; 33406\_at Cluster Incl.  
 AL050345:Novel human gene mapping to chomosome 22 /cds=(1; 34395\_at Cluster Incl.  
 AB002352:Human mRNA for KIAA0354 gene, complete cds /cds=; 35304\_at Cluster Incl.  
 AF052130:Homo sapiens clone 23704 mRNA sequence /cds=UNKN; 35355\_at Cluster Incl.  
 AB020697:Homo sapiens mRNA for KIAA0890 protein, complete; 35742\_at Cluster Incl.
- 10 U95740:Human Chromosome 16 BAC clone CIT987SK-A-362G6 /cd; 35777\_at Cluster Incl.  
 AB000468:Homo sapiens mRNA for zinc finger protein, compl; 37321\_at Cluster Incl.  
 U46570:Human tetratricopeptide repeat protein (tpr1) mRNA; 37399\_at Cluster Incl.  
 D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(5; 38103\_at Cluster Incl.  
 AB014542:Homo sapiens mRNA for KIAA0642 protein, partial ; 38400\_at Cluster Incl.
- 15 AI920820:wn82e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38475\_at Cluster Incl.  
 U50733:Human dynaminin mRNA, complete cds /cds=(78,1298) ; 38751\_i\_at Cluster Incl.  
 AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IM; 39152\_f\_at Cluster Incl.  
 U06632:Homo sapiens p80-coilin mRNA, complete cds /cds=; 39856\_at Cluster Incl.  
 AI708983:at02f03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40184\_at Cluster Incl.
- 20 L37042:Homo sapiens casein kinase I alpha isoform (CSNK1A; 40896\_at Cluster Incl.  
 X13403:Human mRNA for octamer-binding protein Oct-1 /cds=; 41268\_g\_at Cluster Incl.  
 AB028972:Homo sapiens mRNA for KIAA1049 protein, partia; 32511\_at Cluster Incl.  
 AI498132:tm90a12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 688\_at L02426 /FEATURE=  
 /DEFINITION=HUM26SPSIV Human 26S protease (S4) regulator.
- 25 **Metagene** 93; 35096\_at Cluster Incl. U18244:Human excitatory amino acid transporter 4 mRNA, co;  
 37521\_s\_at Cluster Incl. H82458:yv80b07.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 38554\_at  
 Cluster Incl. AA903720:ok60c02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1063\_s\_at U02566  
 /FEATURE= /DEFINITION=HSU02566 Human receptor tyrosine kinase t; 801\_at X82676  
 /FEATURE= /DEFINITION=HSTYRPH Homo sapiens mRNA for tyrosine phosp.
- 30 **Metagene** 94; 39994\_at Cluster Incl. D10925:Human mRNA for HM145 /cds=(22,1089)  
 /gb=D10925 /gi; 770\_at D00632 /FEATURE= /DEFINITION=HUMGSHPIXA Homo sapiens  
 mRNA for glutathione .  
**Metagene** 95; 33708\_at Cluster Incl. AF045584:Homo sapiens PB39 mRNA, complete cds  
 /cds=(76,17; 37248\_at Cluster Incl. U83411:Homo sapiens carboxypeptidase Z precursor, mRNA, c;  
 40154\_at Cluster Incl. AL096725:Homo sapiens mRNA; cDNA DKFZp434B103 (from clone;  
 40856\_at Cluster Incl. U29953:Human pigment epithelium-derived factor gene, comp; 38124\_at  
 Cluster Incl. X55110:Human mRNA for neurite outgrowth-promoting protein; 38406\_f\_at Cluster  
 Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM; 38407\_r\_at Cluster Incl.  
 AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IM; 39158\_at Cluster Incl.

- AB021663:Homo sapiens mRNA for leucine-zipper protein, co; 216\_at M98539 /FEATURE=exon /DEFINITION=HUMPDS03 Human prostaglandin D2 synthase.
- Metagene** 96; 37104\_at Cluster Incl. L40904:H. sapiens peroxisome proliferator activated recep; 34176\_at Cluster Incl. AF091087:Homo sapiens clone 643 unknown mRNA, complete se; 35226\_at
- 5 Cluster Incl. U71207:Human eyes absent homolog (Eab1) mRNA, complete cd; 40255\_at Cluster Incl. AC004531:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-; 506\_s\_at U43185 /FEATURE= /DEFINITION=HSU43185 Human signal transducer and activ.
- Metagene** 97; 36418\_at Cluster Incl. AJ011654:Homo sapiens mRNA for triple LIM domain protein ; 38090\_at Cluster Incl. AL050371:Homo sapiens mRNA; cDNA DKFZp566G2246 (from clon;
- 10 1518\_at J04101 /FEATURE= /DEFINITION=HUMETS1A Human erythroblastosis virus oncog.
- Metagene** 98; 33961\_at Cluster Incl. AL109666:Homo sapiens mRNA full length insert cDNA clone ; 34456\_s\_at Cluster Incl. AB007296:Homo sapiens mRNA for hGLI2, complete cds, clo;
- 35420\_r\_at Cluster Incl. AB020720:Homo sapiens mRNA for KIAA0913 protein, partia; 38190\_r\_at Cluster Incl. AB014545:Homo sapiens mRNA for KIAA0645 protein, comple; 41627\_at Cluster
- 15 Incl. D50645:Homo sapiens mRNA for SDF2, complete cds /cds=(39,; 34727\_at Cluster Incl. AI800578:wg12b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40152\_r\_at Cluster Incl. Z48054:H.sapiens mRNA for peroxisomal targeting signal ; 32197\_at Cluster Incl. AF070548:Homo sapiens clone 24408 2-oxoglutarate carrier ; 36964\_at Cluster Incl. D42053:Human mRNA for KIAA0091 gene, complete cds /cds=(4; 37004\_at Cluster Incl. J02761:Human pulmonary surfactant-
- 20 associated protein B (S; 37317\_at Cluster Incl. L25107:Human LIS mRNA /cds=UNKNOWN /gb=L25107 /gi=602459 ; 39205\_at Cluster Incl. W28793:52f4 Homo sapiens cDNA /gb=W28793 /gi=1308804 /ug=; 39448\_r\_at Cluster Incl. W27095:20c10 Homo sapiens cDNA /gb=W27095 /gi=1306467 /; 41001\_at Cluster Incl. AB023202:Homo sapiens mRNA for KIAA0985 protein, complete; 41280\_r\_at Cluster Incl. AF007134:Homo sapiens clone 23565 unknown mRNA, partial;
- 25 894\_g\_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein ( ; 293\_at Homeotic Protein Hpx-42 ; 244\_at M64673 /FEATURE= /DEFINITION=HUMHSF1 Human heat shock factor 1 (TCF5) mRN.
- Metagene** 99; 35898\_at Cluster Incl. AF100780:Homo sapiens connective tissue growth factor rel; 39971\_at Cluster Incl. M22637:Human LYL-1 protein mRNA, complete cds /cds=UNKNOW;
- 30 40030\_at Cluster Incl. Y15801:Homo sapiens mRNA for PRKY protein /cds=UNKNOWN /g; 32113\_at Cluster Incl. U83115:Human non-lens beta gamma-crystallin like protein ; 39042\_at Cluster Incl. X05615:Human mRNA for thyroglobulin /cds=(41,8344) /gb=X0.
- Metagene** 100; 38505\_at Cluster Incl. AL050151:Homo sapiens mRNA; cDNA DKFZp586J0720 (from clon; 36921\_at Cluster Incl. U02556:Human RP3 mRNA, complete cds /cds=(68,418)
- 35 /gb=U02; 37958\_at Cluster Incl. AL049257:Homo sapiens mRNA; cDNA DKFZp564E153 (from clone; 41225\_at Cluster Incl. AL049417:Homo sapiens mRNA; cDNA DKFZp586O1919 (from clon; 32210\_at Cluster Incl. M83088:Human phosphoglucomutase 1 (PGM1) mRNA, complete c; 32822\_at Cluster Incl. J02966:Human mitochondrial ADP/ADT translocator mRNA, com; 32846\_s\_at Cluster Incl. D13629:Human mRNA for KIAA0004 gene, complete cds /cds=;



- 33423\_g\_at Cluster Incl. AF052155:Homo sapiens clone 24761 mRNA sequence /cds=UN; 34370\_at Cluster Incl. X81198:H.sapiens mRNA (clone p5) for archain /cds=(78,149; 36585\_at Cluster Incl. M36341:Human ADP-ribosylation factor 4 (ARF4) mRNA, compl; 36677\_at Cluster Incl. X70476:H.sapiens subunit of coatomer complex /cds=(68,278; 37345\_at Cluster Incl.
- 5 AF013759:Homo sapiens calumein (Calu) mRNA, complete cds ; 37366\_at Cluster Incl. AL049969:Homo sapiens mRNA; cDNA DKFZp564A072 (from clone; 38113\_at Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial ; 40621\_at Cluster Incl. U63809:Homo sapiens prostate apoptosis response protein p; 2017\_s\_at M64349 /FEATURE= /DEFINITION=HUMCYCD1 Human cyclin D (cyclin D1) mRNA.; 1508\_at D25303 /FEATURE=
- 10 /DEFINITION=HUMIAS Human mRNA for integrin alpha subuni; 120\_at X68742 /FEATURE= /DEFINITION=HSINTASA H.sapiens mRNA for integrin, alpha .
- Metagene 101;** 34502\_g\_at Cluster Incl. L40992:Homo sapiens (clone PEBP2aA1) core-binding facto; 35422\_at Cluster Incl. U01828:Human microtubule-associated protein 2 (MAP2) mRNA; 37222\_at Cluster Incl. X79389:H.sapiens GSTT1 mRNA /cds=(0,722) /gb=X79389 /gi=5; 1972\_s\_at
- 15 U89330 /FEATURE= /DEFINITION=HSU89330 Human alternatively spliced micr; 1035\_g\_at U14394 /FEATURE= /DEFINITION=HSU14394 Human tissue inhibitor of metall; 363\_at Z15114 /FEATURE=cds /DEFINITION=HSPKCG H.sapiens mRNA for protein kinase ; 375\_at Z84718 /FEATURE=mRNA#1 /DEFINITION=HS322B1 Human DNA sequence from clone .
- Metagene 102;** 33642\_s\_at Cluster Incl. U17986:Human GABA/noradrenaline transporter mRNA, compl; 35569\_at Cluster Incl. AB015330:Homo sapiens HRIHFB2007 mRNA, partial cds /cds=(; 41117\_s\_at Cluster Incl. AB016243:Homo sapiens gene for regulatory factor 2 of s; 34179\_at Cluster Incl. Z97183:Human DNA sequence from cosmid B2046 on chromosome; 34733\_at Cluster Incl. X85237:H.sapiens mRNA for splicing factor SF3a120 /cds=(9; 36564\_at Cluster Incl. W27419:31a10 Homo sapiens cDNA /gb=W27419 /gi=1307241 /ug; 37557\_at Cluster Incl.
- 25 U62531:Human AE2 anion exchanger (SLC4A2) mRNA, complete ; 38308\_g\_at Cluster Incl. AB011179:Homo sapiens mRNA for KIAA0607 protein, partia; 38314\_at Cluster Incl. AB002304:Human mRNA for KIAA0306 gene, partial cds /cds=(; 38633\_at Cluster Incl. U35113:Human metastasis-associated mta1 mRNA, complete cd; 39770\_at Cluster Incl. D87437:Human mRNA for KIAA0250 gene, complete cds /cds=(4; 40489\_at Cluster Incl.
- 30 D31840:Human DRPLA mRNA for ORF, complete cds /cds=(238,3; 40850\_at Cluster Incl. L37033:Human FK-506 binding protein homologue (FKBP38) mR; 37370\_i\_at Cluster Incl. L41066:Homo sapiens NF-AT3 mRNA, complete cds /cds=(141; 37386\_i\_at Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=; 37387\_r\_at Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=; 37652\_at Cluster Incl.
- 35 AB002328:Human mRNA for KIAA0330 gene, partial cds /cds=(; 38775\_at Cluster Incl. X13916:Human mRNA for LDL-receptor related protein /cds=(; 38828\_s\_at Cluster Incl. AA628946:af28f05.s1 Homo sapiens cDNA, 3 end /clone=IM; 39530\_at Cluster Incl. L35240:Human enigma gene, complete cds /cds=(0,1367) /gb=; 41337\_at Cluster Incl. AF072902:Homo sapiens gp130 associated protein GAM mRNA, ; 1643\_g\_at U35113 /FEATURE=

- /DEFINITION=HSU35113 Human metastasis-associated mta1; 1011\_s\_at U54778 /FEATURE=  
/DEFINITION=HSU54778 Human 14-3-3 epsilon mRNA, compl; 880\_at M34539 /FEATURE=  
/DEFINITION=HUMFKBP Human FK506-binding protein (FKBP) m; 657\_at L11373 /FEATURE=  
/DEFINITION=HUMPC43ABB Human protocadherin 43 mRNA, comp; 249\_at L41066  
5 /FEATURE= /DEFINITION=HUMNFAT3A Homo sapiens NF-AT3 mRNA, complete.  
**Metagene** 103; 39294\_at Cluster Incl. X16155:Human mRNA for chicken ovalbumin upstream  
promoter; 33785\_at Cluster Incl. AB005298:Homo sapiens BAI 2 mRNA, complete cds /cds=(378;  
32208\_at Cluster Incl. AB002353:Human mRNA for KIAA0355 gene, complete cds /cds=.
- Metagene** 104; 33648\_at Cluster Incl. W28800:52g12 Homo sapiens cDNA /gb=W28800  
10 /gi=1308811 /ug; 34082\_at Cluster Incl. W28356:48e3 Homo sapiens cDNA /gb=W28356  
/gi=1308511 /ug=; 35520\_at Cluster Incl. AI701514:we35h02.x1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 40044\_at Cluster Incl. U16282:Human ELL mRNA, complete cds /cds=(12,1877)  
/gb=U1; 41726\_at Cluster Incl. Z35307:H.sapiens mRNA for endothelin-converting-enzyme 1 ;  
32185\_at Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containi; 41501\_at  
15 Cluster Incl. AF004849:Homo sapiens PKY protein kinase mRNA, complete c; 517\_at U07000  
/FEATURE=cds#4 /DEFINITION=HSU07000 Human breakpoint cluster regio.  
**Metagene** 105; 31740\_s\_at Cluster Incl. AB008913:Homo sapiens mRNA for Pax-4, complete cds  
/cds; 40649\_at Cluster Incl. X64810:H.sapiens encoding PC1/PC3 /cds=(189,2450) /gb=X64;  
40723\_at Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010; 33322\_i\_at  
20 Cluster Incl. X57348:H.sapiens mRNA (clone 9112) /cds=(165,911) /gb=X; 36030\_at Cluster Incl.  
AL080214:Homo sapiens mRNA; cDNA DKFZp586I2223 (from clon; 36079\_at Cluster Incl.  
AF010309:Homo sapiens Pig3 (PIG3) mRNA, complete cds /cds; 40117\_at Cluster Incl.  
D84557:Homo sapiens mRNA for HsMcm6, complete cds /cds=(6; 41171\_at Cluster Incl.  
D45248:Human mRNA for proteasome activator hPA28 subunit ; 35312\_at Cluster Incl.  
25 D21063:Human mRNA for KIAA0030 gene, partial cds /cds=(0; 36170\_at Cluster Incl.  
D83198:Homo sapiens mRNA expressed in thyroid gland /cds=; 37323\_r\_at Cluster Incl.  
X82460:H.sapiens mRNA for 15-hydroxy prostaglandin dehy; 38788\_at Cluster Incl.  
M82827:Human fusion protein mRNA, complete cds /cds=(324; 1184\_at D45248 /FEATURE=  
/DEFINITION=HUMHPA28A Human mRNA for proteasome activa; 709\_at J00314  
30 /FEATURE=mRNA#1 /DEFINITION=HUMTBMM40 Human beta-tubulin gene, clo.  
**Metagene** 106; 37492\_at Cluster Incl. AB007969:Homo sapiens mRNA, chromosome 1 specific  
transer; 37277\_at Cluster Incl. U80017:Homo sapiens basic transcription factor 2 p44 (btf; 39037\_at  
Cluster Incl. L13773:Human AF-4 mRNA, complete cds /cds=(420,4052) /gb=; 39777\_at Cluster  
Incl. AF075587:Homo sapiens protein associated with Myc mRNA, c; 40067\_at Cluster Incl.  
35 M82882:Human cis-acting sequence /cds=UNKNOWN /gb=M82882 ; 38065\_at Cluster Incl.  
X62534:H.sapiens HMG-2 mRNA /cds=(214,843) /gb=X62534 /gi.  
**Metagene** 107; 35605\_at Cluster Incl. AL049653:dJ647M16.1 (Angiopoietin-like factor); likely to;  
34957\_at Cluster Incl. Y18504:Homo sapiens X5L gene /cds=(112,1089) /gb=Y18504 /; 36739\_at  
Cluster Incl. U54617:Human pyruvate dehydrogenase kinase isoform 4 mRNA; 39681\_at Cluster

- Incl. AF060568:Homo sapiens promyelocytic leukemia zinc finger ; 41032\_at Cluster Incl.  
 U56387:Human PC6A protease (hPC6) mRNA, complete cds /cds; 33326\_at Cluster Incl.  
 D42087:Human mRNA for KIAA0118 gene, partial cds /cds=(0,; 33783\_at Cluster Incl.  
 AB007867:Homo sapiens KIAA0407 mRNA, complete cds /cds=(2; 36034\_at Cluster Incl.
- 5 D87447:Human mRNA for KIAA0258 gene, complete cds /cds=(8; 36917\_at Cluster Incl.  
 Z26653:H.sapiens mRNA for laminin M chain (merosin) /cds=; 37230\_at Cluster Incl.  
 AB007938:Homo sapiens mRNA for KIAA0469 protein, complete; 38317\_at Cluster Incl.  
 M99701:Homo sapiens (pp21) mRNA, complete cds /cds=(164,6; 38340\_at Cluster Incl.  
 AB014555:Homo sapiens mRNA for KIAA0655 protein, partial ; 38999\_s\_at Cluster Incl.
- 10 M86707:Homo sapiens myristoyl CoA-protein N-myristoyltr; 40162\_s\_at Cluster Incl.  
 AC003107:Human DNA from chromosome 19-specific cosmid R; 40861\_at Cluster Incl.  
 D14812:Human mRNA for KIAA0026 gene, complete cds /cds=(3; 34377\_at Cluster Incl.  
 J05096:Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, c; 35782\_at Cluster Incl.  
 AB014557:Homo sapiens mRNA for KIAA0657 protein, partial ; 37367\_at Cluster Incl.
- 15 X76228:H.sapiens mRNA for vacuolar H<sup>+</sup> ATPase E subunit /c; 37748\_at Cluster Incl.  
 D86985:Human mRNA for KIAA0232 gene, complete cds /cds=(5; 38734\_at Cluster Incl.  
 M63603:Human phospholamban mRNA, complete cds /cds=(181,3; 39098\_at Cluster Incl.  
 X52896:H.sapiens RNA for dermal fibroblast elastin /cds=U; 40971\_at Cluster Incl. D86982:Human  
 mRNA for KIAA0229 gene, partial cds /cds=(0,; 40973\_at Cluster Incl. A1146846:qb92h04.x1
- 20 Homo sapiens cDNA, 3 end /clone=IMAG; 33136\_at Cluster Incl. AL031714:Human DNA sequence  
 from clone 356B7 on chromosome; 1911\_s\_at M60974 /FEATURE= /DEFINITION=HUMGADD45  
 Human growth arrest and DNA-dam.  
**Metagene** 108; 31641\_s\_at Cluster Incl. AL031282:dJ283E3.2.4 (Matrix Metalloproteinase  
 MMP21/22; 40709\_at Cluster Incl. W27601:35a3 Homo sapiens cDNA /gb=W27601 /gi=1307549
- 25 /ug=; 34218\_at Cluster Incl. U57099:Human APEG-1 mRNA, complete cds /cds=(125,466) /gb;  
 35137\_at Cluster Incl. X69090:H.sapiens mRNA for skeletal muscle 190kD protein /; 36039\_s\_at  
 Cluster Incl. X93498:H.sapiens mRNA for 21-Glutamic Acid-Rich Protein; 38248\_at Cluster Incl.  
 AB011124:Homo sapiens mRNA for KIAA0552 protein, complete; 39423\_f\_at Cluster Incl.  
 AJ000644:Homo sapiens mRNA for SPOP /cds=(157,1281) /gb; 39717\_g\_at Cluster Incl.
- 30 AI597616:tn15f08.x1 Homo sapiens cDNA, 3 end /clone=IM; 41207\_at Cluster Incl.  
 AF043897:Homo sapiens C90RF3 large isoform, mRNA sequence; 33885\_at Cluster Incl.  
 AB020714:Homo sapiens mRNA for KIAA0907 protein, complete; 34870\_at Cluster Incl.  
 AB014513:Homo sapiens mRNA for KIAA0613 protein, partial ; 36142\_at Cluster Incl.  
 X79204:H.sapiens SCA1 mRNA for ataxin /cds=(935,3385) /gb; 36144\_at Cluster Incl.
- 35 D38522:Human mRNA for KIAA0080 gene, partial cds /cds=(0,; 36577\_at Cluster Incl.  
 Z24725:H.sapiens mitogen inducible gene mig-2, complete C; 37304\_at Cluster Incl. U35451:Homo  
 sapiens heterochromatin protein p25 mRNA, com; 38101\_at Cluster Incl. AB011151:Homo sapiens  
 mRNA for KIAA0579 protein, partial ; 38396\_at Cluster Incl. Y09836:H.sapiens mRNA for 3UTR  
 of unknown protein /cds=UN; 40575\_at Cluster Incl. AB011155:Homo sapiens mRNA for

- KIAA0583 protein, partial ; 40994\_at Cluster Incl. L15388:Human G protein-coupled receptor kinase (GRK5) mRNA; 41273\_at Cluster Incl. AL046940:DKFZp586I0517\_r1 Homo sapiens cDNA, 5 end/clon; 32554\_s\_at Cluster Incl. Y12781:Homo sapiens mRNA for transducin (beta) like 1 p; 2056\_at M34641 /FEATURE= /DEFINITION=HUMFGF1A Human fibroblast growth factor (FG;
- 5 2057\_g\_at M34641 /FEATURE= /DEFINITION=HUMFGF1A Human fibroblast growth factor (; 1535\_at U68723 /FEATURE= /DEFINITION=HSU68723 Human checkpoint suppressor 1 mRNA; 1230\_g\_at U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance assoc; 1135\_at L15388 /FEATURE= /DEFINITION=HUMGRK5A Human G protein-coupled receptor k; 822\_s\_at U79115 /FEATURE= /DEFINITION=HSU79115 Human death adaptor molecule RAID;
- 10 738\_at D38524 /FEATURE= /DEFINITION=HUM5N Human mRNA for 5'-nucleotidase ; 498\_at U33821 /FEATURE= /DEFINITION=HSU33821 Homo sapiens tax1-binding protein T.
- Metagene** 109; 40022\_at Cluster Incl. AB008226:Homo sapiens FCMD mRNA for fukutin, complete cds; 41099\_at Cluster Incl. X84740:H.sapiens mRNA for DNA ligase III /cds=(333,3101) ; 41696\_at Cluster Incl. AI620381:tu94d05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33331\_at
- 15 Cluster Incl. U17077:Human BENE mRNA, partial cds /cds=(0,446) /gb=U170; 35216\_at Cluster Incl. X79440:H.sapiens mRNA for NADP+-dependent malic enzyme /c; 35657\_at Cluster Incl. U08998:Human TAR RNA binding protein 2 (TRBP2) mRNA, comp; 36461\_at Cluster Incl. U41804:Human putative T1/ST2 receptor binding protein pre; 37252\_at Cluster Incl. U44755:Human PSE-binding factor PTF delta subunit mRNA, c; 39745\_at Cluster Incl.
- 20 AB011139:Homo sapiens mRNA for KIAA0567 protein, partial ; 40106\_at Cluster Incl. AJ007509:Homo sapiens mRNA for E1B-55kDa-associated prote; 34862\_at Cluster Incl. AA005018:zh96a09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 513\_at U25265 /FEATURE= /DEFINITION=HSU25265 Human MEK5 mRNA, complete cds ; 187\_at U07349 /FEATURE= /DEFINITION=HSU07349 Human B lymphocyte serine/threonine.
- 25 **Metagene** 110; 39253\_s\_at Cluster Incl. M29893:Human low molecular mass GTP-binding protein (ra; 39323\_at Cluster Incl. U45974:Human phosphatidylinositol (4,5) bisphosphate 5-ph; 32057\_at Cluster Incl. U32907:Human p37NB mRNA, complete cds /cds=(281,1222) /gb; 33228\_g\_at Cluster Incl. AI984234:wz57e04.x1 Homo sapiens cDNA, 3 end /clone=IM; 33328\_at Cluster Incl. W28612:49b3 Homo sapiens cDNA /gb=W28612 /gi=1308560 /ug=; 41179\_at Cluster Incl.
- 30 AB029023:Homo sapiens mRNA for KIAA1100 protein, complete; 34363\_at Cluster Incl. Z11793:H.sapiens mRNA for selenoprotein P /cds=(36,1181) ; 37303\_at Cluster Incl. AF057160:Homo sapiens putative poly(ADP-ribosyl) transfer; 37661\_at Cluster Incl. J04027:Human plasma membrane Ca<sup>2+</sup> pumping ATPase mRNA, co; 37671\_at Cluster Incl. S78569:laminin alpha 4 chain [human, fetal lung, mRNA, 62; 41274\_at Cluster Incl. AA908993:ol10d03.s1 Homo sapiens
- 35 cDNA, 3 end /clone=IMAG; 41504\_s\_at Cluster Incl. AF055376:Homo sapiens short form transcription factor C; 33126\_at Cluster Incl. L13435:Human chromosome 3p21.1 gene sequence /cds=UNKNOWN; 1715\_at U37518 /FEATURE= /DEFINITION=HSU37518 Human TNF-related apoptosis induci; 1380\_at M60828 /FEATURE= /DEFINITION=HUMKGF Human keratinocyte growth factor mRNA.

- Metagene 111**; 37161\_at Cluster Incl. W28948:54b12 Homo sapiens cDNA /gb=W28948 /gi=1308896 /ug; 39597\_at Cluster Incl. AB020650:Homo sapiens mRNA for KIAA0843 protein, complete; 41370\_at Cluster Incl. AF090988:Homo sapiens U5 snRNP-specific 40 kDa protein mR; 41399\_at Cluster Incl. AB029034:Homo sapiens mRNA for KIAA1111 protein, partial ; 41712\_at
- 5 Cluster Incl. AB011132:Homo sapiens mRNA for KIAA0560 protein, complete; 31786\_at Cluster Incl. AF051321:Homo sapiens Sam68-like phosphotyrosine protein ; 36537\_at Cluster Incl. AB011093:Homo sapiens mRNA for KIAA0521 protein, partial ; 36858\_at Cluster Incl. D25218:Human mRNA for KIAA0112 gene, partial cds /cds=(0,; 38702\_at Cluster Incl. AF070640:Homo sapiens clone 24781 mRNA sequence /cds=UNKN; 39386\_at Cluster Incl.
- 10 D14811:Human mRNA for KIAA0110 gene, complete cds /cds=(3; 39687\_at Cluster Incl. AI524873:promrna-10.C03.r Homo sapiens cDNA, 5 end /clon; 40774\_at Cluster Incl. X74801:H.sapiens Cctg mRNA for chaperonin /cds=(0,1634) /; 41756\_at Cluster Incl. AJ010842:Homo sapiens mRNA for putative ATP(GTP)-binding ; 32237\_at Cluster Incl. D87454:Human mRNA for KIAA0265 gene, partial cds /cds=(0,; 35313\_at Cluster Incl.
- 15 AB002308:Human mRNA for KIAA0310 gene, complete cds /cds=; 35750\_at Cluster Incl. AL049948:Homo sapiens mRNA; cDNA DKFZp564K0222 (from clon; 36957\_at Cluster Incl. W22296:65A11 Homo sapiens cDNA /clone=(not-directional) /; 37726\_at Cluster Incl. X06323:Human MRL3 mRNA for ribosomal protein L3 homologue; 40189\_at Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M936; 40607\_at Cluster Incl.
- 20 U97105:Homo sapiens N2A3 mRNA, complete cds /cds=(1336,30; 40623\_at Cluster Incl. AI749193:at40e04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40992\_s\_at Cluster Incl. AF055993:Homo sapiens mSin3A associated polypeptide p30; 41360\_at Cluster Incl. AA044787:zk74c11.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1195\_s\_at AF012024 /FEATURE= /DEFINITION=AF012024 Homo sapiens integrin cytoplas.
- 25 **Metagene 112**; 31575\_f\_at Cluster Incl. M14087:Human HL14 gene encoding beta-galactoside-binding; 32396\_f\_at Cluster Incl. AA079018:zm94e12.s1 Homo sapiens cDNA, 3 end /clone=IM; 33633\_at Cluster Incl. AF030335:Homo sapiens purinergic P2Y11 receptor (P2Y11) m; 34071\_at Cluster Incl. Y11918:H.sapiens IMAGE cDNA clone 26881 /cds=UNKNOWN /gb=; 37098\_at Cluster Incl. D38537:Human mRNA for protoporphyrinogen oxidase, complet; 41116\_at Cluster
- 30 Incl. AI799802:wc43d09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41414\_at Cluster Incl. AL050346:Novel human gene mapping to chromosome 22 /cds=(3; 33269\_at Cluster Incl. AB003723:Homo sapiens mRNA for GPI1, complete cds /cds=(1; 35628\_at Cluster Incl. AF023676:Homo sapiens lamin B receptor homolog TM7SF2 (TM; 38425\_at Cluster Incl. U49719:Human hydroxymethylglutaryl-CoA lyase (HMGCL) gene; 40234\_at Cluster Incl.
- 35 X96484:H.sapiens mRNA for DGCR6 protein /cds=(422,676) /g; 991\_g\_at X51602 /FEATURE=cds /DEFINITION=HSFLT Human flt mRNA for receptor-relat.
- Metagene 113**; 34539\_at Cluster Incl. AF065854:Homo sapiens OR7E12P pseudogene, complete sequen; 35585\_at Cluster Incl. X15675:Human pTR7 mRNA for repetitive sequence /cds=UNKNO; 37444\_at Cluster Incl. AF028827:Homo sapiens Tax interaction protein 40 mRNA, pa; 38518\_at

- Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193); 41648\_at Cluster Incl. X78706:H.sapiens mRNA for carnitine acetyltransferase /cd; 35983\_at Cluster Incl. AC004528:Homo sapiens chromosome 19, cosmid R32184 /cds=(; 39328\_at Cluster Incl. M11058:Human 3-hydroxy-3-methylglutaryl coenzyme A reduct; 40054\_at Cluster Incl.
- 5 D43949:Human mRNA for KIAA0082 gene, partial cds /cds=(0,; 40783\_s\_at Cluster Incl. L36151:Homo sapiens phosphatidylinositol 4-kinase mRNA,; 41749\_at Cluster Incl. U53003:Human GT335 mRNA, complete cds /cds=(84,890) /gb=U; 41773\_at Cluster Incl. U58048:Human metalloproteinase PRSM1 mRNA, complete cds /c; 34406\_at Cluster Incl. AB011174:Homo sapiens mRNA for KIAA0602 protein, partial ; 833\_at U40279 /FEATURE=cds
- 10 /DEFINITION=HSITGAD06 Human beta-2 integrin alphaD su.  
**Metagene** 114; 33484\_at Cluster Incl. Y10571:H.sapiens mRNA for dinG gene /cds=(12,1022) /gb=Y1; 34472\_at Cluster Incl. AB012911:Homo sapiens mRNA for Frizzled-6, complete cds /; 36692\_at Cluster Incl. AF052099:Homo sapiens clone 23632 mRNA sequence /cds=UNKN; 38573\_at Cluster Incl. U72209:Human YY1-associated factor 2 (YAF2) mRNA, complet; 38605\_at
- 15 Cluster Incl. AI345944:qp47e09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40347\_at Cluster Incl. AA913812:ol39a08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41379\_at Cluster Incl. AB011166:Homo sapiens mRNA for KIAA0594 protein, partial ; 41381\_at Cluster Incl. AB002306:Human mRNA for KIAA0308 gene, partial cds /cds=(; 41441\_at Cluster Incl. M55654:Human TATA-binding protein mRNA, complete cds /cds; 31872\_at Cluster Incl.
- 20 X79201:H.sapiens mRNA for SYT /cds=(3,1178) /gb=X79201 /g; 31883\_at Cluster Incl. AF025794:Homo sapiens methionine synthase reductase (MTRR; 32621\_at Cluster Incl. M97388:Human TATA binding protein-associated phosphoprote; 32669\_at Cluster Incl. AB014571:Homo sapiens mRNA for KIAA0671 protein, complete; 32706\_at Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cd; 32720\_at Cluster Incl.
- 25 AA151716:zo30d07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32735\_at Cluster Incl. AB023148:Homo sapiens mRNA for KIAA0931 protein, partial ; 33219\_at Cluster Incl. AB029020:Homo sapiens mRNA for KIAA1097 protein, partial ; 34699\_at Cluster Incl. AL050105:Homo sapiens mRNA; cDNA DKFZp586H0519 (from clon; 34728\_g\_at Cluster Incl. AI800578:wg12b07.x1 Homo sapiens cDNA, 3 end /clone=IM; 35231\_at Cluster Incl.
- 30 X12791:Human mRNA for 19kD protein of signal recognition ; 35656\_at Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alte; 36033\_at Cluster Incl. AL049309:Homo sapiens mRNA; cDNA DKFZp564B176 (from clone; 36508\_at Cluster Incl. AF030186:Homo sapiens glypican-4 (GPC4) mRNA, complete cd; 36511\_at Cluster Incl. AB020658:Homo sapiens mRNA for KIAA0851 protein, complete; 37575\_at Cluster Incl.
- 35 AL050192:Homo sapiens mRNA; cDNA DKFZp586C1723 (from clon; 37900\_at Cluster Incl. AF093670:Homo sapiens peroxisomal biogenesis factor (PEX1; 38283\_at Cluster Incl. AB007619:Homo sapiens mRNA for EBAG9, complete cds /cds=(; 38668\_at Cluster Incl. AB011125:Homo sapiens mRNA for KIAA0553 protein, partial ; 38705\_at Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38708\_at Cluster Incl.

- AF054183:Homo sapiens GTP binding protein mRNA, complete ; 38967\_at Cluster Incl.
- AF054175:Homo sapiens mitochondrial proteolipid 68MP homo; 38990\_at Cluster Incl.
- AL031178:Human DNA sequence from clone 341E18 on chromoso; 39034\_at Cluster Incl.
- AL080122:Homo sapiens mRNA; cDNA DKFZp564O123 (from clone; 39382\_at Cluster Incl.
- 5 AB011089:Homo sapiens mRNA for KIAA0517 protein, partial ; 39442\_at Cluster Incl.
- AL080115:Homo sapiens mRNA; cDNA DKFZp564G0222 (from clon; 39691\_at Cluster Incl.
- AB007960:chromosome 1 specific transcript KIAA0491 /cds=U; 39713\_at Cluster Incl.
- AJ132440:Homo sapiens mRNA for PLU-1 protein /cds=(89,472; 39759\_at Cluster Incl.
- AL031781:dJ51J12.1 (human ortholog of zebrafish Quaking p; 40086\_at Cluster Incl.
- 10 D87450:Human mRNA for KIAA0261 gene, partial cds /cds=(0; 40128\_at Cluster Incl.
- D79993:Human mRNA for KIAA0171 gene, complete cds /cds=(1; 40457\_at Cluster Incl.
- AF038250:AF038250 Homo sapiens cDNA /clone=ntcon9 /gb=AF0; 40517\_at Cluster Incl.
- AB002370:Human mRNA for KIAA0372 gene, complete cds /cds=; 40831\_at Cluster Incl.
- AL050190:Homo sapiens mRNA; cDNA DKFZp586B0923 (from clon; 41131\_f\_at Cluster Incl.
- 15 U01923:Human BTK region clone ftp-3 mRNA /cds=UNKNOWN /; 32769\_at Cluster Incl.
- AB023210:Homo sapiens mRNA for KIAA0993 protein, partial ; 32849\_at Cluster Incl.
- D80000:Human mRNA for KIAA0178 gene, partial cds /cds=(0; 33367\_s\_at Cluster Incl.
- D88674:Homo sapiens mRNA for antizyme inhibitor, comple; 33394\_at Cluster Incl.
- AA034074:zi06c05.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 33403\_at Cluster Incl.
- 20 AL050260:Homo sapiens mRNA; cDNA DKFZp547E1010 (from clon; 33877\_s\_at Cluster Incl.
- AB028990:Homo sapiens mRNA for KIAA1067 protein, partia; 33886\_at Cluster Incl.
- AF006516:Homo sapiens eps8 binding protein e3B1 mRNA, com; 34349\_at Cluster Incl.
- AJ011779:Homo sapiens mRNA for SEC63 protein /cds=(98,238; 34781\_at Cluster Incl.
- D84145:Human WS-3 mRNA, complete cds /cds=(87,659) /gb=D8; 34819\_at Cluster Incl.
- 25 D14043:Human mRNA for MGC-24, complete cds /cds=(79,648) ; 34824\_at Cluster Incl.
- AB015344:Homo sapiens HRIHFB2157 mRNA, partial cds /cds=(; 35268\_at Cluster Incl.
- AL050171:Homo sapiens mRNA; cDNA DKFZp586F1122 (from clon; 35271\_at Cluster Incl.
- AF006083:Homo sapiens actin-related protein Arp3 (ARP3) m; 35290\_at Cluster Incl.
- AL050081:Homo sapiens mRNA; cDNA DKFZp566J2146 (from clon; 35306\_at Cluster Incl.
- 30 AB001636:Homo sapiens mRNA for ATP-dependent RNA helicase; 35734\_at Cluster Incl.
- AI935551:wo97g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35761\_at Cluster Incl.
- AL050073:Homo sapiens mRNA; cDNA DKFZp566E2346 (from clon; 35793\_at Cluster Incl.
- AB014560:Homo sapiens mRNA for KIAA0660 protein, complete; 35818\_at Cluster Incl.
- D00265:Homo sapiens mRNA for cytochrome c, partial cds /c; 36110\_at Cluster Incl.
- 35 M28215:Homo sapiens GTP-binding protein (RAB5) mRNA, comp; 36176\_at Cluster Incl.
- U61234:Human tubulin-folding cofactor C mRNA, complete cd; 36579\_at Cluster Incl.
- D50916:Human mRNA for KIAA0126 gene, complete cds /cds=(7; 36604\_at Cluster Incl.
- D83004:Human epidermoid carcinoma mRNA for ubiquitin-conj; 36608\_at Cluster Incl.
- D55654:Human mRNA for cytosolic malate dehydrogenase, com; 36655\_at Cluster Incl.

- L27476:Human X104 mRNA, complete cds /cds=(79,3429) /gb=L; 36943\_r\_at Cluster Incl.
- U81992:Homo sapiens C2H2 zinc finger protein PLAGL1 (PL; 37036\_at Cluster Incl.
- AB002299:Human mRNA for KIAA0301 gene, partial cds /cds=(; 37296\_at Cluster Incl.
- L28997:Homo sapiens ARL1 mRNA, complete cds /cds=(144,689; 37336\_at Cluster Incl.
- 5 D87684:Human mRNA for KIAA0242 gene, partial cds /cds=(0; 37359\_at Cluster Incl.
- D14658:Human mRNA for KIAA0102 gene, complete cds /cds=(3; 37392\_at Cluster Incl.
- X84908:H.sapiens mRNA for phosphorylase-kinase, beta subu; 37663\_at Cluster Incl.
- X70649:Homo sapiens DDX1 gene, complete CDS /cds=(288,251; 37670\_at Cluster Incl.
- J04543:Human synexin mRNA, complete cds /cds=(60,1460) /g; 38016\_at Cluster Incl.
- 10 M94630:Homo sapiens hnRNP-C like protein mRNA, complete c; 38035\_at Cluster Incl.
- AF072928:Homo sapiens myotubularin related protein 6 mRNA; 38040\_at Cluster Incl.
- AF107463:Homo sapiens splicing factor mRNA, complete cds ; 38074\_at Cluster Incl.
- U91932:Homo sapiens AP-3 complex sigma3A subunit mRNA, co; 38102\_at Cluster Incl.
- W28575.51f12 Homo sapiens cDNA /gb=W28575 /gi=1308730 /ug; 38441\_s\_at Cluster Incl.
- 15 X59408:H.sapiens, gene for Membrane cofactor protein /c; 38462\_at Cluster Incl. U64028:Human NADH-ubiquinone oxidoreductase subunit B13 m; 38472\_at Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0; 38835\_at Cluster Incl. U94831:Homo sapiens multispinning membrane protein mRNA, ; 38846\_at Cluster Incl. AA768912:nz82h06.s1 Homo sapiens cDNA /clone=IMAGE-130201; 39099\_at Cluster Incl. X97064:H.sapiens mRNA for Sec23A isoform, 2748bp /cds=(15; 39117\_at Cluster Incl. AB014562:Homo sapiens mRNA for KIAA0662 protein, partial ; 40262\_at Cluster Incl. AF031166:Homo sapiens SRp46 splicing factor retrospudoge; 40901\_at Cluster Incl. U17989:Homo sapiens nuclear autoantigen GS2NA mRNA, compl; 41320\_s\_at Cluster Incl. U69609:Human transcriptional repressor (GCF2) mRNA, com; 41342\_at Cluster Incl. D38076:Human mRNA for RanBP1 (Ran-binding protein 1), com; 41562\_at Cluster Incl.
- 25 L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cd; 41823\_at Cluster Incl. AJ132258:Homo sapiens mRNA for staufer protein, partial /; 32508\_at Cluster Incl.
- AL096857:Novel human mRNA from chromosome 1, which has si; 33107\_at Cluster Incl.
- AB020705:Homo sapiens mRNA for KIAA0898 protein, partial ; 1789\_at U65928 /FEATURE= /DEFINITION=HSU65928 Human Jun activation domain bindin; 1329\_s\_at U74382 /FEATURE=
- 30 /DEFINITION=HSU74382 Human telomeric repeat DNA-bindi; 1238\_at U09759 /FEATURE= /DEFINITION=HSU09759 Human protein kinase (JNK2) mRNA, ; 1046\_at U34605 /FEATURE= /DEFINITION=HSU34605 Human retinoic acid- and interfero; 891\_at M77698 /FEATURE= /DEFINITION=HUMKRP Homo sapiens GLI-Krupple related prot; 812\_at U68111 /FEATURE=mRNA /DEFINITION=HSPPP1R2E6 Human protein phosphatase inh; 630\_at L39874
- 35 /FEATURE=expanded\_cds /DEFINITION=HUMDODDA Homo sapiens deoxycytid; 509\_at U44378 /FEATURE= /DEFINITION=HSU44378 Human homozygous deletion target in; 510\_g\_at U44378 /FEATURE= /DEFINITION=HSU44378 Human homozygous deletion target ; 488\_at U61166 /FEATURE= /DEFINITION=HSU61166 Human SH3 domain-containing protein; 379\_at AB006679 /FEATURE= /DEFINITION=AB006679 Homo sapiens mRNA for ATP binding.



- Metagene 115**; 34099\_f\_at Cluster Incl. W26056:18e1 Homo sapiens cDNA /gb=W26056 /gi=1306323 /u; 35408\_i\_at Cluster Incl. X16281:Human mRNA for zinc finger protein (clone 431) /; 39360\_at Cluster Incl. AF034546:Homo sapiens sorting nexin 3 (SNX3) mRNA, comple; 32232\_at Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subu;
- 5 39826\_f\_at Cluster Incl. W29115:56e8 Homo sapiens cDNA /gb=W29115 /gi=1309081 /u; 1668\_s\_at L15409 /FEATURE= /DEFINITION=HUMHIPLIND Homo sapiens (clone g7) von Hi.
- Metagene 116**; 32021\_at Cluster Incl. AI560890:tq41d05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33035\_at Cluster Incl. AL021397:dj69E11.3 (Yeast YPR037W and worm C02C2.6 predic; 35413\_s\_at Cluster Incl. AA258092:zs30g01.r1 Homo sapiens cDNA, 5 end /clone=IM;
- 10 35870\_at Cluster Incl. AJ007714:Homo sapiens mRNA for lysine-ketoglutarate reduc; 35963\_at Cluster Incl. AI201243:qf70f09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37506\_at Cluster Incl. Z78308:HSZ78308 Homo sapiens cDNA /clone=1.47-(CEPH) /gb=; 37507\_i\_at Cluster Incl. AA675900:g02504r Homo sapiens cDNA, 5 end /clone=g0250; 40713\_at Cluster Incl. AB020634:Homo sapiens mRNA for KIAA0827 protein, complete; 32124\_at Cluster Incl.
- 15 AL030996:dJ1189B24.4 (novel PUTATIVE protein similar to h; 39436\_at Cluster Incl. AF079221:Homo sapiens BCL2/adenovirus E1B 19kDa-interacti; 38807\_at Cluster Incl. AA043348:zk66b12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38814\_at Cluster Incl. AF038954:Homo sapiens vacuolar H(+)-ATPase subunit mRNA, ; 40920\_at Cluster Incl. AF023158:Homo sapiens tyrosine phosphatase (cdc14B) mRNA,; 450\_g\_at U66469 /FEATURE=
- 20 /DEFINITION=HSU66469 Human cell growth regulator CGR19; 147\_at U82130 /FEATURE= /DEFINITION=HSU82130 Human tumor susceptibility protein (. **Metagene 117**; 32030\_at Cluster Incl. X99459:H.sapiens mRNA for sigma 3B protein /cds=(30,611) ; 35984\_at Cluster Incl. AF041381:Homo sapiens putative transcriptional repressor ; 40827\_at Cluster Incl. U04953:Human isoleucyl-tRNA synthetase mRNA, complete cds; 41750\_at Cluster
- 25 Incl. D49489:Human mRNA for protein disulfide isomerase-related; 33369\_at Cluster Incl. AI535653:P9-C4.T3.P9.D4 Homo sapiens cDNA, 3 end /clone\_; 33422\_at Cluster Incl. AF052155:Homo sapiens clone 24761 mRNA sequence /cds=UNKN; 34390\_at Cluster Incl. U90441:Human prolyl 4-hydroxylase alpha (II) subunit mRNA; 35340\_at Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36992\_at Cluster Incl.
- 30 AI653621:tz21b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37046\_at Cluster Incl. AI246726:qk40a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40584\_at Cluster Incl. Y08612:Homo sapiens mRNA for nuclear pore complex protein; 32539\_at Cluster Incl. U51205:Human COP9 homolog (HCOP9) mRNA, complete cds /cds; 890\_at M74524 /FEATURE= /DEFINITION=HUMHHR6A Human HHR6A (yeast RAD 6 homologue).
- 35 **Metagene 118**; 31481\_s\_at Cluster Incl. M92383:Homo sapiens thymosin beta-10 gene, 3end /cds=(0; 32434\_at Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds ; 32321\_at Cluster Incl. X56841:H.sapiens HLA-E gene /cds=(0,363) /gb=X56841 /gi=4; 35012\_at Cluster Incl. M81750:H.sapiens myeloid cell nuclear differentiation ant; 37509\_at Cluster Incl. AF046059:Homo sapiens cytokine receptor related protein 4; 37845\_at Cluster Incl. M58285:Human

- membrane-associated protein (HEM-1) mRNA, co; 38893\_at Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosom; 39581\_at Cluster Incl. AA570193:nf38c11.s1 Homo sapiens cDNA /clone=IMAGE-916052; 40310\_at Cluster Incl. AF051152:Homo sapiens Toll/interleukin-1 receptor-like pr; 40685\_at Cluster Incl. U10868:Human aldehyde dehydrogenase
- 5 ALDH7 mRNA, complete ; 40757\_at Cluster Incl. M18737:Human Hanukah factor serine protease (HuHF) mRNA, ; 41425\_at Cluster Incl. M98833:Human ERGB transcription factor (FLI-1 homolog) mR; 41716\_at Cluster Incl. AB020663:Homo sapiens mRNA for KIAA0856 protein, partial ; 41868\_at Cluster Incl. J04131:Human gamma-glutamyl transpeptidase (GGT) protein ; 31845\_at Cluster Incl. U32645:Human myeloid elf-1 like factor (MEF) mRNA, comple; 32035\_at
- 10 Cluster Incl. M16942:Human MHC class II HLA-DRw53-associated glycoprote; 32083\_at Cluster Incl. AF027826:Homo sapiens putative seven pass transmembrane p; 33238\_at Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinas; 33253\_at Cluster Incl. D50919:Human mRNA for KIAA0129 gene, complete cds /cds=(1; 33777\_at Cluster Incl. D34625:Human TBXAS1 gene for thromboxane synthase, promot; 35172\_at Cluster Incl.
- 15 AF049891:Homo sapiens tyrosylprotein sulfotransferase-2 m; 35995\_at Cluster Incl. AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complet; 37565\_at Cluster Incl. X85750:H.sapiens mRNA for transcript associated with mono; 37966\_at Cluster Incl. AA187563:zp66g11.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 38006\_at Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds; 38332\_at Cluster Incl.
- 20 U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=; 39023\_at Cluster Incl. AF020038:Homo sapiens NADP-dependent isocitrate dehydroge; 39760\_at Cluster Incl. AL031781:dJ51J12.1.3 (human ortholog of mouse KH Domain R; 40407\_at Cluster Incl. U28386:Human nuclear localization sequence receptor hSRP1; 40456\_at Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from clone; 32193\_at Cluster Incl.
- 25 AF030339:Homo sapiens receptor for viral semaphorin prote; 33839\_at Cluster Incl. D26350:Human mRNA for type 2 inositol 1,4,5-trisphosphate; 34889\_at Cluster Incl. AA056747:zk81f02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35320\_at Cluster Incl. AB004857:Homo sapiens mRNA for NRAMP2, complete cds /cds=; 36576\_at Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete ; 36938\_at Cluster Incl. U70063:Human acid ceramidase mRNA,
- 30 complete cds /cds=(17; 37363\_at Cluster Incl. AB007889:Homo sapiens KIAA0429 mRNA, complete cds /cds=(2; 37684\_at Cluster Incl. AB020687:Homo sapiens mRNA for KIAA0880 protein, complete; 38370\_at Cluster Incl. U90902:Human clone 23612 mRNA sequence /cds=UNKNOWN /gb=U; 38378\_at Cluster Incl. M37033:Human CD53 glycoprotein mRNA, complete cds /cds=(9; 38379\_at Cluster Incl. X76534:H.sapiens NMB mRNA /cds=(91,1773) /gb=X76534 /gi=6; 40278\_at Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial ; 40571\_at Cluster Incl. U90942:Human myosin heavy chain 12 (MYO5A) mRNA, complete; 40585\_at Cluster Incl. D25538:Human mRNA for KIAA0037 gene, complete cds /cds=(2; 40910\_at Cluster Incl. U56637:Human capping protein alpha subunit isoform 1 mRNA; 41812\_s\_at Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partia; 41824\_at Cluster Incl.

- AI140114:qa95c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1478\_at L10717 /FEATURE=  
/DEFINITION=HUMTKTCS Homo sapiens T cell-specific tyros; 1405\_i\_at M21121 /FEATURE=  
/DEFINITION=HUMTCSM Human T cell-specific protein (RA; 1062\_g\_at U00672 /FEATURE=  
/DEFINITION=U00672 Human interleukin-10 receptor mRNA; 461\_at U70063 /FEATURE=  
5 /DEFINITION=HSU70063 Human acid ceramidase mRNA, complet.
- Metagene** 119; 36134\_at Cluster Incl. U79299:Human neuronal olfactomedin-related ER localized  
p; 38409\_at Cluster Incl. M61199:Human cleavage signal 1 protein mRNA, complete cds; 38737\_at  
Cluster Incl. X57025:Human IGF-I mRNA for insulin-like growth factor I ; 1625\_at Insulin-Like  
Growth Factor Ib ; 1501\_at X57025 /FEATURE=mRNA /DEFINITION=HSIGFACI Human IGF-I  
10 mRNA for insulin-l.
- Metagene** 120; 38210\_at Cluster Incl. Z35094:H.sapiens mRNA for SURF-2 /cds=(17,787)  
/gb=Z35094; 38889\_at Cluster Incl. AF104304:Homo sapiens Smad anchor for receptor activation;  
39929\_at Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial ; 39984\_g\_at  
Cluster Incl. U73704:Homo sapiens 48 kDa FKBP-associated protein FAP4; 40758\_at Cluster Incl.
- 15 X81788:Homo sapiens ICT1 (alias DS-1) mRNA /cds=(2,622) /; 41671\_at Cluster Incl.  
U97018:Homo sapiens echinoderm microtubule-associated pro; 32672\_at Cluster Incl.  
AL049387:Homo sapiens mRNA; cDNA DKFZp586N1918 (from clon; 33256\_at Cluster Incl.  
Y14494:Homo sapiens mRNA for mitochondrial carrier protei; 33713\_at Cluster Incl.  
AJ005895:Homo sapiens mRNA for (JM3) preprotein transloca; 33751\_at Cluster Incl.
- 20 AL109702:Homo sapiens mRNA full length insert cDNA clone ; 34292\_at Cluster Incl.  
X92475:H.sapiens mRNA for ITBA1 protein /cds=(284,1069) /; 35247\_at Cluster Incl.  
AI557062:PT2.1\_13\_A09.r Homo sapiens cDNA, 3 end /clone\_; 35719\_at Cluster Incl.  
AB011178:Homo sapiens mRNA for KIAA0606 protein, partial ; 37549\_g\_at Cluster Incl.  
U87408:Human clone IMAGE-74593 unknown protein mRNA, pa; 37646\_at Cluster Incl.
- 25 D26018:Human mRNA for KIAA0039 gene, partial cds /cds=(0,; 39394\_at Cluster Incl.  
AF007149:Homo sapiens clone 23568, 23621, 23795, 23873 an; 39705\_at Cluster Incl.  
AB014600:Homo sapiens mRNA for KIAA0700 protein, partial ; 39772\_at Cluster Incl.  
AF007157:Homo sapiens clone 23856 unknown mRNA, partial c; 40462\_at Cluster Incl.  
AF055022:Homo sapiens clone 24684 mRNA sequence /cds=UNKN; 40852\_at Cluster Incl.
- 30 AB025254:Homo sapiens mRNA for tudor repeat associator wi; 32246\_g\_at Cluster Incl.  
AF014837:Homo sapiens m6A methyltransferase (MT-A70) ge; 32823\_at Cluster Incl.  
W28734:51a1 Homo sapiens cDNA /gb=W28734 /gi=1308682 /ug=; 34848\_at Cluster Incl.  
X69141:H.sapiens mRNA for squalene synthase /cds=(91,1344; 34868\_at Cluster Incl.  
AB029012:Homo sapiens mRNA for KIAA1089 protein, partial ; 35274\_at Cluster Incl.
- 35 Y12226:H.sapiens mRNA for gamma-adaptin /cds=(28,2505) /g; 35792\_at Cluster Incl.  
U67963:Human lysophospholipase homolog (HU-K5) mRNA, comp; 36115\_at Cluster Incl.  
L29217:Homo sapiens clk3 mRNA, complete cds /cds=(56,1528; 39557\_at Cluster Incl.  
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AF047185:Homo sapiens NADH-ubiquinone oxidoreductase su; 41349\_at Cluster Incl.

- L43964:Homo sapiens (clone F-T03796) STM-2 mRNA, complete; 32558\_at Cluster Incl.  
 AB021868:Homo sapiens PIAS3 mRNA for protein inhibitor of; 927\_s\_at J05582  
 /FEATURE=mRNA /DEFINITION=HUMPANMU Human pancreatic mucin mRNA, ; 101\_at  
 Y09305 /FEATURE=cds /DEFINITION=HSDYRK4 H.sapiens mRNA for protein kinase.
- 5 **Metagene** 121; 41871\_at Cluster Incl. AI660929:wf20a09.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 35208\_at Cluster Incl. AB020681:Homo sapiens mRNA for KIAA0874 protein,  
 partial ; 35622\_at Cluster Incl. AB001451:Homo sapiens mRNA for Sck, partial cds /cds=(0,1;  
 36899\_at Cluster Incl. M97287:Human MAR/SAR DNA binding protein (SATB1) mRNA, co;  
 38250\_at Cluster Incl. D26488:Human mRNA for KIAA0007 gene, partial cds /cds=(0,; 41167\_at  
 10 Cluster Incl. M64929:Human protein phosphatase 2A alpha subunit mRNA, c; 34316\_at Cluster Incl.  
 W52024:zd13a03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 38013\_at Cluster Incl.  
 AL096842:Homo sapiens mRNA; cDNA DKFZp586D1519 (from clone; 40203\_at Cluster Incl.  
 AJ012375:Homo sapiens mRNA for SUI1 protein translation i; 1226\_at U69611 /FEATURE=  
 /DEFINITION=HSU69611 Human TNF-alpha converting enzyme .
- 15 **Metagene** 122; 35489\_at Cluster Incl. M82962:Human N-benzoyl-L-tyrosyl-p-amino-benzoic acid  
 hyd; 447\_g\_at U89896 /FEATURE= /DEFINITION=HSU89896 Homo sapiens casein kinase I  
 gamm; 372\_f\_at Z84718 /FEATURE=cds#2 /DEFINITION=HS322B1 Human DNA sequence from  
 clone.  
**Metagene** 123; 34959\_at Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA,  
 com; 38879\_at Cluster Incl. D83664:Human mRNA for CAAF1 (calcium-binding protein in a;  
 41365\_at Cluster Incl. Y09788:H.sapiens MUC5B gene /cds=(0,2538) /gb=Y09788 /gi=; 34319\_at  
 Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1352\_at U11870  
 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8 receptor t.
- 20 **Metagene** 124; 35951\_at Cluster Incl. AB018286:Homo sapiens mRNA for KIAA0743 protein,  
 complete; 37459\_at Cluster Incl. X57527:Human COL8A1 mRNA for alpha 1(VIII) collagen /cds=;  
 41864\_at Cluster Incl. AF052181:Homo sapiens clone 24790 mRNA sequence /cds=UNKN;  
 36853\_at Cluster Incl. M64752:Human glutamate receptor subunit (GluH1) mRNA, com; 37628\_at  
 Cluster Incl. M69177:Human monoamine oxidase B (MAOB) mRNA, complete cd; 40078\_at  
 Cluster Incl. AF015287:Homo sapiens serine protease mRNA, complete cds ; 33431\_at Cluster Incl.
- 25 U05291:Human fibromodulin mRNA, partial cds /cds=(0,177) ; 35752\_s\_at Cluster Incl.  
 M15036:Human vitamin K-dependent plasma protein S mRNA,; 40936\_at Cluster Incl.  
 AI651806:wb55f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41294\_at Cluster Incl.  
 AJ238246:Homo sapiens mRNA for sarcolectin /cds=(61,1470); 32593\_at Cluster Incl.  
 D42043:Human mRNA for KIAA0084 gene, partial cds /cds=(0,; 2073\_s\_at L34058 /FEATURE=  
 30 /DEFINITION=HUMCA13A Homo sapiens cadherin-13 mRNA, c; 482\_at U59289 /FEATURE=  
 /DEFINITION=HSU59289 Human H-cadherin mRNA, complete cds; 483\_g\_at U59289  
 /FEATURE= /DEFINITION=HSU59289 Human H-cadherin mRNA, complete c.
- 35 **Metagene** 125; 31670\_s\_at Cluster Incl. U81554:Homo sapiens CaM kinase II isoform mRNA,  
 complet; 31987\_at Cluster Incl. AL049268:Homo sapiens mRNA; cDNA DKFZp564G103 (from

- clone; 33988\_at Cluster Incl. X75861:H.sapiens TEGT gene /cds=(40,753) /gb=X75861 /gi=4;  
 39607\_at Cluster Incl. AL080178:Homo sapiens mRNA; cDNA DKFZp434K171 (from clone;  
 39663\_at Cluster Incl. D63998:Human mRNA for golgi alpha-mannosidaseII, complete; 33302\_at  
 Cluster Incl. AF016028:Homo sapiens sarcospan-2 (SPN2) mRNA, complete c; 37264\_at Cluster  
 5 Incl. U09410:Human zinc finger protein ZNF131 mRNA, partial cds; 37608\_g\_at Cluster Incl.  
 AJ005168:Homo sapiens KHK gene, exons 4-8 /cds=(0,552) ; 38650\_at Cluster Incl. L27560:Human  
 insulin-like growth factor binding protein 5; 38673\_s\_at Cluster Incl. D64137:Human KIP2 gene for  
 Cdk-inhibitor p57KIP2, compl; 39327\_at Cluster Incl. D86983:Human mRNA for KIAA0230 gene,  
 partial cds /cds=(0,; 38841\_at Cluster Incl. AF068195:Homo sapiens putative glialblastoma cell  
 10 differe; 39561\_at Cluster Incl. AL008583:dJ327J16.3 (novel CHROMObox family protein) /cds;  
 40275\_at Cluster Incl. AL046322:DKFZp434I087\_r1 Homo sapiens cDNA, 5 end /clone;  
 40552\_s\_at Cluster Incl. AL049987:Homo sapiens mRNA; cDNA DKFZp564F112 (from clo;  
 41293\_at Cluster Incl. A1123710:oo16h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41829\_at  
 Cluster Incl. AB018274:Homo sapiens mRNA for KIAA0731 protein, partial ; 2050\_s\_at M29870  
 15 /FEATURE= /DEFINITION=HUMRACA Human ras-related C3 botulinum to; 1677\_at M65062  
 /FEATURE= /DEFINITION=HUMIGFBP6 Human insulin-like growth factor ; 1396\_at L27560  
 /FEATURE=mRNA /DEFINITION=HUMIGFBP5X Human insulin-like growth fa; 1114\_at  
 M22490 /FEATURE= /DEFINITION=HUMBMP2B Human bone morphogenetic protein-2.  
**Metagene** 126; 34928\_at Cluster Incl. AF060865:Homo sapiens chromosome 16 zinc finger protein  
 20 Z; 40377\_at Cluster Incl. AB014582:Homo sapiens mRNA for KIAA0682 protein, complete;  
 32661\_s\_at Cluster Incl. D79992:Human mRNA for KIAA0170 gene, complete cds /cds=; 33732\_at  
 Cluster Incl. Y08387:H.sapiens mRNA for mu-ARP2 protein /cds=(54,1415) ; 39022\_at Cluster Incl.  
 AL050110:Homo sapiens mRNA; cDNA DKFZp586J0619 (from clon; 40833\_r\_at Cluster Incl.  
 AL050126:Homo sapiens mRNA; cDNA DKFZp586G011 (from clo; 38020\_at Cluster Incl.  
 25 AB014552:Homo sapiens mRNA for KIAA0652 protein, complete; 38109\_at Cluster Incl.  
 AF020544:Homo sapiens inactive palmitoyl-protein thioeste; 33111\_at Cluster Incl.  
 AI333845:qp99a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 942\_at D31815 /FEATURE=  
 /DEFINITION=HUMSMP30 Human mRNA for SMP-30 (senescence m.  
**Metagene** 127; 34480\_at Cluster Incl. AF016272:Homo sapiens Ksp-cadherin (CDH16) mRNA,  
 30 complete; 40366\_at Cluster Incl. M25322:Human granule membrane protein-140 mRNA, complete ;  
 33284\_at Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKN;  
 38284\_at Cluster Incl. AJ007041:Homo sapiens mRNA for trithorax homologue 2 /cds; 34303\_at  
 Cluster Incl. AL049949:Homo sapiens mRNA; cDNA DKFZp564L0822 (from clon; 36150\_at  
 Cluster Incl. AB020649:Homo sapiens mRNA for KIAA0842 protein, partial ; 37760\_at Cluster Incl.  
 35 AB015019:Homo sapiens mRNA for BAP2-alpha protein, comple; 38064\_at Cluster Incl.  
 X79882:H.sapiens lrp mRNA /cds=(105,2795) /gb=X79882 /gi=; 39119\_s\_at Cluster Incl.  
 AA631972:fmfc39 Homo sapiens cDNA /clone=CR7-5 /gb=AA63; 1196\_at D00591  
 /FEATURE=exons#7-14 /DEFINITION=HUMRCC1 Homo sapiens RCC1 gene, e.  
**Metagene** 128; 32447\_at Cluster Incl. U76388:Human steroidogenic factor 1 mRNA, complete cds

- /c; 35519\_at Cluster Incl. AL049431:Homo sapiens mRNA; cDNA DKFZp586J211 (from clone; 35864\_at Cluster Incl. Y00970:Human mRNA for acrosin (EC 3.4.21.10) /cds=(16,128; 35896\_at Cluster Incl. D87002:Human (lambda) DNA for immunoglobulin light chain /c; 34280\_at Cluster Incl. Y09765:Homo sapiens mRNA for putative GABA receptor epsilon; 35152\_at Cluster Incl.
- 5 AJ001016:Homo sapiens mRNA encoding RAMP3 /cds=(29,475) /; 37272\_at Cluster Incl. X57206:H.sapiens mRNA for 1D-myo-inositol-trisphosphate 3; 38269\_at Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone; 38628\_at Cluster Incl. AF029777:Homo sapiens histone acetyltransferase (GCN5) mRNA; 39358\_at Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid h; 41203\_at Cluster Incl. L49380:Homo sapiens clone B4 transcription factor ZFM1 mRNA; 33454\_at Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /; 33916\_at Cluster Incl. AB023192:Homo sapiens mRNA for KIAA0975 protein, partial ; 37365\_at Cluster Incl. X63368:H.sapiens HSJ1 mRNA /cds=(25,1080) /gb=X63368 /gi=; 37687\_i\_at Cluster Incl. M31932:Human IgG low affinity Fc fragment receptor (FcR; 32592\_at Cluster Incl. AB002321:Human mRNA for KIAA0323 gene, partial cds /cds=(; 1988\_at X76079 /FEATURE=exons#1-4 /DEFINITION=HSPDGF H.sapiens mRNA for platelet; 1664\_at Insulin-Like Growth Factor 2 ; 1119\_at J05249 /FEATURE= /DEFINITION=HUMREPA Human replication protein A 32-kDa ; 448\_s\_at U93237 /FEATURE=mRNA#1 /DEFINITION=HSU93237 Human menin (MEN1) gene, co; 181\_g\_at S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhancer.
- 20 **Metagene** 129; 34993\_at Cluster Incl. X95191:H.sapiens mRNA for delta-sarcoglycan /cds=(0,872) ; 38965\_at Cluster Incl. M55172:Human large aggregating cartilage proteoglycan core; 39206\_s\_at Cluster Incl. X17406:Human mRNA for cartilage specific proteoglycan /; 39207\_r\_at Cluster Incl. X17406:Human mRNA for cartilage specific proteoglycan /; 39250\_at Cluster Incl. X96584:H.sapiens mRNA for NOV protein /cds=(72,1145) /gb=; 39616\_at Cluster Incl.
- 25 AL050227:Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone; 39966\_at Cluster Incl. AF059274:Homo sapiens neuroglycan C mRNA, complete cds /c; 31888\_s\_at Cluster Incl. AF001294:Homo sapiens IPL (IPL) mRNA, complete cds /cds; 32687\_s\_at Cluster Incl. X83857:H.sapiens mRNA for prostaglandin E receptor (EP3; 34285\_at Cluster Incl. AB018338:Homo sapiens mRNA for KIAA0795 protein, partial ; 35729\_at Cluster Incl.
- 30 AB018270:Homo sapiens mRNA for KIAA0727 protein, partial ; 38643\_at Cluster Incl. W87466:zh67c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 39063\_at Cluster Incl. J00073:Human alpha-cardiac actin gene, 5 flank and /cds=(; 41126\_at Cluster Incl. AA978353:oq40b07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41758\_at Cluster Incl. AL096879:Novel human mRNA similar to C. elegans gene WP-C; 32182\_at Cluster Incl.
- 35 AB023182:Homo sapiens mRNA for KIAA0965 protein, partial ; 32838\_at Cluster Incl. S67247:smooth muscle myosin heavy chain isoform SMemb [hu; 35833\_at Cluster Incl. AL080184:Homo sapiens mRNA; cDNA DKFZp434O071 (from clone; 37658\_at Cluster Incl. L13720:Homo sapiens growth-arrest-specific protein (gas) ; 38034\_at Cluster Incl. M16505:Human steroid sulfatase (STS) mRNA, complete cds /; 1424\_s\_at D78577 /FEATURE=expanded\_cds

- /DEFINITION=D78576S2 Human DNA for 14-3-3.
- Metagene 130;** 33004\_g\_at Cluster Incl. AI275502:ql74d06.x1 Homo sapiens cDNA, 3 end /clone=IM; 36767\_at Cluster Incl. K03191:Human cytochrome P-1-450 (TCDD-inducible) mRNA, co; 32714\_s\_at Cluster Incl. L17075:Human TGF-b superfamily receptor type I mRNA, co;
- 5 41260\_at Cluster Incl. U59321:Human DEAD-box protein p72 (P72) mRNA, complete cd; 1025\_g\_at X02612 /FEATURE=expanded\_cds /DEFINITION=HSCYP450 Human gene for cytoc.
- Metagene 131;** 31457\_at Cluster Incl. AF042832:Homo sapiens forkhead-related transcription fact; 38223\_at Cluster Incl. AB024057:Homo sapiens mRNA for vascular Rab-GAP/TBC-conta; 40348\_s\_at Cluster Incl. W25866:14c12 Homo sapiens cDNA /gb=W25866 /gi=1305989 /; 39387\_at
- 10 Cluster Incl. U34044:Human selenium donor protein (selD) mRNA, complete; 40092\_at Cluster Incl. AB002312:Human mRNA for KIAA0314 gene, partial cds /cds=(; 32248\_at Cluster Incl. AL045811:DKFZp434H166\_r1 Homo sapiens cDNA, 5 end /clone; 1217\_g\_at X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase.
- Metagene 132;** 39392\_at Cluster Incl. AJ002190:Homo sapiens cDNA for dihydroxyacetone
- 15 phosphate; 41196\_at Cluster Incl. L38951:Homo sapiens importin beta subunit mRNA, complete ; 37650\_at Cluster Incl. U41315:Human ring zinc-finger protein (ZNF127-Xp) gene an; 37725\_at Cluster Incl. X74008:H.sapiens mRNA for protein phosphatase 1 gamma /cd; 41243\_at Cluster Incl. AB007916:Homo sapiens mRNA for KIAA0447 protein, complete; 1239\_s\_at U13021 /FEATURE=
- 20 /DEFINITION=HSU13021 Human positive regulator of prog; 555\_at U05227 /FEATURE= /DEFINITION=HSU05227 Human Rar protein mRNA, complete cd.
- Metagene 133;** 31680\_at Cluster Incl. M55630:Human topoisomerase I pseudogene 2 /cds=UNKNOWN /g; 38545\_at Cluster Incl. M31682:Human testicular inhibin beta-B-subunit mRNA, 3 e; 40735\_at Cluster Incl. D16626:Human mRNA for histidase, complete cds /cds=(243,2; 41100\_at Cluster Incl. AB023172:Homo sapiens mRNA for KIAA0955 protein, complete; 41460\_at
- 25 Cluster Incl. AF080561:Homo sapiens SYT interacting protein SIP mRNA, c; 31802\_at Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(6; 32644\_at Cluster Incl. D79991:Human mRNA for KIAA0169 gene, partial cds /cds=(0; 34765\_at Cluster Incl. D13645:Human mRNA for KIAA0020 gene, complete cds /cds=(4; 39755\_at Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome; 40050\_at Cluster Incl.
- 30 AF069747:Homo sapiens MTG8-like protein MTGR1a mRNA, comp; 32245\_at Cluster Incl. AF014837:Homo sapiens m6A methyltransferase (MT-A70) gene; 32820\_at Cluster Incl. U71267:Human potential transcriptional repressor NOT4Hp (; 35351\_at Cluster Incl. U89505:Human Hlark mRNA, complete cds /cds=(55,1155) /gb=; 35830\_at Cluster Incl. AB002368:Human mRNA for KIAA0370 gene, partial cds /cds=(; 37676\_at Cluster Incl.
- 35 AF056490:Homo sapiens cAMP-specific phosphodiesterase 8A ; 40891\_f\_at Cluster Incl. X92896:H.sapiens mRNA for ITBA2 protein /cds=(10,327) /; 40946\_at Cluster Incl. AI023044:ow65c01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1248\_at U37689 /FEATURE= /DEFINITION=HSU37689 Human RNA polymerase II subunit (h; 776\_at D13435 /FEATURE= /DEFINITION=HUMPIGF Human mRNA for PIG-F (phosphatidyl-i.

- Metagene 134;** 31562\_at Cluster Incl. U63973:Human rhodopsin kinase mRNA, complete cds /cds=(10; 32364\_at Cluster Incl. AJ011785:Homo sapiens mRNA for Six9 protein /cds=(74,814); 34467\_g\_at Cluster Incl. Y12505:H.sapiens mRNA for serotonin receptor 5-HT4B, sp; 35403\_at Cluster Incl. AB029017:Homo sapiens mRNA for KIAA1094 protein, complete; 37832\_at Cluster
- 5 Incl. AL080062:Homo sapiens mRNA; cDNA DKFZp564I122 (from clone; 38215\_at Cluster Incl. U84894:Human 239AB mRNA, complete cds /cds=(114,1028) /gb; 40024\_at Cluster Incl. D86640:Homo sapiens mRNA for stac, complete cds /cds=(39,; 31812\_at Cluster Incl. M24470:Human glucose-6-phosphate dehydrogenase, complete ; 33277\_at Cluster Incl. AB028996:Homo sapiens mRNA for KIAA1073 protein, complete; 35151\_at Cluster Incl.
- 10 AF089814:Homo sapiens growth suppressor related (DOC-1R) ; 36855\_r\_at Cluster Incl. M81886:Human glutamate receptor type 1 (HBGR1) mRNA, co; 37232\_at Cluster Incl. AB011158:Homo sapiens mRNA for KIAA0586 protein, complete; 37284\_at Cluster Incl. U60800:Human semaphorin (CD100) mRNA, complete cds /cds=(; 38258\_at Cluster Incl. U79290:Human clone 23908 mRNA sequence /cds=UNKNOWN /gb=U; 41127\_at Cluster Incl.
- 15 L14595:Human alanine/serine/cysteine/threonine transporte; 41143\_at Cluster Incl. U12022:Human calmodulin (CALM1) gene /cds=(199,648) /gb=U; 33388\_at Cluster Incl. AL080223:Homo sapiens mRNA; cDNA DKFZp566H2446 (from clon; 36593\_at Cluster Incl. U67368:Human multiple exostosis 2 (EXT2) gene /cds=(30,21; 38785\_at Cluster Incl. X52228:Human mRNA for secreted epithelial tumour mucin an; 39836\_at Cluster Incl. AI925231:wn52c05.x1 Homo sapiens cDNA, 3
- 20 end /clone=IMAG; 41358\_at Cluster Incl. AI827730:wfl1d12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41598\_at Cluster Incl. AA890010:aj89h08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1898\_at L24203 /FEATURE= /DEFINITION=HUMDK Homo sapiens ataxia-telangiectasia gr; 829\_s\_at U21689 /FEATURE=cds /DEFINITION=HSU21689 Human glutathione S-transferas; 114\_r\_at X14474 /FEATURE=cds /DEFINITION=HSTAUI Human mRNA for
- 25 microtubule-assoc.
- Metagene 135;** 33684\_at Cluster Incl. Z71621:H.sapiens Wnt-13 mRNA /cds=(491,1609) /gb=Z71621 /; 37070\_at Cluster Incl. D14720:Homo sapiens gene for peripheral myelin protein ze; 38179\_at Cluster Incl. U31248:Human zinc finger protein (ZNF174) mRNA, complete ; 39661\_s\_at Cluster Incl. AF034102:Homo sapiens NBMPR-insensitive nucleoside tran; 36872\_at Cluster Incl.
- 30 AL120559:DKFZp761B219\_r1 Homo sapiens cDNA, 5 end /clone; 41748\_at Cluster Incl. AA196476:zp99g10.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 37758\_s\_at Cluster Incl. W28479:47d8 Homo sapiens cDNA /gb=W28479 /gi=1308427 /u.
- Metagene 136;** 33462\_at Cluster Incl. D13626:Human mRNA for KIAA0001 gene, complete cds /cds=(2; 36328\_at Cluster Incl. M31651:Homo sapiens sex hormone-binding globulin (SHBG) g; 32032\_at Cluster Incl. L77566:Homo sapiens DGS-I mRNA, 3 end /cds=UNKNOWN /gb=L; 35173\_at Cluster Incl. U03886:Human GS2 mRNA, complete cds /cds=(130,891) /gb=U0; 36012\_at Cluster Incl. Y09631:H.sapiens mRNA for PIBF1 protein, complete /cds=(0; 36641\_at Cluster Incl. U03851:Human capping protein alpha mRNA, partial cds /cds.
- Metagene 137;** 33505\_at Cluster Incl. AI887421:wm05c01.x1 Homo sapiens cDNA, 3 end



- /clone=IMAG; 36067\_at Cluster Incl. AB000887:Homo sapiens mRNA for EBI1-ligand chemokine, com; 39781\_at Cluster Incl. U20982:Human insulin-like growth factor binding protein-4; 36686\_at Cluster Incl. U07919:Human aldehyde dehydrogenase 6 mRNA, complete cds ; 37017\_at Cluster Incl. M22430:Human RASF-A PLA2 mRNA, complete cds /cds=(135,569; 1737\_s\_at M62403
- 5 /FEATURE= /DEFINITION=HUMIGFBP5 Human insulin-like growth facto; 1042\_at U27185 /FEATURE= /DEFINITION=HSU27185 Human RAR-responsive (TIG1) mRNA, ; 614\_at M22430 /FEATURE= /DEFINITION=HUMRASFA Human RASF-A PLA2 mRNA, complete c.
- Metagene** 138; 34034\_at Cluster Incl. D80011:Human mRNA for KIAA0189 gene, complete cds /cds=(3; 34965\_at Cluster Incl. AF031824:Homo sapiens leukocystatin mRNA, complete cds /c;
- 10 38956\_at Cluster Incl. AF052111:Homo sapiens clone 23953 mRNA sequence /cds=UNKN; 41471\_at Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 32096\_at Cluster Incl. AC005546:Homo sapiens chromosome 19, cosmid R29425 /cds=(; 33804\_at Cluster Incl. U43522:Human cell adhesion kinase beta (CAKbeta) mRNA, co; 35714\_at Cluster Incl. U89606:Human pyridoxal kinase mRNA, complete cds /cds=(6; 36856\_at Cluster Incl.
- 15 W28743:51a9 Homo sapiens cDNA /gb=W28743 /gi=1308691 /ug=; 37180\_at Cluster Incl. X14034:Human mRNA for phospholipase C /cds=(152,3910) /gb; 37188\_at Cluster Incl. X92720:H.sapiens mRNA for phosphoenolpyruvate carboxykina; 37645\_at Cluster Incl. Z22576:H.sapiens CD69 gene /cds=(81,680) /gb=Z22576 /gi=3; 39385\_at Cluster Incl. M22324:Human aminopeptidase N/CD13 mRNA encoding aminopep; 40772\_at Cluster Incl.
- 20 AA284298:zc30c10.T7 Homo sapiens cDNA, 3 end /clone=IMAG; 35287\_at Cluster Incl. AF046888:Homo sapiens proliferation inducing ligand APRIL; 37033\_s\_at Cluster Incl. X13710:H.sapiens unspliced mRNA for glutathione peroxid; 37351\_at Cluster Incl. X90858:H.sapiens mRNA for uridine phosphorylase /cds=(352; 1780\_at M19722 /FEATURE= /DEFINITION=HUMFGR Human fgr proto-oncogene encoded p55; 1637\_at U09578 /FEATURE=
- 25 /DEFINITION=HSU09578 Homo sapiens MAPKAP kinase (3pK) m; 1426\_at D89077 /FEATURE= /DEFINITION=D89077 Homo sapiens mRNA for Src-like adapt; 1427\_g\_at D89077 /FEATURE= /DEFINITION=D89077 Homo sapiens mRNA for Src-like ada; 868\_at U13991 /FEATURE= /DEFINITION=HSU13991 Human TATA-binding protein associat; 794\_at X62055 /FEATURE=cds /DEFINITION=HSPTP1C H.sapiens PTP1C mRNA for protein-; 307\_at J03600 /FEATURE=
- 30 /DEFINITION=HUMLOX5 Human lipoxxygenase mRNA, complete cd; 182\_at U01062 /FEATURE=mRNA /DEFINITION=HUMIP3R3 Human type 3 inositol 1,4,5-tri.
- Metagene** 139; 38501\_s\_at Cluster Incl. U37139:Human beta 3-endonexin mRNA, long form and short; 33234\_at Cluster Incl. AA887480:oj54a12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33753\_at Cluster Incl. AB014566:Homo sapiens mRNA for KIAA0666 protein, partial ; 35215\_at
- 35 Cluster Incl. AL049996:Homo sapiens mRNA; cDNA DKFZp564K112 (from clone; 36456\_at Cluster Incl. AL080063:Homo sapiens mRNA; cDNA DKFZp564I052 (from clone; 37590\_g\_at Cluster Incl. AL109698:Homo sapiens mRNA full length insert cDNA clon; 39373\_at Cluster Incl. AF035284:Homo sapiens clone 23716 mRNA sequence /cds=UNKN; 34314\_at Cluster Incl. X59543:Human mRNA for M1 subunit of ribonucleotide reduct; 35352\_at Cluster Incl.

- AB002305:Human mRNA for KIAA0307 gene, complete cds /cds=; 35804\_at Cluster Incl.
- AB022785:Homo sapiens ASH2L gene, complete cds, similar t; 37040\_at Cluster Incl.
- D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,.
- Metagene 140;** 34433\_at Cluster Incl. AF035299:Homo sapiens clone 23863 mRNA, partial cds
- 5 /cds=; 36136\_at Cluster Incl. AF010315:Homo sapiens Pig11 (PIG11) mRNA, complete cds /c;
- 32513\_at Cluster Incl. W27495:31h12 Homo sapiens cDNA /gb=W27495 /gi=1307317 /ug; 1386\_at
- M83738 /FEATURE= /DEFINITION=HUMPTPSA Human protein-tyrosine phosphatase; 141\_s\_at
- U75276 /FEATURE= /DEFINITION=HSU75276 Human TFIIB related factor hBRF (.
- Metagene 141;** 33058\_at Cluster Incl. Y17282:Homo sapiens mRNA for cytokeratin type II
- 10 /cds=(18; 40750\_at Cluster Incl. U18088:Human 3,5 -cyclic AMP phosphodiesterase inactive s;
- 38636\_at Cluster Incl. AB003184:Homo sapiens mRNA for ISLR, complete cds /cds=(9; 39075\_at
- Cluster Incl. AF040958:Homo sapiens lysosomal neuraminidase precursor, ; 39395\_at Cluster Incl.
- AA704137:ag47g01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38780\_at Cluster Incl.
- J04794:Human aldehyde reductase mRNA, complete cds /cds=(; 41584\_at Cluster Incl.
- 15 AF062529:Homo sapiens clone 486790 diphosphoinositol poly; 1830\_s\_at M38449 /FEATURE=
- /DEFINITION=HUMTGFB Human transforming growth factor; 1747\_at AD000092
- /FEATURE=cds#2 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro.
- Metagene 142;** 33537\_at Cluster Incl. X90761:Homo sapiens hHa2 gene /cds=(61,1407)
- /gb=X90761 /; 38576\_at Cluster Incl. AJ223353:Homo sapiens mRNA for histone H2B, clone pJG4-
- 20 5-; 32627\_at Cluster Incl. AF039023:Homo sapiens Ran-GTP binding protein mRNA, parti;
- 32718\_at Cluster Incl. AF038009:Homo sapiens tyrosylprotein sulfotransferase-1 m; 32618\_at
- Cluster Incl. X93086:H.sapiens mRNA for biliverdin IX alpha reductase /.
- Metagene 143;** 31319\_at Cluster Incl. M20707:Human kappa-immunoglobulin germline pseudogene
- (Ch; 31586\_f\_at Cluster Incl. X72475:H.sapiens mRNA for rearranged Ig kappa light cha;
- 25 34094\_i\_at Cluster Incl. U80114:Human immunoglobulin heavy chain variable region; 34095\_f\_at
- Cluster Incl. U80114:Human immunoglobulin heavy chain variable region; 34098\_f\_at Cluster Incl.
- AI799757:wc37g12.x1 Homo sapiens cDNA, 3 end /clone=IM; 35530\_f\_at Cluster Incl.
- X92997:H.sapiens mRNA for IgG lambda light chain V-J-C ; 35566\_f\_at Cluster Incl.
- AF015128:Homo sapiens IgG heavy chain variable region ( ; 36277\_at Cluster Incl. M23323:Human
- 30 membrane protein (CD3-epsilon) gene /cds=(59; 37061\_at Cluster Incl. U29615:Human
- chitotriosidase precursor mRNA, complete cds; 40749\_at Cluster Incl. X07203:Human mRNA for
- CD20 receptor (S7) /cds=(90,983) /g; 40159\_r\_at Cluster Incl. M55067:Human 47-kD autosomal
- chronic granulomatous dise; 38017\_at Cluster Incl. U05259:Human MB-1 gene, complete cds
- /cds=(36,716) /gb=U0; 38018\_g\_at Cluster Incl. U05259:Human MB-1 gene, complete cds
- 35 /cds=(36,716) /gb=; 41585\_at Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein,
- partial ; 1633\_g\_at U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene
- homolo.
- Metagene 144;** 39972\_at Cluster Incl. Z94155:H.sapiens mRNA for P2Y-like G-protein coupled
- rece; 34281\_at Cluster Incl. AF039555:Homo sapiens visinin-like protein 1 (VSNL1) mRNA;

- 35658\_at Cluster Incl. U40380:Human presenilin I-374 (AD3-212) mRNA, complete cd; 35789\_at Cluster Incl. AB028965:Homo sapiens mRNA for KIAA1042 protein, complete; 38467\_at Cluster Incl. U96721:Homo sapiens alternative Hermansky-Pudlak syndrome; 32606\_at Cluster Incl. AA135683:zl10c08.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1378\_g\_at M58603 /FEATURE=
- 5 /DEFINITION=HUMNFKB Human nuclear factor kappa-B DNA .
- Metagene** 145; 31378\_at Cluster Incl. AF041339:Homo sapiens homeodomain protein (PITX3) mRNA, c; 35537\_at Cluster Incl. AF029761:Homo sapiens decoy receptor 2 mRNA, complete cds; 35448\_at Cluster Incl. U37219:Human cyclophilin-like protein CyP-60 mRNA, comple; 38191\_at Cluster Incl. AI040181:ox42d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41445\_at Cluster
- 10 Incl. X02812:Human mRNA for transforming growth factor-beta (TG; 33719\_at Cluster Incl. AF010242:AF010242 Homo sapiens cDNA /gb=AF010242 /gi=2612; 34367\_at Cluster Incl. AF006043:Homo sapiens 3-phosphoglycerate dehydrogenase mR; 39520\_at Cluster Incl. AI924382:wn60d01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41541\_at Cluster Incl. AI971642:wr06e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33151\_s\_at Cluster Incl.
- 15 W25932:15b1 Homo sapiens cDNA /gb=W25932 /gi=1306055 /u; 2066\_at L22474 /FEATURE= /DEFINITION=HUMBAXB Human Bax beta mRNA, complete cds ; 2023\_g\_at M77198 /FEATURE= /DEFINITION=HUMRPKB Human rac protein kinase beta mRN; 2034\_s\_at U10906 /FEATURE= /DEFINITION=HSU10906 Human cyclin-dependent kinase in; 1950\_s\_at AB004922 /FEATURE=cds /DEFINITION=AB004922S1 Homo sapiens gene for Sma; 1542\_at X04571
- 20 /FEATURE=cds /DEFINITION=HSEGFRE Human mRNA for kidney epidermal; 1259\_at L76568 /FEATURE=exons#13-14 /DEFINITION=HUMERCC4G Homo sapiens excision ; 1235\_at M86400 /FEATURE= /DEFINITION=HUMPHPLA2 Human phospholipase A2 mRNA, comp; 1155\_at J03069 /FEATURE=mRNA /DEFINITION=HUMMYCL2A Human MYCL2 gene, complete cd; 1034\_at U14394 /FEATURE= /DEFINITION=HSU14394 Human tissue inhibitor of metallo;
- 25 438\_at X07767 /FEATURE=cds /DEFINITION=HSPKA Human mRNA for cAMP-dependent prote; 104\_at Z21966 /FEATURE=cds /DEFINITION=HSMPOUHOX H.sapiens mPOU homeobox protein.
- Metagene** 146; 35060\_at Cluster Incl. U51224:Human U2AFBPL gene, complete cds /cds=(111,1550) /; 34027\_f\_at Cluster Incl. AA010078:ze16d01.s1 Homo sapiens cDNA, 3 end
- 30 /clone=IM; 39979\_at Cluster Incl. L29433:Human factor X (blood coagulation factor) gene /cd; 40644\_g\_at Cluster Incl. M34480:Human platelet glycoprotein IIb (GPIIb) mRNA, co; 33314\_at Cluster Incl. U69141:Human glutaryl-CoA dehydrogenase mRNA, complete cd; 36543\_at Cluster Incl. J02931:Human placental tissue factor (two forms) mRNA, co; 38649\_at Cluster Incl. AB023187:Homo sapiens mRNA for KIAA0970 protein, complete; 41158\_at Cluster Incl.
- 35 M54927:Human myelin proteolipid protein mRNA, complete cd; 38057\_at Cluster Incl. AL049798:Human DNA sequence from clone 797M17 on chromoso; 38059\_g\_at Cluster Incl. Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=; 39893\_at Cluster Incl. AB010414:Homo sapiens mRNA for G-protein gamma 7, complet; 40185\_at Cluster Incl. S40719:glial fibrillary acidic protein [human, glioma cel.

- Metagene 147;** 31637\_s\_at Cluster Incl. X72631:H.sapiens mRNA encoding Rev-ErbAalpha /cds=UNKNO; 36780\_at Cluster Incl. M25915:Human complement cytolysis inhibitor (CLI) mRNA, c; 41039\_at Cluster Incl. AL022476:dJ323M22.2.1 (novel protein similar to KIAA0173 ; 31896\_at Cluster Incl. AL050281:Homo sapiens mRNA; cDNA DKFZp586G1219 (from clon; 32117\_at
- 5 Cluster Incl. U51698:HSU51698 Homo sapiens cDNA /gb=U51698 /gi=1255268 ; 33810\_at Cluster Incl. AF110377:Homo sapiens PCAF-associated factor 400 (PAF400); 36003\_at Cluster Incl. AJ005698:Homo sapiens mRNA for poly(A)-specific ribonucle; 36545\_s\_at Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, comple; 37956\_at Cluster Incl. U37519:Human aldehyde dehydrogenase (ALDH8) mRNA, complet; 38719\_at Cluster Incl.
- 10 U03985:Human N-ethylmaleimide-sensitive factor mRNA, part; 39370\_at Cluster Incl. W28807:52a3 Homo sapiens cDNA /gb=W28807 /gi=1308755 /ug=; 39404\_s\_at Cluster Incl. D86988:Human mRNA for KIAA0221 gene, complete cds /cds=; 40498\_g\_at Cluster Incl. AF040707:Homo sapiens candidate tumor suppressor gene 2; 40787\_at Cluster Incl. U90911:Human clone 23652 mRNA sequence /cds=UNKNOWN /gb=U; 33920\_at Cluster Incl. AF051782:Homo
- 15 sapiens diaphanous 1 (HDIA1) mRNA, complete; 34380\_at Cluster Incl. AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds=(; 34396\_at Cluster Incl. AB023195:Homo sapiens mRNA for KIAA0978 protein, partial ; 35270\_at Cluster Incl. W16505:zb05e12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 35301\_at Cluster Incl. AL049941:Homo sapiens mRNA; cDNA DKFZp564E2222 (from clon; 35323\_at Cluster Incl. U78525:Homo sapiens eukaryotic translation initiation fac;
- 20 36996\_at Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85; 38423\_at Cluster Incl. L38935:Homo sapiens GT212 mRNA /cds=UNKNOWN /gb=L38935 /g; 33198\_at Cluster Incl. AA206524:zq58b03.r1 Homo sapiens cDNA, 5 end /clone=IMAG.
- Metagene 148;** 32915\_at Cluster Incl. AL109730:Homo sapiens mRNA full length insert cDNA clone ; 33546\_at Cluster Incl. AI923984:wn49d12.x1 Homo sapiens cDNA, 3 end /clone=IMAG;
- 25 33571\_at Cluster Incl. X80590:H.sapiens PHKG1 mRNA /cds=(119,1282) /gb=X80590 /g; 35378\_at Cluster Incl. AI051683:oy77h08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41641\_at Cluster Incl. AJ223603:Homo sapiens mRNA encoding rat C4.4-like protein; 33266\_at Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRN; 37278\_at Cluster Incl. X92762:H.sapiens mRNA for tafazzins protein /cds=(288,116; 38442\_at Cluster Incl.
- 30 U19718:Human microfibril-associated glycoprotein (MFAP2) ; 40205\_g\_at Cluster Incl. X71877:H.sapiens mRNA for chymotrypsin-like protease CT; 40565\_at Cluster Incl. AI358867:qy24a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1799\_at U64315 /FEATURE= /DEFINITION=HSU64315 Human DNA repair endonuclease subu; 480\_at U56816 /FEATURE= /DEFINITION=HSU56816 Human kinase Myt1 (Myt1) mRNA, comp; 160037\_at Z48482
- 35 /FEATURE=cds /DEFINITION=HSMMPM2 H.sapiens mRNA for membrane-ty.
- Metagene 149;** 36102\_at Cluster Incl. AF038962:Homo sapiens voltage dependent anion channel pro; 696\_at Homeotic Protein Hox5.4 .
- Metagene 150;** 34578\_at Cluster Incl. U34976:Human gamma-sarcoglycan mRNA, complete cds /cds=(1; 39603\_at Cluster Incl. AB007926:Homo sapiens mRNA for KIAA0457 protein, partial ;

- 36825\_at Cluster Incl. X82200:H.sapiens Staf50 mRNA /cds=(122,1450) /gb=X82200 /; 35839\_at Cluster Incl. D78130:Homo sapiens mRNA for squalene epoxidase, complete; 40954\_at Cluster Incl. H94881:yu57f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-.
- Metagene 151;** 699\_s\_at Mucin 1, Epithelial, Alt. Splice 6 ; 203\_at M68891 /FEATURE=
- 5 /DEFINITION=HUMGATA Human GATA-binding protein (GATA2) m.
- Metagene 152;** 39583\_at Cluster Incl. AF030435:Homo sapiens glioma amplified on chromosome 1 pr; 36552\_at Cluster Incl. AL080220:Homo sapiens mRNA; cDNA DKFZp586P0123 (from clone; 36567\_at Cluster Incl. W26700:11h4 Homo sapiens cDNA /gb=W26700 /gi=1305802 /ug=;
- 39418\_at Cluster Incl. AJ007398:Homo sapiens mRNA for PBK1 protein /cds=(5,1558); 35363\_at
- 10 Cluster Incl. AL080113:Homo sapiens mRNA; cDNA DKFZp586K2322 (from clone; 39512\_s\_at Cluster Incl. AA457029:aa38b10.s1 Homo sapiens cDNA, 3 end /clone=IM; 41539\_at Cluster Incl. U77782:Human N-methyl-D-aspartate receptor 2C subunit pre; 33122\_at Cluster Incl. N95393:zb68c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-.
- Metagene 153;** 31622\_f\_at Cluster Incl. M10943:Human metallothionein-I $\epsilon$  gene (hMT-I $\epsilon$ )
- 15 /cds=(0,1; 31623\_f\_at Cluster Incl. K01383:Human metallothionein-I-A gene, complete coding ; 38164\_at Cluster Incl. U57629:Human retinitis pigmentosa GTPase regulator (RPGR); 39594\_f\_at Cluster Incl. R93527:yq35f10.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41446\_f\_at Cluster Incl. H68340:yr82b10.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32079\_at Cluster Incl. AB014539:Homo sapiens mRNA for KIAA0639 protein, partial ; 39411\_at Cluster Incl.
- 20 AL080156:Homo sapiens mRNA; cDNA DKFZp434J214 (from clone; 40074\_at Cluster Incl. X16396:Human mRNA for NAD-dependent methylene tetrahydrof; 33825\_at Cluster Incl. X68733:H.sapiens gene for alpha1-antichymotrypsin, exon I; 36130\_f\_at Cluster Incl. R92331:yq03h03.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 36960\_at Cluster Incl. U89278:Human polyhomeotic 2 homolog (HPH2) mRNA, complete; 38044\_at Cluster Incl.
- 25 AF035283:Homo sapiens clone 23916 mRNA sequence /cds=UNKN; 39120\_at Cluster Incl. AA224832:nc33b06.s1 Homo sapiens cDNA /clone=IMAGE-100990; 40202\_at Cluster Incl. D31716:Human mRNA for GC box bindig protein, complete cds; 926\_at J03910 /FEATURE=mRNA /DEFINITION=HUMMT2A Human (clone 14VS) metallothione; 609\_f\_at M13485 /FEATURE=cds /DEFINITION=HUMMT1B2 Human metallothionein I-B gene.
- 30 **Metagene 154;** 39640\_at Cluster Incl. AB016789:Homo sapiens mRNA for Glutamine-fructose-6-phosp; 37191\_at Cluster Incl. D87463:Human mRNA for KIAA0273 gene, complete cds /cds=(4; 39040\_at Cluster Incl. W28360:46f9 Homo sapiens cDNA /gb=W28360 /gi=1308371 /ug=;
- 39331\_at Cluster Incl. X79535:H.sapiens mRNA for beta tubulin, clone nuk\_278 /cd; 35326\_at Cluster Incl. AF004876:Homo sapiens 54Tm (54tm) mRNA, complete cds /cd; 40638\_at Cluster
- 35 Incl. X70944:H.sapiens mRNA for PTB-associated splicing factor ; 41250\_at Cluster Incl. U24169:Human JTV-1 (JTV-1) mRNA, complete cds /cds=(113,1; 1979\_s\_at X55504 /FEATURE=cds /DEFINITION=HSP120A H.sapiens mRNA for P120 antige; 296\_at Tubulin, Beta ; 297\_g\_at Tubulin, Beta .
- Metagene 155;** 39261\_at Cluster Incl. L16896:Human zinc finger protein mRNA, complete cds

- /cds=; 32140\_at Cluster Incl. Y08110:H.sapiens mRNA for mosaic protein LR11 /cds=(80,67;  
34223\_at Cluster Incl. M59818:Human granulocyte colony-stimulating factor recept; 1353\_g\_at  
U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8 receptor; 596\_s\_at  
M59820 /FEATURE=mRNA /DEFINITION=HUMGCSFR3 Human granulocyte colony-sti; 245\_at  
5 M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRN.  
**Metagene** 156; 31431\_at Cluster Incl. U12255:Human IgG Fc receptor hFcRn mRNA, complete cds  
/cd; 31432\_g\_at Cluster Incl. U12255:Human IgG Fc receptor hFcRn mRNA, complete cds /;  
31609\_s\_at Cluster Incl. L33799:Human procollagen C-proteinase enhancer protein ; 35016\_at  
Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cd; 35517\_at Cluster Incl.
- 10 M12807:Human T-cell surface glycoprotein T4 mRNA, complet; 33956\_at Cluster Incl.  
AB018549:Homo sapiens MD-2 mRNA, complete cds /cds=(125,6; 35411\_at Cluster Incl.  
AB018551:Homo sapiens ATPBL mRNA for coiled-coil protein.; 35965\_at Cluster Incl.  
X51757:Human heat-shock protein HSP70B gene /cds=(0,1931); 36270\_at Cluster Incl.  
U04343:Human CD86 antigen mRNA, complete cds /cds=(147,11; 36773\_f\_at Cluster Incl.
- 15 M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), ; 36789\_f\_at Cluster Incl.  
AF025534:Homo sapiens leucocyte immunoglobulin-like rec; 38894\_g\_at Cluster Incl.  
AL008637:Human DNA sequence from clone 833B7 on chromos; 38964\_r\_at Cluster Incl.  
U12707:Human Wiskott-Aldrich syndrome protein (WASP) mR; 39263\_at Cluster Incl.  
M87434:Human 71 kDa 25 oligoadenylate synthetase (p69 2-; 39319\_at Cluster Incl.
- 20 U20158:Human 76 kDa tyrosine phosphoprotein SLP-76 mRNA, ; 40296\_at Cluster Incl.  
AL023653:Human DNA sequence from clone 753P9 on chromosom; 40365\_at Cluster Incl.  
M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(; 41609\_at Cluster Incl.  
U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /; 31870\_at Cluster Incl.  
X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908; 32046\_at Cluster Incl.
- 25 D10495:Homo sapiens mRNA for protein kinase C delta-type.; 32068\_at Cluster Incl.  
U62027:Human anaphylatoxin C3a receptor (HNFAG09) mRNA, c; 32737\_at Cluster Incl.  
M64595:Human small G protein (Gx) mRNA, 3 end /cds=(0,54; 34268\_at Cluster Incl.  
X91809:H.sapiens mRNA for GAIP protein /cds=(288,941) /gb; 34665\_g\_at Cluster Incl.  
X62573:H.sapiens RNA for Fc receptor, TC9 /cds=UNKNOWN ; 35659\_at Cluster Incl.
- 30 U00672:Human interleukin-10 receptor mRNA, complete cds /; 36007\_at Cluster Incl.  
AL050137:Homo sapiens mRNA; cDNA DKFZp586L151 (from clone; 36465\_at Cluster Incl.  
U51127:Human interferon regulatory factor 5 (Humirf5) mRN; 36889\_at Cluster Incl.  
M33195:Human Fc-epsilon-receptor gamma-chain mRNA, comple; 37200\_at Cluster Incl.  
J04162:Human leukocyte IgG receptor (Fc-gamma-R) mRNA, co; 37918\_at Cluster Incl.
- 35 M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150; 38287\_at Cluster Incl.  
AA808961.nw16h03.s1 Homo sapiens cDNA /clone=IMAGE-124066; 38323\_at Cluster Incl.  
AC005162:Homo sapiens BAC clone RG113D17 from 7p14-p15 /c; 38686\_at Cluster Incl.  
X71490:H.sapiens mRNA for vacuolar proton ATPase, subunit; 39049\_at Cluster Incl.  
AJ243937:Homo sapiens mRNA for G18.1a and G18.1b proteins; 39070\_at Cluster Incl.

- U03057:Human actin bundling protein (HSN) mRNA, complete ; 39345\_at Cluster Incl.  
 AI525834:PT1.3\_06\_D01.r Homo sapiens cDNA, 5 end /clone\_ ; 39347\_at Cluster Incl.  
 X97074:H.sapiens mRNS for clathrin-associated protein /cd; 39428\_at Cluster Incl.  
 AF055581:Homo sapiens adaptor protein Lnk mRNA, complete ; 40081\_at Cluster Incl.
- 5 L26232:Human phospholipid transfer protein mRNA, complete; 40505\_at Cluster Incl.  
 AA883502:am25h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41168\_at Cluster Incl.  
 AF029750:Homo sapiens tapasin (NGS-17) mRNA, complete cds; 41198\_at Cluster Incl.  
 AF055008:Homo sapiens clone 24720 epithelin 1 and 2 mRNA.; 41723\_s\_at Cluster Incl.  
 M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5; 32157\_at Cluster Incl.
- 10 S57501:protein phosphatase type 1 catalytic subunit [huma; 33339\_g\_at Cluster Incl.  
 M97936:Human transcription factor ISGF-3 mRNA sequence ; 33871\_s\_at Cluster Incl.  
 J02876:Human placental folate binding protein mRNA, com; 35807\_at Cluster Incl. M21186:Human  
 neutrophil cytochrome b light chain p22 phag; 36661\_s\_at Cluster Incl. X06882:Human gene for  
 CD14 differentiation antigen /cds; 36959\_at Cluster Incl. U49278:Homo sapiens UEV-1 (UBE2V)
- 15 mRNA, partial cds /cds=; 36994\_at Cluster Incl. M62762:Human vacuolar H<sup>+</sup> ATPase proton  
 channel subunit mR; 37310\_at Cluster Incl. X02419:H.sapiens uPA gene /cds=(119,1414)  
 /gb=X02419 /gi=; 37328\_at Cluster Incl. X07743:Human mRNA for pleckstrin (P47) /cds=(60,1112)  
 /gb; 37383\_f\_at Cluster Incl. X58536:Human mRNA for HLA class I locus C heavy chain /;  
 37402\_at Cluster Incl. D26129:Human mRNA for ribonuclease A (RNase A), complete ; 38745\_at
- 20 Cluster Incl. X76488:H.sapiens mRNA for lysosomal acid lipase /cds=(145; 38796\_at Cluster Incl.  
 X03084:Human mRNA for C1q B-chain of complement system /c; 39829\_at Cluster Incl.  
 AB016811:Homo sapiens mRNA for ADP ribosylation factor-li; 32616\_at Cluster Incl.  
 M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(29; 33121\_g\_at Cluster Incl.  
 AF045229:Homo sapiens regulator of G protein signaling ; 1919\_at X16316 /FEATURE=cds
- 25 /DEFINITION=HSVAVPO Human mRNA for vav oncogene ; 1810\_s\_at D10495 /FEATURE=  
 /DEFINITION=HUMPKSCD Homo sapiens mRNA for protein ki; 1768\_s\_at X59932  
 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase; 1375\_s\_at  
 M32304 /FEATURE= /DEFINITION=HUMMET Human metalloproteinase inhibitor ; 1107\_s\_at  
 M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-induced 17; 957\_at
- 30 Arrestin, Beta 2 ; 548\_s\_at S80267 /FEATURE= /DEFINITION=S80267 p72syk {G insertion  
 nucleotide 92} ; 478\_g\_at U51127 /FEATURE= /DEFINITION=HSU51127 Human interferon  
 regulatory facto; 317\_at D55696 /FEATURE= /DEFINITION=D55696 Homo sapiens mRNA for  
 cysteine protea; 172\_at U57650 /FEATURE= /DEFINITION=HSU57650 Human SH2-containing  
 inositol 5-pho; 117\_at X51757 /FEATURE=cds /DEFINITION=HSP70B Human heat-shock protein
- 35 HSP70B g; 133\_at X87212 /FEATURE=cds /DEFINITION=HSCATHCGE H.sapiens mRNA for  
 cathepsin C ; 160022\_at X03663 /FEATURE=cds /DEFINITION=HSCFMS Human mRNA for c-  
 fms proto-onco.
- Metagene** 157; 39988\_at Cluster Incl. M74447:Human PSF-2 mRNA, complete cds /cds=(96,2207)  
 /gb=; 33230\_at Cluster Incl. AJ131186:Homo sapiens mRNA for nuclear matrix protein NMP;

- 34182\_at Cluster Incl. U18932:Human heparan sulfate-N-deacetylase/N-sulfotransfe.
- Metagene 158;** 33634\_at Cluster Incl. AF038007:Homo sapiens FIC1 mRNA, complete cds /cds=(0,375; 34919\_at Cluster Incl. AJ223957:Homo sapiens mRNA for ARNO3 protein /cds=(25,122; 35001\_at Cluster Incl. Z85986:Human DNA sequence from clone 108K11 on
- 5 chromosome; 39254\_at Cluster Incl. AL050011:Homo sapiens mRNA; cDNA DKFZp564G013 (from clone; 41089\_at Cluster Incl. M83363:Human plasma membrane calcium-pumping ATPase (PMCA; 37979\_at Cluster Incl. X80507:H.sapiens YAP65 mRNA /cds=(0,1364) /gb=X80507 /gi=; 37711\_at Cluster Incl. S57212:hMEF2C=myocyte enhancer-binding factor 2 [human, s; 1671\_s\_at L35253 /FEATURE= /DEFINITION=HUMMAPKNS Human p38 mitogen activated pro; 1190\_at
- 10 Z48541 /FEATURE=cds /DEFINITION=HSPTPU2GN H.sapiens mRNA for protein tyr.
- Metagene 159;** 31587\_at Cluster Incl. X96969:H.sapiens mRNA for urea transporter /cds=(273,1466; 32933\_r\_at Cluster Incl. AL050122:Homo sapiens mRNA; cDNA DKFZp586E121 (from clo; 34788\_at Cluster Incl. AL049365:Homo sapiens mRNA; cDNA DKFZp586A0618 (from clon; 41497\_at Cluster Incl. AI401296:tg92c03.x1 Homo sapiens cDNA, 3 end /clone=IMAG;
- 15 41507\_at Cluster Incl. AI700753:we41b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG.
- Metagene 160;** 34950\_at Cluster Incl. AB018303:Homo sapiens mRNA for KIAA0760 protein, partial ; 37447\_at Cluster Incl. AF015257:Homo sapiens flow-induced endothelial G protein-; 41667\_s\_at Cluster Incl. AJ006068:Homo sapiens mRNA for dTDP-D-glucose 4,6-dehyd; 41715\_at Cluster Incl. Y11312:H.sapiens mRNA for phosphoinositide 3-kinase /cds=; 31799\_at Cluster Incl.
- 20 AF070618:Homo sapiens clone 24627 mRNA sequence /cds=UNKN; 33294\_at Cluster Incl. D29958:Human mRNA for KIAA0116 gene, partial cds /cds=(0,; 33796\_at Cluster Incl. U73960:Human ADP-ribosylation factor-like protein 4 mRNA,; 40480\_s\_at Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete ; 41220\_at Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete; 36610\_at Cluster Incl.
- 25 D21852:Human mRNA for KIAA0029 gene, partial cds /cds=(38.
- Metagene 161;** 32998\_at Cluster Incl. L19315:Human cholecystokinin A receptor mRNA, complete cd; 32968\_s\_at Cluster Incl. AL050253:H.sapiens mRNA similar to D29763 mouse mRNA fo; 41394\_at Cluster Incl. AF038440:Homo sapiens phospholipase D2 (PLD2) mRNA, splic; 41689\_at Cluster Incl. R16035:ya51h07.r2 Homo sapiens cDNA, 5 end /clone=IMAGE-; 40830\_at Cluster
- 30 Incl. AF012106:Homo sapiens DnaJ protein (HSPF2) mRNA, complete; 967\_g\_at X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S..
- Metagene 162;** 35414\_s\_at Cluster Incl. U77914:Human soluble protein Jagged mRNA, partial cds /; 41700\_at Cluster Incl. M62424:Human thrombin receptor mRNA, complete cds /cds=(2; 32647\_at Cluster Incl. AF060902:Homo sapiens vesicle soluble NSF attachment prot; 35643\_at Cluster Incl.
- 35 X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /g; 39065\_s\_at Cluster Incl. D83077:Homo sapiens mRNA for TPRD, complete cds /cds=(1; 39351\_at Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,4; 39397\_at Cluster Incl. M64497:Human apolipoprotein AI regulatory protein (ARP-1); 41743\_i\_at Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRN; 32214\_at Cluster Incl.



- AF003938:Homo sapiens thioredoxin-like protein mRNA, comp; 33402\_at Cluster Incl.  
 AL035081:H.sapiens mRNA similar to Xenopus laevis mRNA fo; 33429\_at Cluster Incl.  
 AL050225:Homo sapiens mRNA; cDNA DKFZp586M1523 (from clon; 33866\_at Cluster Incl.  
 X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /c; 33875\_at Cluster Incl.
- 5 AI547262:PN001\_AH\_H03.r Homo sapiens cDNA, 5 end /clone\_; 33930\_at Cluster Incl.  
 AB020724:Homo sapiens mRNA for KIAA0917 protein, partial ; 36647\_at Cluster Incl.  
 AA526812:ni92a08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38123\_at Cluster Incl.  
 D14878:Human mRNA for protein D123, complete cds /cds=(28; 39169\_at Cluster Incl.  
 AF054184:Homo sapiens Sec61 gamma mRNA, complete cds /cds; 39814\_s\_at Cluster Incl.
- 10 AI052724:oz27a12.x1 Homo sapiens cDNA, 3 end /clone=IM; 40556\_at Cluster Incl.  
 D42073:Human mRNA for reticulocalbin, complete cds /cds=(; 2044\_s\_at M15400  
 /FEATURE=mRNA /DEFINITION=HUMRBS Human retinoblastoma susceptib; 1884\_s\_at  
 M15796 /FEATURE= /DEFINITION=HUMCYL Human cyclin protein gene, complet; 1798\_at  
 U41060 /FEATURE= /DEFINITION=HSU41060 Human breast cancer, estrogen regu; 1728\_at
- 15 L13689 /FEATURE=mRNA /DEFINITION=HUMBMI1X Human prot-oncogene (BMI-1) mR;  
 994\_at X58288 /FEATURE=mRNA /DEFINITION=HSHRPTPU H.sapiens hR-PTPu gene for prot.  
**Metagene 163;** 36706\_at Cluster Incl. Y15057:Homo sapiens mRNA for STK9 protein  
 /cds=(221,3313); 37237\_at Cluster Incl. D38293:Homo sapiens mRNA for clathrin-like protein,  
 compl; 37589\_at Cluster Incl. AL109698:Homo sapiens mRNA full length insert cDNA clone ;
- 20 37957\_at Cluster Incl. AL031177:dJ889M15.3 (novel protein) /cds=(0,1186) /gb=AL0; 38296\_at  
 Cluster Incl. AL050196:Homo sapiens mRNA; cDNA DKFZp586D2223 (from clon; 35368\_at  
 Cluster Incl. AF046001:Homo sapiens zinc finger transcription factor (Z; 35743\_at Cluster Incl.  
 U79569:Human no arches (nar) mRNA, complete cds /cds=(36;; 1523\_g\_at U43408 /FEATURE=  
 /DEFINITION=HSU43408 Human tyrosine kinase (Tnk1) mRN; 1187\_at X84740
- 25 /FEATURE=mRNA /DEFINITION=HSDNALIG3 H.sapiens mRNA for DNA ligase.  
**Metagene 164;** 34477\_at Cluster Incl. AF000994:Homo sapiens ubiquitous TPR motif, Y isoform  
 (UT; 35885\_at Cluster Incl. AF000986:Homo sapiens Drosophila fat facets related Y pro; 37583\_at  
 Cluster Incl. U52191:Human SMCY (H-Y) mRNA, complete cds /cds=(275,4894; 38355\_at Cluster  
 Incl. AF000984:Homo sapiens dead box, Y isoform (DBY) mRNA, alt; 40097\_at Cluster Incl.
- 30 AF000987:Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, co; 41214\_at Cluster Incl.  
 M58459:Human ribosomal protein (RPS4Y) isoform mRNA, comp.  
**Metagene 165;** 34812\_at Cluster Incl. W26099:22f11 Homo sapiens cDNA /gb=W26099  
 /gi=1306645 /ug; 34854\_at Cluster Incl. AC004382:Homo sapiens Chromosome 16 BAC clone  
 CIT987SK-A-; 32591\_at Cluster Incl. AI494623:qz17b06.x1 Homo sapiens cDNA, 3 end
- 35 /clone=IMAG; 1729\_at L41690 /FEATURE= /DEFINITION=HUMTRADD Homo sapiens TNF  
 receptor-1 associ; 1317\_at X70040 /FEATURE=cds /DEFINITION=HSRON H.sapiens RON mRNA  
 for tyrosine ki; 1254\_at L36861 /FEATURE=expanded\_cds /DEFINITION=HUMGCAPB Homo  
 sapiens guanylate.  
**Metagene 166;** 32331\_at Cluster Incl. X60673:Human AK3 mRNA for adenylate kinase 3

- /cds=UNKNOWN; 40322\_at Cluster Incl. D12763:Homo sapiens mRNA for ST2 protein  
 /cds=(46,1032) /; 33769\_at Cluster Incl. AF087020:Homo sapiens protein zero related protein (PZR)  
 ; 36490\_s\_at Cluster Incl. X15331:Human mRNA for phosphoribosylpyrophosphate synth; 37952\_at  
 Cluster Incl. M35999:Human platelet glycoprotein IIIa (GPIIIa) mRNA, co; 39002\_at Cluster Incl.
- 5 AJ010063:Homo sapiens telethonin gene /cds=(10,513) /gb=A; 41782\_g\_at Cluster Incl.  
 U22815:Human LAR-interacting protein 1a mRNA, complete ; 35305\_at Cluster Incl.  
 X95762:H.sapiens mRNA for aminopeptidase P-like /cds=(0,1; 36101\_s\_at Cluster Incl.  
 M63978:Human vascular endothelial growth factor gene /c; 39810\_at Cluster Incl. AC005253:Homo  
 sapiens chromosome 19, cosmid R26445 /cds=(; 1735\_g\_at M60556 /FEATURE=mRNA#1
- 10 /DEFINITION=HUMTGFB3B Human transforming growth; 1454\_at U68019 /FEATURE=  
 /DEFINITION=HSU68019 Homo sapiens mad protein homolog (; 1318\_at X74262 /FEATURE=cds  
 /DEFINITION=HSRBAP48 H.sapiens RbAp48 mRNA encoding ; 759\_at D38145 /FEATURE=  
 /DEFINITION=HUMPTGIS Human mRNA for prostacyclin synthas; 275\_at L05147 /FEATURE=  
 /DEFINITION=HUMDSPHS Human dual specificity phosphatase ; 231\_at M55153 /FEATURE=
- 15 /DEFINITION=HUMTGASE Human transglutaminase (TGase) mRNA.  
**Metagene** 167; 33613\_at Cluster Incl. AA806239:oc21e02.s1 Homo sapiens cDNA /clone=IMAGE-  
 134153; 35606\_at Cluster Incl. D16583:Human gene for L-histidine decarboxylase, complete;  
 36749\_at Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /; 37121\_at  
 Cluster Incl. S69115:granulocyte colony-stimulating factor induced gene; 37454\_at Cluster Incl.
- 20 AJ001634:Homo sapiens mRNA for CC-chemokine MCP-4 /cds=(4; 37493\_at Cluster Incl.  
 H04668:yj49e08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 37823\_at Cluster Incl.  
 Y16645:Homo sapiens mRNA for monocyte chemotactic protein; 38131\_at Cluster Incl.  
 AF010316:Homo sapiens Pig12 (PIG12) mRNA, complete cds /c; 38222\_at Cluster Incl.  
 AF007893:Homo sapiens P2Y6 receptor pseudogene, complete ; 40671\_g\_at Cluster Incl.
- 25 AI148772:qc69h01.x1 Homo sapiens cDNA, 3 end /clone=IM; 41045\_at Cluster Incl. U77643:Homo  
 sapiens K12 protein precursor mRNA, complete ; 41385\_at Cluster Incl. AB023204:Homo sapiens  
 mRNA for KIAA0987 protein, partial ; 41433\_at Cluster Incl. M73255:Human vascular cell  
 adhesion molecule-1 (VCAM1) ge; 31895\_at Cluster Incl. AB002803:Homo sapiens BACH1  
 mRNA, complete cds /cds=(118,; 31898\_at Cluster Incl. D86967:Human mRNA for KIAA0212
- 30 gene, complete cds /cds=(5; 32034\_at Cluster Incl. AF041259:Homo sapiens breast cancer putative  
 transcriptio; 32666\_at Cluster Incl. U19495:Human intercrine-alpha (hIRH) mRNA, complete cds /;  
 34663\_at Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-; 36070\_at  
 Cluster Incl. AL049389:Homo sapiens mRNA; cDNA DKFZp586O0118 (from clon; 36879\_at  
 Cluster Incl. M63193:Human platelet-derived endothelial cell growth fac; 37215\_at Cluster Incl.
- 35 AF046798:untitled /cds=(113,2656) /gb=AF046798 /gi=317040; 37603\_at Cluster Incl.  
 X52015:H.sapiens mRNA for interleukin-1 receptor antagoni; 38652\_at Cluster Incl.  
 AF070644:Homo sapiens clone 24742 mRNA sequence /cds=UNKN; 39043\_at Cluster Incl.  
 AF006084:Homo sapiens Arp2/3 protein complex subunit p41-; 39338\_at Cluster Incl.  
 AI201310:qf71b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39421\_at Cluster Incl.

- D43969:Human AML1 mRNA for AML1c protein (alternatively s; 40520\_g\_at Cluster Incl.  
Y00638:Human mRNA for leukocyte common antigen (T200) /; 41184\_s\_at Cluster Incl.  
X87344:H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LM; 32860\_g\_at Cluster Incl.  
M97935:Homo sapiens transcription factor ISGF-3 mRNA, c; 33452\_at Cluster Incl.
- 5 M15518:Human tissue-type plasminogen activator (t-PA) mRN; 33834\_at Cluster Incl.  
L36033:Human pre-B cell stimulating factor homologue (SDF; 36986\_at Cluster Incl.  
AL031295:Human DNA sequence from clone 886K2 on chromosom; 36988\_at Cluster Incl.  
M80783:Human B12 protein mRNA, complete cds /cds=(153,110; 38369\_at Cluster Incl.  
U70451:Human myeloid differentiation primary response pro; 38389\_at Cluster Incl.
- 10 X04371:Human 1.6Kb mRNA for 2-5A synthetase induced by in; 40639\_at Cluster Incl.  
AL021683:Homo sapiens cDNA homologous to Yeast SCO1 & SCO; 32614\_at Cluster Incl.  
AB018278:Homo sapiens mRNA for KIAA0735 protein, complete; 1456\_s\_at M63838  
/FEATURE= /DEFINITION=HUMIFI16A Human interferon-gamma induced ; 1039\_s\_at U22431  
/FEATURE= /DEFINITION=HSU22431 Human hypoxia-inducible factor 1; 999\_at X59812
- 15 /FEATURE=cds /DEFINITION=HSVD3HYD H.sapiens CYP 27 mRNA for vitam; 943\_at D43968  
/FEATURE= /DEFINITION=HUMAML1BA Human AML1 mRNA for AML1b protein ; 859\_at  
U03688 /FEATURE= /DEFINITION=HSU03688 Human dioxin-inducible cytochrome P; 583\_s\_at  
M30257 /FEATURE= /DEFINITION=HUMCAM1V Human vascular cell adhesion mole; 570\_at  
M83221 /FEATURE= /DEFINITION=HUMIRELA Homo sapiens I-Rel mRNA, complete c; 479\_at
- 20 U53446 /FEATURE= /DEFINITION=HSU53446 Human mitogen-responsive phosphopro; 393\_s\_at  
X90976 /FEATURE= /DEFINITION=HSRNAML11 H.sapiens mRNA for an acute myel.  
**Metagene** 168; 35553\_at Cluster Incl. AF042181:Homo sapiens testis-specific Y-encoded-like prot.  
**Metagene** 169; 31526\_f\_at Cluster Incl. X63547:H.sapiens mRNA for tre oncogene (clone 213)  
/cds; 33620\_at Cluster Incl. X16667:Human HOX2G mRNA from the Hox2 locus /cds=(363,165;  
25 34077\_at Cluster Incl. X95876:H.sapiens mRNA for G-protein coupled receptor /cds; 34503\_at  
Cluster Incl. AF007146:Homo sapiens clone 23686 and 23885 mRNA sequence; 36289\_f\_at Cluster  
Incl. U27333:Human alpha (1,3) fucosyltransferase (FUT6) mRNA; 32048\_at Cluster Incl.  
AL049675:Human gene from PAC 886K2, chromosome 1 /cds=UNK; 34755\_at Cluster Incl.  
AJ236876:Homo sapiens mRNA for poly(ADP-ribose) polymeras; 38350\_f\_at Cluster Incl.
- 30 AF005392:Homo sapiens alpha tubulin (TUBA2) gene, parti; 2038\_g\_at M13995  
/FEATURE=mRNA /DEFINITION=HUMBCL2B Human B-cell leukemia/lympho; 1652\_at  
U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene homolog ; 685\_f\_at  
K03460 /FEATURE=cds /DEFINITION=HUMTUBA2H Human alpha-tubulin isotype H.  
**Metagene** 170; 37631\_at Cluster Incl. U14391:Human myosin-IC mRNA, complete cds
- 35 /cds=(375,3704); 40417\_at Cluster Incl. D43950:Human mRNA for KIAA0098 gene, partial cds  
/cds=(0; 32830\_g\_at Cluster Incl. X97544:H.sapiens mRNA for TIM17 preprotein translocase ;  
33820\_g\_at Cluster Incl. X13794:H.sapiens lactate dehydrogenase B gene exon 1 an; 35272\_at  
Cluster Incl. AI541042:pec1.2-1.D12.r Homo sapiens cDNA, 5 end /clone\_; 38125\_at Cluster Incl.  
M14083:Human beta-migrating plasminogen activator inhibit; 40637\_at Cluster Incl.

- Y00371:Human hsc70 gene for 71 kd heat shock cognate prot; 1179\_at Heat Shock Protein, 70 Kda ; 1180\_g\_at Heat Shock Protein, 70 Kda ; 672\_at J03764 /FEATURE=cds /DEFINITION=HUMPAIA Human, plasminogen activator inhi; 115\_at X14787 /FEATURE=cds /DEFINITION=HSTS Human mRNA for thrombospondin .
- 5 **Metagene** 171; 31488\_s\_at Cluster Incl. S81916:phosphoglycerate kinase {alternatively spliced} ; 31728\_at Cluster Incl. M29335:Human MHC class II DO-alpha mRNA, partial cds /cds; 31947\_r\_at Cluster Incl. X74143:H.sapiens HBF-2 mRNA for transcription factor /c; 32408\_s\_at Cluster Incl. AL022101:dJ845O24.4 (Heterogenous Nuclear Ribonucleopro; 35036\_at Cluster Incl. U94333:Human Clq/MBL/SPA receptor C1qR(p) mRNA, complete ; 34909\_at Cluster Incl.
- 10 AC004990:Homo sapiens PAC clone DJ1185107 from 7q11.23-q2; 37434\_at Cluster Incl. W28907:53e12 Homo sapiens cDNA /gb=W28907 /gi=1308855 /ug; 37770\_at Cluster Incl. AF026445:Homo sapiens cofactor of initiator function (CIF; 38500\_at Cluster Incl. AB002450:Homo sapiens mRNA from chromosome 5q21-22, clone; 38552\_f\_at Cluster Incl. AI984786:wr85c06.x1 Homo sapiens cDNA, 3 end /clone=IM; 39613\_at Cluster Incl.
- 15 X74837:H.sapiens HUMM9 mRNA /cds=(689,2566) /gb=X74837 /g; 36513\_at Cluster Incl. U37283:Human microfibril-associated glycoprotein-2 MAGP-2; 39368\_at Cluster Incl. AL031668:Human DNA sequence from clone 64K7 on chromosome; 32790\_at Cluster Incl. D59253:Human mRNA for NCBP interacting protein 1, complet; 38085\_at Cluster Incl. AI740522:wg16b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39883\_at Cluster Incl.
- 20 AF091078:Homo sapiens clone 559 unknown mRNA, complete se; 40941\_at Cluster Incl. W27026:19d10 Homo sapiens cDNA /gb=W27026 /gi=1306398 /ug; 2074\_at L34954 /FEATURE=cds /DEFINITION=HUMCONNEX Human connexin 40 gene, compl; 1968\_g\_at X76079 /FEATURE=exons#1-4 /DEFINITION=HSPDGF H.sapiens mRNA for platel; 1773\_at L00635 /FEATURE= /DEFINITION=HUMFPTB Human farnesyl-protein transferase ; 1734\_at
- 25 M60556 /FEATURE=mRNA#1 /DEFINITION=HUMTGFB3B Human transforming growth f; 1457\_at M64174 /FEATURE= /DEFINITION=HUMPTKJAK1 Human protein-tyrosine kinase (J; 1321\_s\_at U43916 /FEATURE= /DEFINITION=HSU43916 Human tumor-associated membrane ; 1267\_at M55284 /FEATURE= /DEFINITION=HUMPKCL Human protein kinase C-L (PRKCL) mR; 1236\_s\_at M89914 /FEATURE= /DEFINITION=HUMNF1B Human neurofibromin (NF1)
- 30 gene, c; 1164\_at Ubiquitin-Conjugating Enzyme Ubch5 ; 1074\_at M28209 /FEATURE= /DEFINITION=HUMRAB1A Homo sapiens GTP-binding protein (; 865\_at U08316 /FEATURE= /DEFINITION=HSU08316 Human insulin-stimulated protein ki; 262\_at M21154 /FEATURE=mRNA /DEFINITION=HUMAMD Human S-adenosylmethionine decarb. **Metagene** 172; 37781\_at Cluster Incl. AB023138:Homo sapiens mRNA for KIAA0921 protein, partial ; 40677\_at Cluster Incl. AF054984:Homo sapiens clone 23709 mRNA sequence /cds=UNKN; 37998\_at Cluster Incl. U09877:Human helicase-like protein (HLP) mRNA, complete c; 35801\_at Cluster Incl. AF026816:Homo sapiens putative oncogene protein mRNA, par; 37355\_at Cluster Incl. D38255:Homo sapiens mRNA for CAB1, complete cds /cds=(121; 443\_at X17360 /FEATURE=mRNA /DEFINITION=HSHOX51 Human HOX 5.1 gene for HOX 5.1 p; 251\_at

- L41816 /FEATURE=mRNA /DEFINITION=HUMCKI Homo sapiens cam kinase I mRNA, c.  
**Metagene** 173; 31495\_at Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor,  
 complete; 32488\_at Cluster Incl. X14420:Human mRNA for pro-alpha-1 type 3 collagen /cds=(1;  
 32305\_at Cluster Incl. J03464:Human collagen alpha-2 type I mRNA, complete cds; ; 35937\_at  
 5 Cluster Incl. U65416:Human MHC class I molecule (MICB) gene, complete c; 36758\_at Cluster Incl.  
 AF070578:Homo sapiens clone 24674 mRNA sequence /cds=UNKN; 31900\_at Cluster Incl.  
 U33429:human K+ channel beta 2 subunit mRNA, complete cds; 33243\_at Cluster Incl.  
 AF099935:Homo sapiens MDC-3.13 isoform 2 mRNA, complete c; 39400\_at Cluster Incl.  
 AB028978:Homo sapiens mRNA for KIAA1055 protein, partial ; 39438\_at Cluster Incl.  
 10 AF039081:Homo sapiens Cre binding protein-like 2 mRNA, co; 40797\_at Cluster Incl.  
 AF009615:Homo sapiens ADAM10 (ADAM10) mRNA, complete cds ; 32148\_at Cluster Incl.  
 AI701049:wc78b08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33936\_at Cluster Incl.  
 D86181:Homo sapiens DNA for galactocerebrosidase /cds=(14; 35786\_at Cluster Incl.  
 AB007945:Homo sapiens mRNA for KIAA0476 protein, complete; 36607\_at Cluster Incl.  
 15 Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=; 36976\_at Cluster Incl.  
 D21255:Human mRNA for OB-cadherin-2, complete cds /cds=(4; 38427\_at Cluster Incl.  
 L25286:Homo sapiens alpha-1 type XV collagen mRNA, comple; 38446\_at Cluster Incl.  
 X56199:Human XIST, coding sequence a mRNA (locus DXS399; 39517\_at Cluster Incl.  
 AF035313:Homo sapiens clone 23851 mRNA sequence /cds=UNKN; 2087\_s\_at D21254  
 20 /FEATURE= /DEFINITION=HUMOSF4A Human mRNA for OB-cadherin-1, co; 1877\_g\_at  
 Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related ; 1700\_at U82987 /FEATURE=  
 /DEFINITION=HSU82987 Human Bcl-2 binding component 3 (b; 1589\_s\_at L42243  
 /FEATURE=cds#2 /DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8); 1136\_at L16991  
 /FEATURE= /DEFINITION=HUMCDC8X Human thymidylate kinase (CDC8) mR; 402\_s\_at  
 25 X69819 /FEATURE=cds /DEFINITION=HSICAM3RN H.sapiens ICAM-3 mRNA ; 160027\_s\_at  
 Y00285 /FEATURE=cds /DEFINITION=HSIGFIIR Human mRNA for insuline-lik.  
**Metagene** 174; 38915\_at Cluster Incl. AB011135:Homo sapiens mRNA for KIAA0563 protein,  
 complete; 36496\_at Cluster Incl. AF014398:Homo sapiens myo-inositol monophosphatase 2 mRNA;  
 36566\_at Cluster Incl. AJ222967:Homo sapiens mRNA for cystinosin /cds=(339,1442); 36915\_at  
 30 Cluster Incl. AI810485:wb89b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38440\_s\_at Cluster  
 Incl. AA015605:ze20c12.s1 Homo sapiens cDNA, 3 end /clone=IM; 33178\_at Cluster Incl.  
 AF003837:Homo sapiens Jagged1 (JAG1) mRNA, complete cds /; 760\_at Y09216 /FEATURE=  
 /DEFINITION=HSDYRK2 H.sapiens mRNA for protein kinase, D.  
**Metagene** 175; 34549\_g\_at Cluster Incl. X55764:Human mRNA for cytochrome P-450 (11 Beta)  
 35 /cds=(; 40651\_s\_at Cluster Incl. AF039523:untitled /cds=(0,1334) /gb=AF039523 /gi=282812;  
 40741\_at Cluster Incl. M30185:Human cholesteryl ester transfer protein mRNA, com; 34706\_at  
 Cluster Incl. AB011090:Homo sapiens mRNA for KIAA0518 protein, partial ; 37274\_at Cluster Incl.  
 AF018631:untitled /cds=(35,1666) /gb=AF018631 /gi=2674074; 37554\_at Cluster Incl.  
 U62801:Human protease M mRNA, complete cds /cds=(245,979); 33455\_at Cluster Incl.

- X02747:Human mRNA for aldolase B /cds=(125,1219) /gb=X027; 38464\_at Cluster Incl.
- X87237:H.sapiens mRNA for processing a-glucosidase I /cds; 40523\_at Cluster Incl.
- AI371038:ta29f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40927\_at Cluster Incl.
- W26324:28h9 Homo sapiens cDNA /gb=W26324 /gi=1307086 /ug=; 41279\_f\_at Cluster Incl.
- 5 AF007134:Homo sapiens clone 23565 unknown mRNA, partial; 41588\_at Cluster Incl.
- AA022949:ze72h02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1908\_at L16464 /FEATURE= /DEFINITION=HUMETSONC Human ETS oncogene (PEP1) mRNA, c.
- Metagene** 176; 32916\_at Cluster Incl. X54134:Human HPTP epsilon mRNA for protein tyrosine phosph; 38138\_at Cluster Incl. D38583:Human mRNA for calgizzarin, complete cds /cds=(120; 39670\_at Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from clon; 39982\_r\_at Cluster Incl. D13265:Human mRNA for macrophage scavenger receptor typ; 34774\_at Cluster Incl. U44772:Human palmitoyl protein thioesterase mRNA, complet; 36128\_at Cluster Incl. L40397:Homo sapiens (clone S31i125) mRNA, 3 end of cds /; 37324\_at Cluster Incl. X01060:Human mRNA for transferrin receptor /cds=(263,2545; 37689\_s\_at Cluster Incl.
- 15 X68090:H.sapiens Fc-gamma-RIIA gene for IgG Fc receptor; 37741\_at Cluster Incl. M77836:Human pyrroline 5-carboxylate reductase mRNA, comp; 1786\_at U08023 /FEATURE= /DEFINITION=HSU08023 Human cellular proto-oncogene (c-m; 1140\_at L25851 /FEATURE= /DEFINITION=HUMINAE Homo sapiens integrin alpha E precu; 642\_s\_at L76528 /FEATURE=expanded\_cds /DEFINITION=HUMPS1A11 Homo sapiens preseni; 467\_at U63717
- 20 /FEATURE= /DEFINITION=HSU63717 Homo sapiens osteoclast stimulating; 338\_at AF005887 /FEATURE= /DEFINITION=AF005887 Homo sapiens ATF family member AT.
- Metagene** 177; 35055\_at Cluster Incl. X53281:H.sapiens BTF3b mRNA /cds=(239,727) /gb=X53281 /gi; 32111\_at Cluster Incl. AL050164:Homo sapiens mRNA; cDNA DKFZp586C1622 (from clon; 34216\_at Cluster Incl. AA478904:zv20c05.r1 Homo sapiens cDNA, 5 end
- 25 /clone=IMAG; 35635\_at Cluster Incl. AL080202:Homo sapiens mRNA; cDNA DKFZp434F172 (from clone; 36515\_at Cluster Incl. AJ238764:Homo sapiens mRNA for UDP-N-acetylglucosamine-2-; 40508\_at Cluster Incl. AF025887:Homo sapiens glutathione S-transferase A4-4 (GST; 41136\_s\_at Cluster Incl. Y00264:Human mRNA for amyloid A4 precursor of Alzheimer; 41231\_f\_at Cluster Incl. X13546:Human HMG-17 gene for non-histone chromosomal pr; 32244\_at Cluster Incl.
- 30 AB018280:Homo sapiens mRNA for KIAA0737 protein, complete; 33827\_at Cluster Incl. AL049783:Novel human gene mapping to chromosome 13 /cds=(1; 34340\_at Cluster Incl. AA173896:zp03b02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 34366\_g\_at Cluster Incl. AF042386:Homo sapiens cyclophilin-33B (CYP-33) mRNA, co; 34860\_g\_at Cluster Incl. Z98046:dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE); 35294\_at Cluster Incl.
- 35 M25077:Human SS-A/Ro ribonucleoprotein autoantigen 60 kd ; 36201\_at Cluster Incl. D13315:Human mRNA for lactoyl glutathione lyase /cds=(87,; 39865\_at Cluster Incl. AI890903:wm91f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40617\_at Cluster Incl. AC004381:Homo sapiens Chromosome 16 BAC clone CIT987SK-44; 40642\_at Cluster Incl. AI312646:qp77f01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41837\_at Cluster Incl.

- AA149431:z126a08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1640\_at U17714 /FEATURE=  
/DEFINITION=HSU17714 Homo sapiens putative tumor suppre; 1577\_at M23263 /FEATURE=  
/DEFINITION=HUMARB Human androgen receptor mRNA, comple; 490\_g\_at U63329  
/FEATURE=cds /DEFINITION=HSU63329 Human mutY homolog (hMYH) gene; 178\_f\_at  
5 U38964 /FEATURE=cds /DEFINITION=HSU38964 Human PMS2 related (hPMSR2) ge.  
**Metagene** 178; 33589\_at Cluster Incl. AF052103:Homo sapiens clone 23726 mRNA sequence  
/cgs=UNKN; 33984\_at Cluster Incl. M16660:Human 90-kDa heat-shock protein gene, cDNA,  
comple; 34222\_at Cluster Incl. AL035289:H.sapiens gene from PAC 1026E2, partial /cgs=(1;  
33352\_at Cluster Incl. X57985:H.sapiens genes for histones H2B.1 and H2A /cgs=(4; 36203\_at  
10 Cluster Incl. X16277:Human gene for ornithine decarboxylase ODC (EC 4.1; 38030\_at Cluster Incl.  
AB002330:Human mRNA for KIAA0332 gene, partial cds /cgs=(; 40252\_g\_at Cluster Incl.  
U00943:Human clone A9A2BRB2 (CAC)n/(GTG)n repeat-contai; 1850\_at U07418 /FEATURE=  
/DEFINITION=HSHMLHI Human DNA mismatch repair (hmlh1) m; 1081\_at M33764  
/FEATURE=cgs /DEFINITION=HUMSODB Human ornithine decarboxylase ge; 946\_at D50663  
15 /FEATURE= /DEFINITION=D50663 Human mRNA for TCTEL1 gene, complete .  
**Metagene** 179; 37462\_i\_at Cluster Incl. L21990:Human spliceosomal protein (SAP 62) gene,  
comple; 38918\_at Cluster Incl. AF083105:Homo sapiens HMG box factor SOX-13 mRNA, complet;  
40362\_at Cluster Incl. X61498:H.sapiens mRNA for NF-kB subunit /cgs=(163,2964) /; 41018\_at  
Cluster Incl. AL050015:Homo sapiens mRNA; cDNA DKFZp564O243 (from clone; 41413\_at  
20 Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane ; 31837\_at Cluster Incl.  
U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 complete; 35154\_at Cluster Incl.  
W68046:zd42a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35205\_at Cluster Incl.  
AL050280:Homo sapiens mRNA; cDNA DKFZp586B0519 (from clon; 35244\_at Cluster Incl.  
AB007929:Homo sapiens mRNA for KIAA0460 protein, partial ; 35675\_at Cluster Incl.  
25 AF037261:Homo sapiens SH3-containing adaptor molecule-1 m; 37931\_at Cluster Incl.  
X05299:Human mRNA (~95%) for major centromere autoantigen; 38310\_at Cluster Incl.  
AB014591:Homo sapiens mRNA for KIAA0691 protein, complete; 38721\_at Cluster Incl.  
W72733:zd77h11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39711\_at Cluster Incl.  
J03075:Human 80K-H protein (kinase C substrate) mRNA, com; 40093\_at Cluster Incl.  
30 X83425:H.sapiens LU gene for Lutheran blood group glycop; 40817\_at Cluster Incl.  
M96824:Human nucleobindin precursor mRNA, complete cds /c; 41134\_at Cluster Incl.  
AB023181:Homo sapiens mRNA for KIAA0964 protein, complete; 32254\_at Cluster Incl.  
AL050223:Homo sapiens mRNA; cDNA DKFZp586L1323 (from clon; 32836\_at Cluster Incl.  
U56417:Human lysophosphatidic acid acyltransferase-alpha ; 33398\_at Cluster Incl.  
35 AB014570:Homo sapiens mRNA for KIAA0670 protein, partial ; 33425\_at Cluster Incl.  
X97548:H.sapiens mRNA for TIF1beta zinc finger protein /c; 33841\_at Cluster Incl.  
R48209:yj63d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 33879\_at Cluster Incl.  
U79528:Human SR31747 binding protein 1 mRNA, complete cds; 36152\_at Cluster Incl.  
X79353:H.sapiens XAP-4 mRNA for GDP-dissociation inhibito; 36162\_at Cluster Incl.

- X64364:H.sapiens mRNA for M6 antigen /cds=(57,866) /gb=X6; 36183\_at Cluster Incl.  
 X86779:H.sapiens mRNA for FAST kinase /cds=(21,1670) /gb=; 36958\_at Cluster Incl.  
 X95735:Homo sapiens mRNA for zyxin /cds=(71,1789) /gb=X95; 37307\_at Cluster Incl.  
 X04828:Human mRNA for G(i) protein alpha-subunit (adenyla; 37346\_at Cluster Incl.
- 5 M57567:Human ADP-ribosylation factor (hARF5) mRNA, comple; 38766\_at Cluster Incl.  
 AB002307:Human mRNA for KIAA0309 gene, partial cds /cds=(; 40235\_at Cluster Incl.  
 L13738:Human activated p21cdc42Hs kinase (ack) mRNA, comp; 40580\_r\_at Cluster Incl.  
 M24398:Human parathymosin mRNA, complete cds /cds=(300,; 40998\_at Cluster Incl.  
 AF071309:Homo sapiens OPA-containing protein mRNA, comple; 32553\_at Cluster Incl.
- 10 M94046:Human zinc finger protein (MAZ) mRNA /cds=UNKNOWN ; 1926\_at U48801  
 /FEATURE= /DEFINITION=HSU48801 Human vascular endothelial growth ; 1642\_at U35113  
 /FEATURE= /DEFINITION=HSU35113 Human metastasis-associated mta1 m; 1487\_at L38487  
 /FEATURE=mRNA /DEFINITION=HUMHERRA1 Human estrogen receptor-relat; 1158\_s\_at  
 J04046 /FEATURE=mRNA /DEFINITION=HUMCAMA Human calmodulin mRNA, comple;
- 15 497\_at U32680 /FEATURE= /DEFINITION=HSU32680 Human CLN3 mRNA, complete cds ;  
 388\_at X80907 /FEATURE= /DEFINITION=HSPHOSINK H.sapiens mRNA for p85 beta subuni;  
 371\_at Z56281 /FEATURE=cds /DEFINITION=HSIRF3MR H.sapiens mRNA for interferon re;  
 175\_s\_at U33053 /FEATURE= /DEFINITION=HSU33053 Human lipid-activated protein kin.  
**Metagene** 180; 33072\_at Cluster Incl. AF041245:Homo sapiens orexin receptor-2 mRNA, complete  
 20 cd; 37508\_f\_at Cluster Incl. AA675900:g02504r Homo sapiens cDNA, 5 end /clone=g0250;  
 37519\_at Cluster Incl. M10058:Human asialoglycoprotein receptor H1 mRNA, complet; 41003\_at  
 Cluster Incl. U41816:Human C-1 mRNA, complete cds /cds=(11,403) /gb=U41; 41435\_at Cluster  
 Incl. AB014554:Homo sapiens mRNA for KIAA0654 protein, partial ; 34655\_at Cluster Incl.  
 AI951832:wx38b09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36165\_at Cluster Incl.
- 25 W51774:zc48b04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39472\_s\_at Cluster Incl.  
 W25985:17e6 Homo sapiens cDNA /gb=W25985 /gi=1306252 /u; 32505\_at Cluster Incl.  
 W28652:50f5 Homo sapiens cDNA /gb=W28652 /gi=1308663 /ug=; 1477\_s\_at M61853  
 /FEATURE=mRNA /DEFINITION=HUM2C18 Human cytochrome P4502C18 (CY; 554\_at  
 U03634 /FEATURE= /DEFINITION=HSU03634 Human P47 LBC oncogene mRNA, comple.
- 30 **Metagene** 181; 32478\_f\_at Cluster Incl. AL031133:dJ281H8.4 (Ubiquitin-Like protein SMT3 LIKE)  
 /; 35018\_at Cluster Incl. U61538:Human calcium-binding protein chp mRNA, complete c; 36379\_at  
 Cluster Incl. AF085808:Homo sapiens uroplakin III mRNA, complete cds /c; 32970\_f\_at Cluster  
 Incl. U77327:Human Ki-1/57 intracellular antigen mRNA, partia; 32731\_at Cluster Incl.  
 AB018247:Homo sapiens mRNA for Fe65L2, complete cds /cds=; 32739\_at Cluster Incl.
- 35 AA001791:zh86c04.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 33814\_at Cluster Incl.  
 AF005046:Homo sapiens serine/threonine kinase mRNA, compl; 37246\_at Cluster Incl.  
 AF070535:Homo sapiens clone 24432 mRNA sequence /cds=UNKN; 40084\_at Cluster Incl.  
 U03494:Human transcription factor LSF mRNA, complete cds ; 35815\_at Cluster Incl.  
 AL049470:Homo sapiens mRNA; cDNA DKFZp586L012 (from clone; 36132\_at Cluster Incl.



- S74728:antiquitin=26g turgor protein homolog [human, kidn; 39094\_at Cluster Incl.  
 AI991631:wr12h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40640\_at Cluster Incl.  
 U62317:Chromosome 22q13 BAC Clone CIT987SK-384D8 complete; 32528\_at Cluster Incl.  
 Z50853:H.sapiens mRNA for CLPP /cds=(19,852) /gb=Z50853 /.
- 5 **Metagene** 182; 31478\_at Cluster Incl. M16653:Human pancreatic elastase IIB mRNA, complete cds  
 /; 35505\_at Cluster Incl. AI290660:qm12b10.x1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 32878\_f\_at Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542;  
 32881\_at Cluster Incl. U88834:Human clone 295, 5cM region surrounding hepatocyte; 34430\_at  
 Cluster Incl. U70732:Human glutamate pyruvate transaminase (GPT) gene, ; 35443\_at Cluster Incl.
- 10 AF060543:Homo sapiens importin alpha 7 subunit mRNA, comp; 36710\_at Cluster Incl.  
 Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds; 31828\_r\_at Cluster Incl.  
 AF027516:Homo sapiens trans-golgi network glycoprotein ; 35175\_f\_at Cluster Incl.  
 X70940:H.sapiens mRNA for elongation factor 1 alpha-2 /; 35703\_at Cluster Incl. X06374:Human  
 mRNA for platelet-derived growth factor PDGF; 40777\_at Cluster Incl. X87838:H.sapiens mRNA
- 15 for beta-catenin /cds=(214,2559) /g; 33449\_at Cluster Incl. AF054185:Homo sapiens proteasome  
 subunit HSPC mRNA, compl; 35768\_at Cluster Incl. AB014561:Homo sapiens mRNA for  
 KIAA0661 protein, complete; 35810\_at Cluster Incl. AI525393:PT1.1\_07\_A11.r Homo sapiens  
 cDNA, 5 end /clone\_ ; 39185\_at Cluster Incl. AF091083:Homo sapiens clone 628 unknown mRNA,  
 complete se; 40540\_at Cluster Incl. AI926989:wo68e11.x1 Homo sapiens cDNA, 3 end
- 20 /clone=IMAG; 2062\_at L19182 /FEATURE= /DEFINITION=HUMMAC25X Human MAC25  
 mRNA, complete cds ; 2007\_g\_at U31601 /FEATURE= /DEFINITION=HSU31601 Human tyrosine  
 protein kinase (J; 1492\_f\_at M33317 /FEATURE=mRNA /DEFINITION=HUMCYIIA4A Human  
 cytochrome P450IIA4 ; 566\_at M79462 /FEATURE= /DEFINITION=HUMPML1 Human PML-1  
 mRNA, complete CDS ; 559\_s\_at S38742 /FEATURE= /DEFINITION=S38742 HOX11=HOX11
- 25 homeodomain {homeobox} ; 469\_at U66406 /FEATURE= /DEFINITION=HSU66406 Human  
 putative EPH-related PTK rece; 254\_at M11353 /FEATURE= /DEFINITION=HUMHISH3C Human  
 H3.3 histone class C mRNA, c.
- Metagene** 183; 35130\_at Cluster Incl. X15722:Human mRNA for glutathione reductase (EC 1.6.4.2)  
 ; 36798\_g\_at Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,12; 37940\_f\_at  
 Cluster Incl. AA806768:ob91d06.s1 Homo sapiens cDNA /clone=IMAGE-1338; 40051\_at Cluster
- 30 Incl. D31762:Human mRNA for KIAA0057 gene, complete cds /cds=(7.  
**Metagene** 184; 31363\_at Cluster Incl. W27607:35b12 Homo sapiens cDNA /gb=W27607  
 /gi=1307555 /ug; 31694\_at Cluster Incl. X82877:H.sapiens Na<sup>+</sup>-D-glucose cotransport regulator  
 gene; 34088\_at Cluster Incl. AF043469:Homo sapiens neurexophilin 4 (NPH4) mRNA, partia;  
 34985\_at Cluster Incl. AF035408:Homo sapiens cartilage intermediate layer protei; 41075\_at Cluster
- 35 Incl. AF087003:Homo sapiens fibrousheathin I mRNA, complete cds; 41654\_at Cluster Incl.  
 X02994:Human mRNA for adenosine deaminase (adenosine amin; 36085\_at Cluster Incl.  
 X63749:H.sapiens DNA for Rod transducin alpha-subunit /cd.
- Metagene** 185; 31372\_at Cluster Incl. W28203:43g3 Homo sapiens cDNA /gb=W28203

- /gi=1308169 /ug=; 31921\_at Cluster Incl. U56421:Human olfactory receptor (OLF3) gene, complete cds; 31975\_at Cluster Incl. X55503:H.sapiens pseudogene for metallothionein and AG/CT; 33622\_at Cluster Incl. Z26308:H.sapiens isoform 1 gene for L-type calcium channel; 32271\_at Cluster Incl. X16707:Human fra-1 mRNA /cds=(34,849) /gb=X16707 /gi=3146; 36703\_at Cluster Incl.
- 5 U86358:Human chemokine (TECK) mRNA, complete cds /cds=(0; 39657\_at Cluster Incl. X07695:Human mRNA for cytokeratin 4 C-terminal region /cd; 40300\_g\_at Cluster Incl. AF091890:Homo sapiens G-protein coupled receptor RE2 mR; 35685\_at Cluster Incl. Z14000:H.sapiens RING1 gene /cds=(75,1208) /gb=Z14000 /gi; 36929\_at Cluster Incl. U17760:Human laminin S B3 chain (LAMB3) gene /cds=(399,39; 38624\_at Cluster Incl.
- 10 AF054506:Homo sapiens erythroid K-CI cotransporter splici; 37299\_at Cluster Incl. J04501:Human muscle glycogen synthase mRNA, complete cds ; 38377\_at Cluster Incl. U47742:Human monocytic leukaemia zinc finger protein (MOZ; 41838\_at Cluster Incl. X99270:H.sapiens Xq28, 2000bp sequence contg. ORF /cds=(5; 731\_f\_at Mucin 3, Intestinal ; 331\_at Microtubule-Associated Protein Tau, Alt. Splice 5, Exon 4a .
- 15 **Metagene** 186; 31738\_at Cluster Incl. W28912:53f11 Homo sapiens cDNA /gb=W28912 /gi=1308860 /ug; 33650\_at Cluster Incl. W25911:14h11 Homo sapiens cDNA /gb=W25911 /gi=1306034 /ug; 33668\_at Cluster Incl. AF037643:Homo sapiens 60S ribosomal protein L12 (RPL12) p; 34532\_at Cluster Incl. AF035318:Homo sapiens clone 23705 mRNA sequence /cds=UNKN; 39325\_at Cluster Incl. U81523:Human endometrial bleeding associated factor mRNA,;
- 20 39659\_at Cluster Incl. L37936:Human nuclear-encoded mitochondrial elongation fac; 40014\_at Cluster Incl. AF055020:Homo sapiens clone 24722 unknown mRNA, partial c; 40324\_r\_at Cluster Incl. AF070585:Homo sapiens clone 24675 mRNA sequence /cds=UN; 41418\_at Cluster Incl. AB020628:Homo sapiens mRNA for KIAA0821 protein, complete; 33782\_r\_at Cluster Incl. AA587372:nn82f03.s1 Homo sapiens cDNA, 3 end /clone=IM; 34730\_g\_at Cluster Incl.
- 25 AB029037:Homo sapiens mRNA for KIAA1114 protein, comple; 35138\_at Cluster Incl. Y11997:H.sapiens mRNA for A-kinase anchoring protein AKAP; 35727\_at Cluster Incl. AI249721:qj64d06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36531\_r\_at Cluster Incl. AC005757:Homo sapiens chromosome 19, cosmid R32611 /cds; 36846\_s\_at Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM; 37585\_at Cluster Incl.
- 30 X13482:Human mRNA for U2 snRNP-specific A protein /cds=(5; 38265\_at Cluster Incl. AI538172:ti75f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38311\_at Cluster Incl. AF055012:Homo sapiens clone 24615 mRNA sequence /cds=UNKN; 39749\_at Cluster Incl. U51007:Human 26S protease subunit S5a mRNA, complete cds ; 40110\_at Cluster Incl. U49283:Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta ; 40869\_at Cluster Incl.
- 35 AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, com; 41205\_at Cluster Incl. U84404:Human E6-associated protein E6-AP/ubiquitin-protei; 32774\_at Cluster Incl. AI541050:pec1.2-1.E08.r Homo sapiens cDNA, 5 end /clone\_ ; 34345\_at Cluster Incl. AF026031:Homo sapiens putative mitochondrial outer membra; 34882\_at Cluster Incl. Y12065:Homo sapiens mRNA for nucleolar protein hNop56 /cd; 35736\_at Cluster Incl.

- AL050091: Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone; 36145\_at Cluster Incl.  
 U51586: Human siah binding protein 1 (SiahBP1) mRNA, parti; 36602\_at Cluster Incl.  
 D21064: Human mRNA for KIAA0123 gene, partial cds /cds=(0,; 37041\_at Cluster Incl.  
 AB023160: Homo sapiens mRNA for KIAA0943 protein, partial ; 38053\_s\_at Cluster Incl.
- 5 AF015767: Homo sapiens brain and reproductive organ-expr; 38060\_at Cluster Incl.  
 AI541336: pec1.2-7.A07.r Homo sapiens cDNA, 5 end /clone\_; 40210\_at Cluster Incl.  
 X75593: H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X7559; 40926\_at Cluster Incl.  
 U36341: Human Xq28 cosmid, creatine transporter (SLC6A8) g; 41600\_at Cluster Incl.  
 U59435: Human cell cycle protein p38-2G4 homolog (hG4-1) m; 1357\_at U20657 /FEATURE=
- 10 /DEFINITION=HSU20657 Human ubiquitin protease (Unph) pr; 1308\_g\_at D14533 /FEATURE=  
 /DEFINITION=HUMXPAC Human mRNA for XPAC protein ; 1009\_at U51004 /FEATURE=  
 /DEFINITION=HSU51004 Homo sapiens protein kinase C inh; 662\_at L13848 /FEATURE=  
 /DEFINITION=HUMRNAHELA Human RNA helicase A mRNA, comple; 571\_at M86667  
 /FEATURE= /DEFINITION=HUMNAP H.sapiens NAP (nucleosome assembly pr; 472\_at U48730
- 15 /FEATURE= /DEFINITION=HSU48730 Homo sapiens transcription factor S; 229\_at M37197  
 /FEATURE=mRNA /DEFINITION=HUMCBF Human CCAAT-box-binding factor (C.  
**Metagene** 187; 32303\_at Cluster Incl. L16464: Human ETS oncogene (PEP1) mRNA, complete cds  
 /cds=; 36761\_at Cluster Incl. AL079276: Homo sapiens mRNA full length insert cDNA clone ;  
 40688\_at Cluster Incl. AJ223280: Homo sapiens mRNA for 36 kDa phosphotyrosine pr; 32225\_at  
 20 Cluster Incl. X04297: Human mRNA for Na,K-ATPase alpha-subunit /cds=(318; 39519\_at Cluster  
 Incl. AB014592: Homo sapiens mRNA for KIAA0692 protein, partial ; 1650\_g\_at U61836  
 /FEATURE=mRNA /DEFINITION=HSU61836 Human putative cyclin G1 int.
- Metagene** 188; 36439\_at Cluster Incl. AL080134: Homo sapiens mRNA; cDNA DKFZp434G043  
 (from clone; 39658\_at Cluster Incl. AB007901: Homo sapiens KIAA0441 mRNA, complete cds  
 25 /cds=(1; 1096\_g\_at M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein  
 CD19 (.
- Metagene** 189; 38863\_at Cluster Incl. L07540: Human replication factor C, 36-kDa subunit mRNA,  
 c; 41852\_at Cluster Incl. U22377: Human Zn-15 related zinc finger protein (rif) mRNA; 32743\_at  
 Cluster Incl. AB007922: Homo sapiens mRNA for KIAA0453 protein, partial ; 951\_at D88378  
 30 /FEATURE= /DEFINITION=D88378 Homo sapiens mRNA for proteasome inh; 205\_g\_at M74297  
 /FEATURE= /DEFINITION=HUMHOX14 Human homeobox 1.4 protein mRNA, .
- Metagene** 190; 36307\_at Cluster Incl. D87468: Human mRNA for KIAA0278 gene, partial cds  
 /cds=(0,; 37128\_at Cluster Incl. AB005216: Homo sapiens mRNA for Nck, Ash and phospholipase;  
 37473\_at Cluster Incl. AF061812: Homo sapiens keratin 16 (KRT16A) mRNA, complete ; 37858\_at  
 35 Cluster Incl. AF057036: Homo sapiens acetylcholinesterase collagen-like ; 40302\_at Cluster Incl.  
 AL031186: bK984G1.1 (PUTATIVE C-terminal end of a novel pr; 32716\_at Cluster Incl.  
 X62535: H.sapiens mRNA for diacylglycerol kinase /cds=(103; 33758\_f\_at Cluster Incl.  
 U25988: Human pregnancy-specific glycoprotein 13 (PSG13); 36621\_at Cluster Incl.  
 M16961: Human alpha-2-HS-glycoprotein alpha and beta chain; 37408\_at Cluster Incl.

- AB014609:Homo sapiens mRNA for KIAA0709 protein, complete; 39821\_s\_at Cluster Incl.  
 N95168:zb55f1.1.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40904\_at Cluster Incl.  
 AI857673:wk96c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40960\_at Cluster Incl.  
 D29805:Human mRNA for beta-1,4-galactosyltransferase, com.
- 5 **Metagene** 191; 31668\_f\_at Cluster Incl. W28193:43d12 Homo sapiens cDNA /gb=W28193  
 /gi=1308141 /; 38226\_at Cluster Incl. W27152:23h11 Homo sapiens cDNA /gb=W27152  
 /gi=1306731 /ug; 37045\_at Cluster Incl. D87443:Human mRNA for KIAA0254 gene, complete cds  
 /cds=(5; 38438\_at Cluster Incl. M58603:Human nuclear factor kappa-B DNA binding subunit (;  
 39139\_at Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG.
- 10 **Metagene** 192; 32420\_at Cluster Incl. U18549:Human GPR6 G protein-coupled receptor gene,  
 comple; 35923\_at Cluster Incl. D13305:Human mRNA for brain cholecystokinin receptor /cds;  
 36252\_at Cluster Incl. U43030:Human cardiotrophin-1 (CTF1) mRNA, complete cds /c; 39629\_at  
 Cluster Incl. U03090:Homo sapiens Ca<sup>2+</sup>-dependent phospholipase A2 mRNA,; 39333\_at Cluster  
 Incl. M26576:Human alpha-1 collagen type IV gene /cds=(0,5009) ; 32162\_r\_at Cluster Incl.
- 15 AI817548:wk24e08.x1 Homo sapiens cDNA, 3 end /clone=IM; 41325\_at Cluster Incl.  
 AF006823:Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> chan; 33201\_at Cluster Incl.  
 AW007029:ws49c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 2047\_s\_at M23410  
 /FEATURE= /DEFINITION=HUMPLAKO Human plakoglobin (PLAK) mRNA, c.  
**Metagene** 193; 32444\_at Cluster Incl. X69392:H.sapiens mRNA for ribosomal protein L26  
 /cds=(6,4; 32484\_at Cluster Incl. U94888:Homo sapiens CC-chemokine receptor 10 (CCR10)  
 mRNA; 32492\_g\_at Cluster Incl. U25441:Human dopamine D3 receptor (DRD3) gene, complete;  
 35590\_s\_at Cluster Incl. X81832:H.sapiens mRNA for glucose-dependant insulinotro; 37517\_at  
 Cluster Incl. AB028962:Homo sapiens mRNA for KIAA1039 protein, partial ; 38507\_at Cluster Incl.  
 X16867:Human mRNA for cytochrome P-450IID (clone pMP34) /; 31815\_r\_at Cluster Incl.
- 25 AB009462:Homo sapiens hLRp105 mRNA for LDL receptor rel; 32646\_at Cluster Incl.  
 AB007918:Homo sapiens mRNA for KIAA0449 protein, partial ; 33268\_at Cluster Incl.  
 L25270:Human XE169 mRNA, complete cds /cds=(531,5213) /gb; 33768\_at Cluster Incl.  
 L19267:Homo sapiens 59 protein mRNA, 3 end /cds=(0,1661); 36084\_at Cluster Incl.  
 D38548:Human mRNA for KIAA0076 gene, complete cds /cds=(8; 33836\_at Cluster Incl.
- 30 AC002045:Human Chromosome 16 BAC clone CIT987SK-A-589H1 /; 37404\_at Cluster Incl.  
 AF030152:Homo sapiens regulator of G protein signaling 12; 38019\_at Cluster Incl. L37043:Homo  
 sapiens casein kinase I epsilon mRNA, complet; 38055\_at Cluster Incl. AI683748:tw53e07.x1 Homo  
 sapiens cDNA, 3 end /clone=IMAG; 39845\_at Cluster Incl. AF020760:Homo sapiens serine protease  
 (Omi) mRNA, complet; 33135\_at Cluster Incl. U17566:Human 65 kDa hydrophobic protein mRNA,  
 complete cd; 1627\_at Tyrosine Kinase ; 1008\_f\_at U50648 /FEATURE=mRNA  
 /DEFINITION=HSIIPKR17 Human interferon-inducible ; 678\_at J04948 /FEATURE=mRNA  
 /DEFINITION=HUMALP1GC Human alkaline phosphatase (AL; 454\_at U66617 /FEATURE=  
 /DEFINITION=HSU66617 Human SWI/SNF complex 60 KDa subuni.  
**Metagene** 194; 36468\_at Cluster Incl. U84551:Human dystrobrevin (DTN) gene /cds=(1,1713)

- /gb=U8; 40476\_s\_at Cluster Incl. U58198:Human interleukin enhancer binding factor 3 mRNA;  
 36592\_at Cluster Incl. S85655:prohibitin [human, mRNA, 1043 nt] /cds=(50,868) /g; 1874\_at  
 D21090 /FEATURE= /DEFINITION=HUMHHR23B Human mRNA for XP-C repair comple;  
 491\_at U46116 /FEATURE=mRNA /DEFINITION=HSPTPRG28 Human receptor tyrosine phosph;  
 5 267\_at L34075 /FEATURE= /DEFINITION=HUMFRAPX Human FKBP-rapamycin associated pro;  
 123\_at X75756 /FEATURE=cds /DEFINITION=HSPKCMU H.sapiens mRNA for protein kinase.  
**Metagene** 195; 33466\_at Cluster Incl. AF038182:Homo sapiens clone 23860 mRNA sequence  
 /cds=UNKN; 35733\_at Cluster Incl. AF006082:Homo sapiens actin-related protein Arp2 (ARP2) m;  
 1820\_g\_at Guanine Nucleotide-Binding Protein Rap2, Ras-Oncogene Related ; 1284\_at  
 10 Serine/Threonine Kinase ; 1253\_at L33801 /FEATURE= /DEFINITION=HUMGLSYKIN Human  
 protein kinase mRNA, compl.  
**Metagene** 196; 32893\_s\_at Cluster Incl. M30474:Human kidney gamma-glutamyl transpeptidase  
 type ; 37463\_r\_at Cluster Incl. L21990:Human spliceosomal protein (SAP 62) gene, comple;  
 41035\_at Cluster Incl. AB018318:Homo sapiens mRNA for KIAA0775 protein, complete; 37970\_at  
 15 Cluster Incl. AB028989:Homo sapiens mRNA for KIAA1066 protein, partial ; 40472\_at Cluster Incl.  
 AF007155:Homo sapiens clone 23763 unknown mRNA, partial c; 38759\_at Cluster Incl.  
 U97502:Homo sapiens butyrophilin (BT3.3) gene /cds=(73,22; 38799\_at Cluster Incl.  
 AF068706:Homo sapiens gamma2-adaptin (G2AD) mRNA, complet; 1341\_at X52056  
 /FEATURE=cds /DEFINITION=HSSPI1 Human mRNA for spi-1 proto-oncoge; 335\_r\_at  
 20 Spliceosomal Protein Sap 62 .  
**Metagene** 197; 31724\_at Cluster Incl. L38518:Homo sapiens sonic hedgehog protein (SHH) mRNA,  
 co; 32990\_at Cluster Incl. S75989:gamma-aminobutyric acid transporter type 3 [human; 33580\_r\_at  
 Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosom; 32379\_f\_at Cluster  
 Incl. W28740:51a5 Homo sapiens cDNA /gb=W28740 /gi=1308688 /u; 35437\_at Cluster Incl.  
 25 M88461:Human neuropeptide Y peptide YY receptor mRNA, com; 40319\_at Cluster Incl.  
 H05552:yl75c01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 31893\_at Cluster Incl.  
 L13687:Homo sapiens ADP-ribosylation factor-like protein ; 34224\_at Cluster Incl.  
 AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B; 35666\_at Cluster Incl.  
 U38276:Human semaphorin III family homolog mRNA, complete; 37553\_at Cluster Incl.  
 30 D50863:Human mRNA for TESK1, complete cds /cds=(272,2152); 37894\_at Cluster Incl.  
 U83410:Human CUL-2 (cul-2) mRNA, complete cds /cds=(146,2; 37982\_at Cluster Incl.  
 Z25821:H.sapiens gene for mitochondrial dodecenoyl-CoA de; 39077\_at Cluster Incl.  
 U41843:Human Dr1-associated corepressor (DRAP1) mRNA, com; 40778\_at Cluster Incl.  
 AF035555:Homo sapiens short chain L-3-hydroxyacyl-CoA deh; 33347\_at Cluster Incl.  
 35 AA883868:am26e11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 34347\_at Cluster Incl.  
 AL049955:Homo sapiens mRNA; cDNA DKFZp564J0123 (from clon; 34351\_at Cluster Incl.  
 AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosph; 34358\_at Cluster Incl.  
 Z49254:H.sapiens L23-related mRNA /cds=(54,515) /gb=Z4925; 34784\_at Cluster Incl.  
 Z83844:Human DNA sequence from clone 37E16 on chromosome ; 35773\_i\_at Cluster Incl.

- AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM; 35774\_r\_at Cluster Incl.  
 AA527880:nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IM; 35813\_at Cluster Incl.  
 AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35819\_at Cluster Incl.  
 X06994:Human mRNA for cytochrome c1 /cds=(8,985) /gb=X069; 36936\_at Cluster Incl.
- 5 U58766:Human FX protein mRNA, complete cds /cds=(74,1039); 38397\_at Cluster Incl.  
 U09196:Human 1.1 kb mRNA upregulated in retinoic acid tre; 38451\_at Cluster Incl.  
 T58471:yb61c11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39499\_s\_at Cluster Incl.  
 W25794:13e8 Homo sapiens cDNA /gb=W25794 /gi=1305935 /u; 40206\_at Cluster Incl.  
 AI767675:wh38d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41306\_at Cluster Incl.
- 10 AA004795:zh96a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32536\_at Cluster Incl.  
 Z37986:H.sapiens mRNA for phenylalkylamine binding protei; 32564\_at Cluster Incl.  
 AA083129:zn31a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1551\_g\_at U19796 /FEATURE=  
 /DEFINITION=HSU19796 Human melanoma antigen p15 mRNA.; 1112\_g\_at M22092  
 /FEATURE=cds /DEFINITION=HUMNCAM2 Human neural cell adhesion mo; 592\_at M34079
- 15 /FEATURE= /DEFINITION=HUMTBP1 Human immunodeficiency virus tat tra.  
**Metagene** 198; 34422\_r\_at Cluster Incl. U82818:Homo sapiens UCP3S mRNA, complete cds  
 /cds=(153; 38546\_at Cluster Incl. AB006537:Homo sapiens mRNA for interleukin 1 receptor acc;  
 39238\_at Cluster Incl. AF040705:Homo sapiens putative tumor suppressor protein u; 41663\_at  
 Cluster Incl. AF038202:Homo sapiens clone 23570 mRNA sequence /cds=UNKN; 41686\_s\_at
- 20 Cluster Incl. AL042668:DKFZp434O1721\_r1 Homo sapiens cDNA, 5 end /cl; 31842\_at Cluster Incl.  
 AF038195:Homo sapiens clone 23661 unknown protein mRNA, c; 32115\_r\_at Cluster Incl.  
 X68486:H.sapiens mRNA for A2a adenosine receptor /cds=(; 38324\_at Cluster Incl.  
 AD000684:Homo sapiens DNA from chromosome 19-cosmid R3087; 32775\_r\_at Cluster Incl.  
 AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=; 38792\_at Cluster Incl.
- 25 AD001528:Homo sapiens spermidine aminopropyltransferase m; 40976\_at Cluster Incl.  
 AF052432:Homo sapiens katanin p80 subunit mRNA, complete ; 32535\_at Cluster Incl.  
 X63556:H.sapiens mRNA for fibrillin /cds=(0,9010) /gb=X63; 32615\_at Cluster Incl. J05032:Human  
 aspartyl-tRNA synthetase alpha-2 subunit mRN; 1775\_at L24559 /FEATURE=  
 /DEFINITION=HUMDNSPOLA Homo sapiens DNA polymerase alph; 1419\_g\_at D29675
- 30 /FEATURE=exon /DEFINITION=HUMNOSB Human inducible nitric oxide ; 1055\_g\_at M87339  
 /FEATURE= /DEFINITION=HUMACT1A Human replication factor C, 37-k.  
**Metagene** 199; 34991\_at Cluster Incl. U58331:Human placental delta sarcoglycan mRNA, complete  
 c; 36799\_at Cluster Incl. L37882:Human frizzled gene product mRNA, complete cds /cd; 39251\_at  
 Cluster Incl. M74091:Human cyclin mRNA /cds=UNKNOWN /gb=M74091 /gi=1806; 37906\_at
- 35 Cluster Incl. Z37976:H.sapiens mRNA for latent transforming growth fact; 39764\_at Cluster Incl.  
 Z22534:H.sapiens ALK-2 mRNA /cds=(103,1632) /gb=Z22534 /g; 34354\_at Cluster Incl.  
 M80634:Human keratinocyte growth factor receptor mRNA, co; 37743\_at Cluster Incl.  
 U60060:Human FEZ1 mRNA, complete cds /cds=(99,1277) /gb=U; 38087\_s\_at Cluster Incl.  
 W72186:zd69b10.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 628\_at L37882 /FEATURE=

- /DEFINITION=HUMFRIZ Human frizzled gene product mRNA, co; 320\_at D83703 /FEATURE=  
/DEFINITION=D83703 Homo sapiens mRNA for peroxisome asse.
- Metagene** 200; 34164\_at Cluster Incl. R42599:yg02e11.s1 Homo sapiens cDNA, 3 end  
/clone=IMAGE-; 34425\_at Cluster Incl. AF031469:Homo sapiens MHC class I related protein 1  
5 isofo; 38538\_at Cluster Incl. AB014602:Homo sapiens mRNA for KIAA0702 protein, complete;  
39601\_at Cluster Incl. AF061836:Homo sapiens putative tumor suppressor protein (; 39609\_at  
Cluster Incl. U80457:Human transcription factor SIM2 short form mRNA, c; 33323\_r\_at Cluster  
Incl. X57348:H.sapiens mRNA (clone 9112) /cds=(165,911) /gb=X; 33812\_at Cluster Incl.  
AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clon; 37572\_at Cluster Incl.
- 10 A W043690:wy80b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37969\_at Cluster Incl.  
M59979:Human prostaglandin endoperoxide synthase mRNA, co; 39789\_at Cluster Incl.  
U96094:Human sarcolipin (SLN) mRNA, complete cds /cds=(16; 34779\_at Cluster Incl.  
R90942:yp92b03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39459\_at Cluster Incl.  
W28765:51d2 Homo sapiens cDNA /gb=W28765 /gi=1308713 /ug=; 39482\_at Cluster Incl.
- 15 W26787:15d8 Homo sapiens cDNA /gb=W26787 /gi=1306078 /ug=; 40271\_at Cluster Incl.  
D42085:Human mRNA for KIAA0095 gene, complete cds /cds=(6; 40981\_at Cluster Incl.  
U00930:Human clone C4E 1.63 (CAC)n/(GTG)n repeat-containi; 1065\_at U02687 /FEATURE=  
/DEFINITION=HSU02687 Human growth factor receptor tyros; 348\_at D14678 /FEATURE=  
/DEFINITION=HUMMHCB Human mRNA for kinesin-related prote.
- 20 **Metagene** 201; 31672\_g\_at Cluster Incl. D82351:Human retropseudogene MSSP-1 DNA, complete  
cds /; 40015\_at Cluster Incl. AB002301:Human mRNA for KIAA0303 gene, partial cds /cds=(;  
34705\_at Cluster Incl. AJ224335:Homo sapien mRNA for putative secretory protein.; 35694\_at  
Cluster Incl. AB014587:Homo sapiens mRNA for KIAA0687 protein, partial ; 40061\_at Cluster Incl.  
D83784:Human mRNA for KIAA0198 gene, partial cds /cds=(0; 37674\_at Cluster Incl.
- 25 Y00451:Human mRNA for 5-aminolevulinate synthase /cds=(83; 39528\_at Cluster Incl.  
L24564:Human Rad mRNA, complete cds /cds=(123,1049) /gb=L; 1776\_at L24564 /FEATURE=  
/DEFINITION=HUMRAD Human Rad mRNA, complete cds .
- Metagene** 202; 31715\_at Cluster Incl. U93720:Homo sapiens TEX28 mRNA, complete cds  
/cds=(144,13; 33555\_at Cluster Incl. AF041261:Homo sapiens immunoglobulin-like transcript 7 mR;  
30 37867\_at Cluster Incl. Z48051:H.sapiens gene for myelin oligodendrocyte glycopro; 41247\_at  
Cluster Incl. H12054:ym11b12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 32520\_at Cluster  
Incl. M24900:Human triiodothyronine recptor (THRA1, ear1), and ; 1904\_at D50692 /FEATURE=  
/DEFINITION=HUMAMY1 Homo sapiens mRNA for c-myc binding; 1097\_s\_at L31584  
/FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled rec; 734\_at Mucin 4,
- 35 Tracheobronchial ; 586\_s\_at M31153 /FEATURE=cds /DEFINITION=HUMCYP178 Human steroid  
17-alpha-hydrox; 494\_at U31120 /FEATURE=mRNA /DEFINITION=HSU31120 Human  
interleukin-13 (IL-13) pr.
- Metagene** 203; 33947\_at Cluster Incl. U18550:Human GPR3 G protein-coupled receptor gene,  
comple; 35707\_at Cluster Incl. AI057614:oy31f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG;

- 36037\_g\_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c; 37924\_g\_at Cluster Incl. AA846749:aj99c10.s1 Homo sapiens cDNA, 3 end /clone=IM; 39054\_at Cluster Incl. X08020:Human mRNA for glutathione S-transferase subunit 4; 39059\_at Cluster Incl. AF034544:Homo sapiens delta7-sterol reductase mRNA, compl; 40107\_at Cluster Incl.
- 5 AF054987:Homo sapiens clone 23831 aldolase C mRNA, comple; 37371\_at Cluster Incl. M81780:Homo sapiens acid sphingomyelinase (SMPD1) gene, c; 40912\_s\_at Cluster Incl. X81372:H.sapiens mRNA for biphenyl hydrolase-related pr; 804\_s\_at X86371 /FEATURE=cds /DEFINITION=HSRNAHUGL H.sapiens mRNA for tumour sup; 556\_s\_at M96233 /FEATURE=expanded\_cds /DEFINITION=HUMGSTM4A Human glutathione tr.
- 10 **Metagene** 204; 32425\_at Cluster Incl. U62431:Human nicotinic acetylcholine receptor alpha2 subu; 35090\_g\_at Cluster Incl. AB005060:Homo sapiens mRNA for NTAK, complete cds /cds=; 33561\_at Cluster Incl. X80031:Homo sapiens COL4A3 mRNA /cds=(161,5173) /gb=X8003; 35382\_at Cluster Incl. AF043244:Homo sapiens apoptosis repressor ARC (ARC) mRNA,; 36312\_at Cluster Incl. L40377:Homo sapiens cytoplasmic antiproteinase 2 (CAP2) m; 38563\_at Cluster Incl.
- 15 AF039652:Homo sapiens ribonuclease H type II mRNA, comple; 39272\_g\_at Cluster Incl. AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IM; 33746\_at Cluster Incl. D88208:Homo sapiens hSGT1 mRNA for hSgt1p, complete cds /; 36454\_at Cluster Incl. AF037335:Homo sapiens carbonic anhydrase precursor (CA 12; 34373\_at Cluster Incl. Z97054:Human DNA sequence from PAC 339A18 on chromosome X; 34816\_at Cluster Incl.
- 20 A1143868:qe04e11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34871\_at Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 36653\_g\_at Cluster Incl. J03824:Human uroporphyrinogen III synthase mRNA, comple; 177\_at U38545 /FEATURE= /DEFINITION=HSU38545 Human ARF-activated phosphatidylcho.
- Metagene** 205; 41380\_at Cluster Incl. AF053003:Homo sapiens dipthamide biosynthesis protein-2 ; 41403\_at Cluster Incl. AI032612:ow17e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36001\_at Cluster Incl. Y18643:Homo sapiens mRNA for methyltransferase-like prote; 39073\_at Cluster Incl. AL038662:DKFZp566I0346\_r1 Homo sapiens cDNA, 5 end /clon; 32751\_at Cluster Incl. AF007140:Homo sapiens clone 23711 unknown mRNA, partial c; 37668\_at Cluster Incl. M69039:Human pre-mRNA splicing factor SF2p32, complete se; 41321\_s\_at Cluster Incl.
- 30 AA528077:nh90a11.s1 Homo sapiens cDNA, 3 end /clone=IM; 1985\_s\_at X73066 /FEATURE=cds /DEFINITION=HSNM23H1A H.sapiens NM23-H1 mRNA ; 1521\_at X17620 /FEATURE=mRNA /DEFINITION=HSNM23 Human mRNA for Nm23 protein, inv.
- Metagene** 206; 35118\_at Cluster Incl. M12625:Human lecithin-cholesterol acyltransferase mRNA, c; 41083\_at Cluster Incl. AC006276:Homo sapiens chromosome 19, cosmid R28379 /cds=(; 41084\_at Cluster Incl. AI659108:tu08c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35621\_at Cluster Incl. L77213:Homo sapiens phosphomevalonate kinase mRNA, comple; 36095\_at Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /; 37342\_s\_at Cluster Incl. AF070531:Homo sapiens clone 24764 mRNA sequence /cds=UN; 1274\_s\_at L22005 /FEATURE= /DEFINITION=HUMCDC34H Human ubiquitin conjugating enz.



- Metagene** 207; 31315\_at Cluster Incl. D84143:Human immunoglobulin (mAb59) light chain V region ; 34105\_f\_at Cluster Incl. A1147237:qb36f02.x1 Homo sapiens cDNA, 3 end /clone=IM; 32905\_s\_at Cluster Incl. M30038:Human tryptase mRNA, complete cds /cds=(17,844) ; 33499\_s\_at Cluster Incl. AF067420:Homo sapiens SNC73 protein (SNC73) mRNA, compl; 33500\_i\_at Cluster
- 5 Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype; 33501\_r\_at Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype; 37864\_s\_at Cluster Incl. Y14737:Homo sapiens mRNA for immunoglobulin lambda heav; 38194\_s\_at Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C regi; 32070\_at Cluster Incl. X97267:H.sapiens LPAP gene /cds=(63,683) /gb=X97267 /gi=1; 33273\_f\_at Cluster Incl. X57809:Human rearranged
- 10 immunoglobulin lambda light cha; 33274\_f\_at Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC-region; 37219\_at Cluster Incl. X72755:H.sapiens Humig mRNA /cds=(39,416) /gb=X72755 /gi=; 37965\_at Cluster Incl. AA181053:zp66g11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41164\_at Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region; 41165\_g\_at Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant regi;
- 15 41237\_at Cluster Incl. D32129:Human mRNA for HLA class-I (HLA-A26) heavy chain, ; 35338\_at Cluster Incl. X17094:Human fur mRNA for furin /cds=(216,2600) /gb=X1709; 37006\_at Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41827\_f\_at Cluster Incl. AI932613:wo05c02.x1 Homo sapiens cDNA, 3 end /clone=IM; 32547\_at Cluster Incl. X56253:Human MPR46 gene for 46kd mannose 6-phosphate rece; 2009\_at U33284 /FEATURE=
- 20 /DEFINITION=HSU33284 Human protein tyrosine kinase PYK2.
- Metagene** 208; 31524\_f\_at Cluster Incl. Z80782:H.sapiens H2B/k gene /cds=(0,380) /gb=Z80782 /gi; 31528\_f\_at Cluster Incl. Z83738:H.sapiens hH2B/e gene /cds=(0,380) /gb=Z83738 /g; 34157\_f\_at Cluster Incl. AI200373:qf98c03.x1 Homo sapiens cDNA, 3 end /clone=IM; 35576\_f\_at Cluster Incl. AL009179:dJ97D16.4 (Histone H2B) /cds=(25,405) /gb=AL00; 32980\_f\_at Cluster
- 25 Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IM; 32121\_at Cluster Incl. U86453:Human phosphatidylinositol 3-kinase catalytic subu.
- Metagene** 209; 41007\_at Cluster Incl. AF052497:Homo sapiens clone B18 unknown mRNA /cds=UNKNOWN; 33815\_at Cluster Incl. J03626:Human UMP synthase mRNA, complete cds /cds=UNKNOWN; 34712\_at Cluster Incl. AB023227:Homo sapiens mRNA for KIAA1010 protein, partial ; 39783\_at Cluster Incl. D43947:Human mRNA for KIAA0100 gene, complete cds /cds=(3;
- 30 32211\_at Cluster Incl. AB009398:Homo sapiens mRNA for 26S proteasome subunit p40; 34776\_at Cluster Incl. W27541:32c12 Homo sapiens cDNA /gb=W27541 /gi=1307345 /ug; 37032\_at Cluster Incl. U08021:Human nicotinamide N-methyltransferase (NNMT) mRNA; 40948\_at Cluster Incl. M96759:Human rod outer segment membrane protein 1 (ROM1) .
- 35 **Metagene** 210; 31320\_at Cluster Incl. U18548:Human GPR12 G protein coupled-receptor gene, compl; 31503\_at Cluster Incl. W28732:50h7 Homo sapiens cDNA /gb=W28732 /gi=1308680 /ug=; 31720\_s\_at Cluster Incl. M10905:Human cellular fibronectin mRNA /cds=(0,2383) /g; 33002\_at Cluster Incl. AF047487:Homo sapiens Nck-2 (NCK2) mRNA, complete cds /cd; 33064\_at Cluster Incl. L07738:Homo sapiens DHP-sensitive calcium channel gamma s; 33647\_s\_at Cluster Incl.

- AA224768:nc12d09.r1 Homo sapiens cDNA /clone=IMAGE-1007; 35126\_at Cluster Incl.  
 AB026542:Homo sapiens WAVE2 mRNA for WASP-family protein,; 36338\_at Cluster Incl.  
 W28504:48e7 Homo sapiens cDNA /gb=W28504 /gi=1308515 /ug=; 36217\_at Cluster Incl.  
 Z35102:H.sapiens mRNA for Ndr protein kinase /cds=(595,19; 31800\_at Cluster Incl.
- 5 AL050136:Homo sapiens mRNA; cDNA DKFZp586L141 (from clone; 32038\_s\_at Cluster Incl.  
 A1739308:wi30c12.x1 Homo sapiens cDNA, 3 end /clone=IM; 40452\_at Cluster Incl. U83246:Homo  
 sapiens copine I mRNA, complete cds /cds=(156; 38831\_f\_at Cluster Incl. AF053356:Homo sapiens  
 chromosome 7q22 sequence /cds=(25; 39100\_at Cluster Incl. X73608:H.sapiens mRNA for testican  
 /cds=(434,1753) /gb=X7; 40634\_at Cluster Incl. M86667:H.sapiens NAP (nucleosome assembly  
 protein) mRNA, ; 41552\_g\_at Cluster Incl. AW044624:wy78c04.x1 Homo sapiens cDNA, 3 end  
 /clone=IM; 1928\_s\_at U78733 /FEATURE=mRNA#1 /DEFINITION=HSSMAD2S8 Homo sapiens  
 mad protein ; 1704\_at S76992 /FEATURE= /DEFINITION=S76992 VAV2=VAV oncogene  
 homolog [human, fe; 1588\_at L42243 /FEATURE=cds#1 /DEFINITION=HUM1FNAM08 Homo  
 sapiens (clone 51H8) a; 594\_s\_at M55265 /FEATURE=mRNA /DEFINITION=HUMACKII Human  
 casein kinase II alpha ; 359\_at Y10659 /FEATURE=cds /DEFINITION=HSIL13RA H.sapiens IL-  
 13Ra mRNA ; 311\_s\_at Fibronectin, Alt. Splice 1 ; 248\_at L40388 /FEATURE=mRNA  
 /DEFINITION=HUMTRIP15M Homo sapiens thyroid receptor.
- 10 **Metagene** 211; 33001\_s\_at Cluster Incl. AF035960:Homo sapiens transglutaminase X mRNA,  
 alternat; 38678\_at Cluster Incl. AA733050:zg79b05.s1 Homo sapiens cDNA, 3 end /clone=3995;  
 20 37691\_at Cluster Incl. X63380:Homo sapiens mRNA for serum response factor-relate; 651\_at  
 L07493 /FEATURE= /DEFINITION=HUM14RPA Homo sapiens replication protein A .  
**Metagene** 212; 31759\_at Cluster Incl. W26220:22d9 Homo sapiens cDNA /gb=W26220  
 /gi=1306631 /ug=; 35598\_at Cluster Incl. AA904505:ol26b03.s1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 35485\_at Cluster Incl. X80818:H.sapiens mRNA for metabotropic glutamate  
 receptor; 35950\_at Cluster Incl. U90841:Homo sapiens SSX4 (SSX4) mRNA, complete cds /cds=(;  
 25 37801\_at Cluster Incl. AF112972:Homo sapiens TJ6 mRNA, complete cds /cds=(5,2575; 37195\_at  
 Cluster Incl. M14565:Human cholesterol side-chain cleavage enzyme P450s; 38991\_at Cluster Incl.  
 U55980:HSU55980 Homo sapiens cDNA, 3 end /clone=25453 /c; 40501\_s\_at Cluster Incl.  
 X73114:H.sapiens mRNA for slow MyBP-C /cds=(81,3452) /g; 39451\_i\_at Cluster Incl.
- 30 AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA,; 1483\_at L34059 /FEATURE=  
 /DEFINITION=HUMCA4A Homo sapiens cadherin-4 mRNA, compl; 1024\_at X02612  
 /FEATURE=expanded\_cds /DEFINITION=HSCYP450 Human gene for cytochr.  
**Metagene** 213; 32011\_g\_at Cluster Incl. Z82180:Human DNA sequence from clone E81G9 on  
 chromosom; 33695\_at Cluster Incl. AC004221:Homo sapiens DNA from chromosome 19, cosmid  
 35 R291; 33237\_at Cluster Incl. AB018344:Homo sapiens mRNA for KIAA0801 protein, complete;  
 36055\_at Cluster Incl. AC003030:Homo sapiens chromosome 19, overlapping cosmids ; 37172\_at  
 Cluster Incl. M75106:Human prepro-plasma carboxypeptidase B mRNA, compl; 38660\_at Cluster  
 Incl. F27891:HSPD16170 Homo sapiens cDNA /clone=s4000025D03 /gb; 39085\_at Cluster Incl.  
 M37984:Human slow twitch skeletal muscle/cardiac muscle t; 38729\_at Cluster Incl.

- M88279:Human immunophilin (FKBP52) mRNA, complete cds /cd; 39500\_s\_at Cluster Incl.  
 AL049299:Homo sapiens mRNA; cDNA DKFZp564P233 (from clo; 41556\_s\_at Cluster Incl.  
 AF019386:Homo sapiens heparan sulfate 3-O-sulfotransfer; 1026\_s\_at U41068 /FEATURE=cds  
 /DEFINITION=HSCOLLA5 Human collagen alpha2(XI) (CO.
- 5 **Metagene** 214; 38589\_i\_at Cluster Incl. M14630:Human prothymosin alpha mRNA, complete cds  
 /cds=; 40661\_at Cluster Incl. D78579:Homo sapiens mRNA for neuron derived orphan recept;  
 34398\_at Cluster Incl. D86956:Human mRNA for KIAA0201 gene, complete cds /cds=(3; 37024\_at  
 Cluster Incl. AF010312:Homo sapiens Pig7 (PIG7) mRNA, complete cds /cds; 752\_s\_at D85429  
 /FEATURE=expanded\_cds /DEFINITION=D85429 Homo sapiens gene for h; 452\_at U66615  
 10 /FEATURE= /DEFINITION=HSU66615 Human SWI/SNF complex 155 KDa subun; 303\_at  
 Guanine Nucleotide Exchange Factor 1 .  
**Metagene** 215; 34690\_at Cluster Incl. U66616:Human SWI/SNF complex 170 KDa subunit  
 (BAF170) mRN; 39334\_s\_at Cluster Incl. L10377:Human (clone CTG-B37) mRNA sequence  
 /cds=UNKNOWN.
- 15 **Metagene** 216; 32460\_at Cluster Incl. S67368:GABRB2=gamma-aminobutyric acid A receptor beta  
 2 s; 33661\_at Cluster Incl. U66589:Human ribosomal protein L5 pseudogene mRNA, comple;  
 32071\_at Cluster Incl. AB002293:Human mRNA for KIAA0295 gene, partial cds /cds=(; 34709\_r\_at  
 Cluster Incl. Z75331:H.sapiens mRNA for nuclear protein SA-2 /cds=(64; 34772\_at Cluster Incl.  
 AB023142:Homo sapiens mRNA for KIAA0925 protein, partial ; 36891\_at Cluster Incl.  
 20 AL022237:bK1191B2.3.1 (PUTATIVE novel Acyl Transferase si; 37932\_at Cluster Incl.  
 Y12490:Homo sapiens mRNA for Golgi-associated microtubule; 38383\_at Cluster Incl.  
 U73338:Human methionine synthase mRNA, complete cds /cds=; 38753\_at Cluster Incl.  
 AF039022:Homo sapiens exportin t mRNA, complete cds /cds=; 1476\_s\_at U22376  
 /FEATURE=cds#5 /DEFINITION=HSU22376 Human (c-myb) gene, complet.
- 25 **Metagene** 217; 33583\_r\_at Cluster Incl. AA523313:ni41h09.s1 Homo sapiens cDNA, 3 end  
 /clone=IM; 32310\_f\_at Cluster Incl. AI341574:qq94h09.x1 Homo sapiens cDNA, 3 end /clone=IM;  
 37151\_at Cluster Incl. AF052120:Homo sapiens clone 23836 mRNA sequence /cds=UNKN;  
 37882\_at Cluster Incl. X63468:H.sapiens mRNA for transcription factor TFIIE alph; 36462\_at  
 Cluster Incl. U50383:Human retinoic acid-responsive protein (NN8-4AG) m; 36498\_at Cluster Incl.
- 30 AI936759:wp69b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36888\_at Cluster Incl.  
 AB020648:Homo sapiens mRNA for KIAA0841 protein, partial ; 39762\_at Cluster Incl.  
 AB007885:Homo sapiens KIAA0425 mRNA, complete cds /cds=(1; 38468\_at Cluster Incl.  
 U65676:Human Hermansky-Pudlak syndrome protein (HPS) mRNA.  
**Metagene** 218; 31523\_f\_at Cluster Incl. Z80780:H.sapiens H2B/h gene /cds=(0,380) /gb=Z80780  
 35 /gi; 31663\_at Cluster Incl. AB016902:Homo sapiens HGC6.3 mRNA, complete cds /cds=(287;  
 31727\_at Cluster Incl. U91510:Human CD39L1 mRNA, complete cds /cds=(21,1439) /gb; 33472\_at  
 Cluster Incl. Z11737:H.sapiens mRNA for flavin-containing monooxygenase; 36759\_at Cluster Incl.  
 U29589:Human m3 muscarinic acetylcholine receptor (CHRM3); 31857\_r\_at Cluster Incl.  
 D50924:Human mRNA for KIAA0134 gene, complete cds /cds=; 33251\_at Cluster Incl.

- AB018322:Homo sapiens mRNA for KIAA0779 protein, partial ; 36458\_at Cluster Incl.  
 AB023235:Homo sapiens mRNA for KIAA1018 protein, complete; 34352\_at Cluster Incl.  
 AA631698:np79a08.s1 Homo sapiens cDNA /clone=IMAGE-113250; 39560\_at Cluster Incl.  
 H10776:ym07h11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 40984\_at Cluster Incl.
- 5 W28255:44b8 Homo sapiens cDNA /gb=W28255 /gi=1308203 /ug=; 41842\_at Cluster Incl.  
 AI701156:we10f09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1840\_g\_at Ras-Like Protein Tc4 ;  
 526\_s\_at U13696 /FEATURE=cds /DEFINITION=HSU13696 Human homolog of yeast mutL (h;  
 323\_at Serine Kinase Psk-H1 .  
**Metagene** 219; 31519\_f\_at Cluster Incl. M90356:Human BTF3 protein homologue gene, complete
- 10 cds ; 31932\_f\_at Cluster Incl. M90357:Human basic transcription factor 3a (BTF3a) gene;  
 32334\_f\_at Cluster Incl. AB009010:Homo sapiens mRNA for polyubiquitin UbC, compl;  
 32335\_r\_at Cluster Incl. AB009010:Homo sapiens mRNA for polyubiquitin UbC, compl; 38476\_at  
 Cluster Incl. L13434:Human chromosome 3p21.1 gene sequence, complete cd; 39844\_at Cluster  
 Incl. AI806379:wf27b10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1256\_at L38929
- 15 /FEATURE=mRNA /DEFINITION=HUMPTPD Homo sapiens protein tyrosine p.  
**Metagene** 220; 31475\_at Cluster Incl. AF082559:Homo sapiens truncated TRF1-interacting ankyrin-  
 ; 33987\_at Cluster Incl. M36340:Human ADP-ribosylation factor 1 (ARF1) mRNA, compl;  
 35652\_g\_at Cluster Incl. AF002715:Homo sapiens MAP kinase kinase kinase (MTK1) m; 38655\_at  
 Cluster Incl. AI525633:PT1.3\_04\_A08.r Homo sapiens cDNA, 5 end /clone\_ ; 38712\_at Cluster Incl.
- 20 AL035291:H.sapiens gene from PACs 125H23 and 105D12 /cds=; 39348\_at Cluster Incl.  
 X99209:H.sapiens mRNA for arginine methyltransferase /cds; 41151\_at Cluster Incl.  
 U45973:Human phosphatidylinositol (4,5)bisphosphate 5-pho; 32826\_at Cluster Incl.  
 AJ133133:Homo sapiens mRNA for ecto-ATP diphosphohydrolas; 32832\_at Cluster Incl.  
 AF084928:Homo sapiens erythroblast macrophage protein EMP; 33409\_at Cluster Incl.
- 25 AA158243:zo76c01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33444\_at Cluster Incl.  
 D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(1; 33922\_at Cluster Incl.  
 U17838:Human zinc finger protein RIZ mRNA, complete cds /; 35273\_at Cluster Incl.  
 AF007151:Homo sapiens clone 23967 unknown mRNA, partial c; 39162\_at Cluster Incl.  
 AA156987:zl19b05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40175\_at Cluster Incl.
- 30 AI141670:ot08b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32565\_at Cluster Incl.  
 U66619:Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA; 2053\_at M34064  
 /FEATURE= /DEFINITION=HUMNCADH Human N-cadherin mRNA, complete cd; 487\_g\_at  
 U60521 /FEATURE= /DEFINITION=HSU60521 Human protease proMch6 (Mch6) mRN; 456\_at  
 U66619 /FEATURE= /DEFINITION=HSU66619 Human SWI/SNF complex 60 KDa subuni.
- 35 **Metagene** 221; 36747\_at Cluster Incl. AF052172:Homo sapiens clone 24617 mRNA sequence  
 /cds=UNKN; 39288\_at Cluster Incl. AI951798:wx37f11.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 40484\_g\_at Cluster Incl. U49857:Human transcriptional activator mRNA, complete  
 c; 33436\_at Cluster Incl. Z46629:Homo sapiens SOX9 mRNA /cds=(359,1888) /gb=Z46629 .  
**Metagene** 222; 32648\_at Cluster Incl. U15979:Human (dlk) mRNA, complete cds /cds=(173,1321)

- /gb; 35706\_at Cluster Incl. N32859: yw88d02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-;
- 38315\_at Cluster Incl. AB015228: Homo sapiens mRNA for RALDH2-T, complete cds /cd;
- 41505\_r\_at Cluster Incl. AF055376: Homo sapiens short form transcription factor C.
- Metagene 223;** 37648\_at Cluster Incl. D63487: Human mRNA for KIAA0153 gene, partial cds
- 5 /cds=(0,; 37892\_at Cluster Incl. J04177: Human alpha-1 type XI collagen (COL11A1) mRNA, com;
- 33907\_at Cluster Incl. AF012072: Homo sapiens eIF4GII mRNA, complete cds /cds=(25;
- 33101\_g\_at Cluster Incl. AB017551: Homo sapiens mRNA for 16G2, complete cds /cds=.
- Metagene 224;** 32969\_r\_at Cluster Incl. Y12661: H.sapiens vgf gene /cds=(212,2062) /gb=Y12661
- /g; 34495\_r\_at Cluster Incl. AJ011733: Homo sapiens mRNA for synaptogyrin 4 protein /; 35887\_at
- 10 Cluster Incl. L34219: Homo sapiens retinaldehyde-binding protein (CRALBP; 38166\_r\_at Cluster
- Incl. AF010403: Homo sapiens ALR mRNA, complete cds /cds=(0,15; 40163\_r\_at Cluster Incl.
- AC003107: Human DNA from chromosome 19-specific cosmid R; 39157\_at Cluster Incl.
- AL021937: dJ149A16.5 (PUTATIVE novel protein similar to mo; 39177\_r\_at Cluster Incl.
- M54994: Human bile salt-activated lipase (BAL) mRNA, com; 39859\_r\_at Cluster Incl.
- 15 AF071504: Homo sapiens syntaxin 11 mRNA, complete cds /c; 40172\_g\_at Cluster Incl.
- AF062739: Homo sapiens GSK-3 binding protein FRAT2 (FRAT; 40930\_at Cluster Incl.
- W25958: 18h6 Homo sapiens cDNA /gb=W25958 /gi=1306360 /ug=; 1028\_at U43431 /FEATURE=
- /DEFINITION=HSU43431 Human DNA topoisomerase III mRNA, .
- Metagene 225;** 38937\_at Cluster Incl. AF022152: Homo sapiens AP-3 complex beta3B subunit
- 20 mRNA, c; 40329\_at Cluster Incl. AL031228: dJ1033B10.10 (membrane protein with histidine ri;
- 36822\_at Cluster Incl. U51334: Human putative RNA binding protein (RBP56) mRNA, c; 38663\_at
- Cluster Incl. AI033692: ow26f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39079\_at Cluster
- Incl. D85758: Homo sapiens mRNA for human protein homologous to ; 32761\_at Cluster Incl.
- AB002322: Human mRNA for KIAA0324 gene, partial cds /cds=(; 34836\_at Cluster Incl.
- 25 U18420: Human ras-related small GTP binding protein Rab5 (; 36161\_at Cluster Incl.
- M34175: Human beta adaptin mRNA, complete cds /cds=(177,29; 38122\_at Cluster Incl.
- D87075: Human mRNA for KIAA0238 gene, partial cds /cds=(0,; 40636\_at Cluster Incl.
- AI807620: wf49b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1997\_s\_at U19599 /FEATURE=
- /DEFINITION=HSU19599 Human (BAX delta) mRNA, complete; 508\_at U43923 /FEATURE=
- 30 /DEFINITION=HSU43923 Human transcription factor SUPT4H m.
- Metagene 226;** 34610\_at Cluster Incl. W25845: 13h9 Homo sapiens cDNA /gb=W25845
- /gi=1305968 /ug=; 32965\_f\_at Cluster Incl. W28645: 52e8 Homo sapiens cDNA /gb=W28645
- /gi=1308800 /u; 36696\_at Cluster Incl. AB000359: Homo sapiens PIGCP1 pseudogene /cds=(0,416)
- /gb=; 38901\_at Cluster Incl. AB020698: Homo sapiens mRNA for KIAA0891 protein, partial ;
- 35 39285\_at Cluster Incl. L28957: Homo sapiens CTP-phosphocholine cytidyltransferase; 39290\_f\_at
- Cluster Incl. W28257: 44c1 Homo sapiens cDNA /gb=W28257 /gi=1308205 /u; 41619\_at Cluster
- Incl. AL022398: dJ434O14.4 (Interferon Regulatory Factor 6) /cds; 34692\_r\_at Cluster Incl.
- AF006087: Homo sapiens Arp2/3 protein complex subunit p2; 35201\_at Cluster Incl. X16135: Human
- mRNA for novel heterogeneous nuclear RNP pro; 35204\_at Cluster Incl. U52840: Homo sapiens

- semaphorin F homolog mRNA, complete c; 39024\_at Cluster Incl. AF042357:AF042357 Homo sapiens cDNA /gb=AF042357 /gi=4104; 39399\_at Cluster Incl. AJ006417:Homo sapiens mRNA for beta-tubulin folding cofac; 40442\_f\_at Cluster Incl. W26019:18b9 Homo sapiens cDNA /gb=W26019 /gi=1306304 /u; 41199\_s\_at Cluster Incl. W27050:19f7 Homo sapiens cDNA
- 5 /gb=W27050 /gi=1306422 /u; 32752\_at Cluster Incl. W72440:zd65e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35345\_at Cluster Incl. X83618:H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coen; 38029\_at Cluster Incl. J02939:Human membrane glycoprotein 4F2 antigen heavy chai; 38127\_at Cluster Incl. Z48199:H.sapiens syndecan-1 gene (exons 2-5) /cds=(0,866); 38412\_at Cluster Incl. U53588:Homo sapiens MHC class 1 region /cds=(199,579) /gb; 39464\_at
- 10 Cluster Incl. W28493:47h11 Homo sapiens cDNA /gb=W28493 /gi=1308459 /ug; 39539\_at Cluster Incl. AI684866:wa86e09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39816\_g\_at Cluster Incl. AA883101:am24d05.s1 Homo sapiens cDNA, 3 end /clone=IM; 40186\_at Cluster Incl. Y08302:H.sapiens mRNA for MAP kinase phosphatase 4 /cds=(; 40886\_at Cluster Incl. L41498:Homo sapiens longation factor 1-alpha 1 (PTI-1) mR; 40888\_f\_at Cluster Incl.
- 15 W28170:43a12 Homo sapiens cDNA /gb=W28170 /gi=1308118 /; 41301\_at Cluster Incl. W28608:49b1 Homo sapiens cDNA /gb=W28608 /gi=1308556 /ug=; 33105\_at Cluster Incl. W28790:54g3 Homo sapiens cDNA /gb=W28790 /gi=1308945 /ug=; 33110\_at Cluster Incl. AI356682:qy22a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33211\_at Cluster Incl. AW051889:wz04f05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 2013\_at U35117 /FEATURE=
- 20 /DEFINITION=HSU35117 Human transcription factor Dp-2 mR; 1644\_at U36764 /FEATURE= /DEFINITION=HSU36764 Human TGF-beta receptor interactin; 1565\_s\_at M96995 /FEATURE= /DEFINITION=HUMEGFGRBA Homo sapiens epidermal growth ; 1358\_s\_at U22970 /FEATURE=mRNA#1 /DEFINITION=HSU22970 Human interferon-inducible; 1240\_at U13022 /FEATURE= /DEFINITION=HSU13022 Human negative regulator of progra; 1142\_at Fibroblast
- 25 Growth Factor Receptor K-Sam, Alt. Splice 1 ; 945\_at D50063 /FEATURE= /DEFINITION=HUMP40MOV Human mRNA for proteasome subunit ; 725\_i\_at Chorionic Somatomammotropin Hormone Cs-5 ; 540\_at S67070 /FEATURE= /DEFINITION=S67070 heat shock protein HSP72 homolog [hum.
- Metagene** 227; 34948\_at Cluster Incl. AI820065:wg56a09.x1 Homo sapiens cDNA, 3 end
- 30 /clone=IMAG; 34254\_at Cluster Incl. U14417:Human Ral guanine nucleotide dissociation stimulat; 39407\_at Cluster Incl. M22488:Human bone morphogenetic protein 1 (BMP-1) mRNA /c; 36642\_at Cluster Incl. J00287:Human pepsinogen gene /cds=(55,1221) /gb=J00287 /g; 39564\_s\_at Cluster Incl. C20962:HUMGS0002427 Homo sapiens cDNA, 3 end /clone\_en; 1516\_g\_at Rad2 ; 1185\_at D49410 /FEATURE=expanded\_cds /DEFINITION=HUMIL3RA12 Human gene for inter; 852\_at
- 35 S70348 /FEATURE= /DEFINITION=S70348 integrin beta 3 {alternatively splice.
- Metagene** 228; 36311\_at Cluster Incl. U40370:Human 3,5 cyclic nucleotide phosphodiesterase (HS; 37461\_at Cluster Incl. AF004327:Homo sapiens angiotensin-2 mRNA, complete cds /; 39315\_at Cluster Incl. D13628:Human mRNA for KIAA0003 gene, complete cds /cds=(9; 1951\_at AF004327 /FEATURE= /DEFINITION=AF004327 Homo sapiens angiotensin-2 mRNA.

- Metagene 229;** 32289\_at Cluster Incl. U40317:Human protein tyrosine phosphatase PTPsigma (PTPsi; 33569\_at Cluster Incl. D50532:Homo sapiens mRNA for macrophage lectin 2, complet; 34897\_at Cluster Incl. W26524:32g4 Homo sapiens cDNA /gb=W26524 /gi=1307385 /ug=;
- 39968\_at Cluster Incl. U50136:Human leukotriene C4 synthase (LTC4S) gene, comple; 32725\_at
- 5 Cluster Incl. AF042083:Homo sapiens BH3 interacting domain death agonis; 36052\_at Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced p; 32238\_at Cluster Incl. AF001383:Homo sapiens amphiphysin II mRNA, complete cds /; 32764\_at Cluster Incl. AI796048:wh41g06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40280\_at Cluster Incl. U72508:Human B7 mRNA, complete cds /cds=(112,1050) /gb=U7; 1595\_at L06139 /FEATURE=
- 10 /DEFINITION=HUMTEKRPTK Homo sapiens receptor protein-ty.
- Metagene 230;** 31874\_at Cluster Incl. Y07846:H.sapiens mRNA for GAR22 protein /cds=(132,1145) /; 35619\_at Cluster Incl. AB014534:Homo sapiens mRNA for KIAA0634 protein, partial ; 36880\_at Cluster Incl. U07736:Human quinone oxidoreductase2 (NQO2) gene /cds=(27; 37266\_at Cluster Incl. U69645:Human zinc finger protein mRNA, complete cds /cds=; 38313\_at
- 15 Cluster Incl. AB028985:Homo sapiens mRNA for KIAA1062 protein, partial ; 39712\_at Cluster Incl. AI541308:pec1.2-4.F11.r Homo sapiens cDNA, 5 end /clone\_ ; 40127\_at Cluster Incl. M95929:Human homeobox protein (PHOX1) mRNA, 3 end /cds=(; 32176\_at Cluster Incl. AB011110:Homo sapiens mRNA for KIAA0538 protein, partial ; 34408\_at Cluster Incl. AF004222:Homo sapiens RTN2-A (RTN2) mRNA, complete cds /c; 38761\_s\_at Cluster Incl.
- 20 AA487755:ab13f01.r1 Homo sapiens cDNA, 5 end /clone=IM; 2052\_g\_at M31767 /FEATURE=mRNA /DEFINITION=HUMDNAMET Human O6-methylguanine-DNA ; 1099\_s\_at L38503 /FEATURE= /DEFINITION=HUMGSTT2A Homo sapiens glutathione S-tran; 355\_s\_at D38037 /FEATURE= /DEFINITION=HUMOTK4 Human mRNA for FK506-binding prote.
- Metagene 231;** 31605\_at Cluster Incl. U72518:Human destrin-2 pseudogene mRNA, complete cds /cds; 35377\_at Cluster Incl. AL080159:Homo sapiens mRNA; cDNA DKFZp434M154 (from clone; 38173\_at Cluster Incl. AB028999:Homo sapiens mRNA for KIAA1076 protein, partial ; 41098\_at Cluster Incl. AB002379:Human mRNA for KIAA0381 gene, partial cds /cds=(; 41449\_at Cluster Incl. AJ000534:Homo sapiens mRNA for epsilon-sarcoglycan /cds=(; 34187\_at Cluster Incl. D28483:Human scr3 mRNA for RNA binding protein SCR3, comp; 36053\_at Cluster Incl.
- 30 AF041248:Homo sapiens cyclin-dependent kinase inhibitor (; 37203\_at Cluster Incl. L07765:Human carboxylesterase mRNA, complete cds /cds=(67; 38974\_at Cluster Incl. AF021819:Homo sapiens RNA-binding protein regulatory subu; 32163\_f\_at Cluster Incl. AA216639:zq95f07.s1 Homo sapiens cDNA, 3 end /clone=IM; 33884\_s\_at Cluster Incl. AB014584:Homo sapiens mRNA for KIAA0684 protein, partia; 41514\_s\_at Cluster Incl. W26628:34a4 Homo sapiens cDNA /gb=W26628
- 35 /gi=1307471 /u; 1879\_at M14949 /FEATURE=cds /DEFINITION=HUMRASR2 Human R-ras gene, exons 2 throu; 1802\_s\_at X03363 /FEATURE=cds /DEFINITION=HSERB2R Human c-erb-B-2 mRNA ; 1132\_s\_at L12060 /FEATURE=mRNA /DEFINITION=HUMRARG7A Homo sapiens retinoic acid ; 568\_at M80335 /FEATURE= /DEFINITION=HUMPKACATO Homo sapiens protein kinase A cat.

- Metagene 232**; 31645\_at Cluster Incl. AB020625:Homo sapiens mRNA for butyrophilin like receptor; 31967\_at Cluster Incl. AF035835:Homo sapiens nephrin (NPHS1) mRNA, complete cds ; 33594\_at Cluster Incl. AB017788:Homo sapiens hdkk-4 mRNA, complete cds /cds=(0,6; 32882\_at Cluster Incl. AF059203:Homo sapiens acyl coenzyme A-cholesterol acyltra; 33520\_at Cluster Incl.
- 5 M13232:Human factor VII serine protease precursor mRNA, c; 34475\_at Cluster Incl. L34408:Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA; 34999\_at Cluster Incl. AF060231:Homo sapiens herpesvirus entry protein C (HVEC) ; 35427\_at Cluster Incl. W28256:44b9 Homo sapiens cDNA /gb=W28256 /gi=1308204 /ug=; 38943\_at Cluster Incl. U36787:Human putative holocytochrome c-type synthetase mR; 39569\_at Cluster Incl. U72849:untitled /cds=(98,6199)
- 10 /gb=U72849 /gi=4097997 /ug; 40681\_at Cluster Incl. AB008375:Homo sapiens mRNA for osteoblast specific cystei; 41469\_at Cluster Incl. L10343:Humalafin gene, complete cds /cds=(516,869) /gb=; 36558\_at Cluster Incl. M92302:Human voltage-dependent calcium channel beta-1 sub; 40408\_at Cluster Incl. L06845:Human cysteinyl-tRNA synthetase mRNA, partial cds ; 40849\_s\_at Cluster Incl. U88528:Human transcription factor LZIP mRNA, complete c; 32831\_at
- 15 Cluster Incl. AA453183:zx46b09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 36127\_g\_at Cluster Incl. U18919:Human chromosome 17q12-21 mRNA, clone pOV-2, par; 36997\_at Cluster Incl. J04809:Human cytosolic adenylate kinase (AK1) gene, compl; 39503\_s\_at Cluster Incl. AB006713:Homo sapiens mRNA for dihydropyrimidinase rela; 1902\_at M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision repair protein ; 1497\_at L04270
- 20 /FEATURE= /DEFINITION=HUMTNFRP Homo sapiens (clone CD18) tumor n; 702\_f\_at Homeotic Protein Hpx-5 .
- Metagene 233**; 36266\_at Cluster Incl. U79275:Human clone 23947 mRNA, partial cds /cds=(0,401) /; 37174\_at Cluster Incl. D14660:Human mRNA for KIAA0104 gene, complete cds /cds=(3; 36625\_at Cluster Incl. L40401:Homo sapiens (clone zap128) mRNA, 3 end of cds /c.
- 25 **Metagene 234**; 41215\_s\_at Cluster Incl. D13891:Human mRNA for Id-2H, complete cds /cds=(96,500); 36591\_at Cluster Incl. X06956:Human HALPHA44 gene for alpha-tubulin, exons 1-3 /; 36617\_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=45; 36618\_g\_at Cluster Incl. X77956:H.sapiens Id1 mRNA /cds=(35,499) /gb=X77956 /gi=; 36619\_r\_at Cluster Incl. S78825:Id1 (Id1-b)=transcription regulator helix-loop-h; 37043\_at Cluster Incl.
- 30 AL021154:dJ150O5.2 (Inhibitor of DNA binding 3 (dominant ; 38755\_at Cluster Incl. X84709:H.sapiens mRNA for mediator of receptor-induced to; 1955\_s\_at AF035528 /FEATURE= /DEFINITION=AF035528 Homo sapiens Smad6 mRNA, compl; 1857\_at AF010193 /FEATURE= /DEFINITION=AF010193 Homo sapiens MAD-related gene SM.
- Metagene 235**; 34078\_s\_at Cluster Incl. M61854:Human cytochrome P4502C19 (CYP2C19) mRNA, clone ; 35087\_at Cluster Incl. AF007147:Homo sapiens clone 23712 mRNA sequence /cds=UNKN; 36766\_at Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /; 33263\_at Cluster Incl. X67098:H.sapiens rTS alpha mRNA containing four open read; 33763\_at Cluster Incl. AI829671:wf09b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40770\_f\_at Cluster Incl. AB017019:Homo sapiens mRNA for JKTBP2, complete cds /cd; 318\_at D64142



- /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone H1x, compl; 319\_g\_at D64142 /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone H1x, com.
- Metagene** 236; 35109\_at Cluster Incl. AB018299:Homo sapiens mRNA for KIAA0756 protein, partial ; 37500\_at Cluster Incl. D50419:Homo sapiens mRNA for OTK18, complete cds /cds=(34; 41411\_at Cluster Incl. AI566877:tn24f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40070\_at Cluster Incl. D50912:Human mRNA for KIAA0122 gene, partial cds /cds=(0; 32776\_at Cluster Incl. M35416:Human GTP-binding protein (RALB) mRNA, complete cd; 39484\_at Cluster Incl. W28518:48a1 Homo sapiens cDNA /gb=W28518 /gi=1308466 /ug=; 1356\_at U18321 /FEATURE= /DEFINITION=HSU18321 Human ionizing radiation resistanc; 1273\_r\_at L22005 /FEATURE=
- 10 /DEFINITION=HUMCDC34H Human ubiquitin conjugating enz.
- Metagene** 237; 31439\_f\_at Cluster Incl. X63095:H.sapiens mRNA for rhesus polypeptide (RhVI) /cd; 32480\_at Cluster Incl. X07495:Human mRNA for cp19 homeobox from HOX-3 locus /cds; 34577\_at Cluster Incl. U10694:Human MAGE-9 antigen (MAGE9) gene, complete cds /c; 36378\_at Cluster Incl. AF085807:Homo sapiens uroplakin Ia mRNA, partial cds /cds; 34902\_at Cluster Incl.
- 15 AB007961:Homo sapiens mRNA, chromosome 1 specific transcr; 36764\_at Cluster Incl. AC004125:Homo sapiens Chromosome 16 BAC clone CIT987SK-62; 38491\_at Cluster Incl. U11732:Human ets-like gene (tel) mRNA, complete cds /cds=; 34189\_at Cluster Incl. D31891:Human mRNA for KIAA0067 gene, complete cds /cds=(8; 40491\_at Cluster Incl. W84531:zd90h11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35254\_at Cluster Incl.
- 20 AB007447:Homo sapiens mRNA for Fln29, complete cds /cds=(; 666\_at L20965 /FEATURE= /DEFINITION=HUMPDEA Human phosphodiesterase mRNA, comple.
- Metagene** 238; 36417\_s\_at Cluster Incl. AF035295:Homo sapiens clone 23623 mRNA, partial cds /cd; 36224\_g\_at Cluster Incl. AI827895:wf12b02.x1 Homo sapiens cDNA, 3 end /clone=IM; 31807\_at Cluster Incl. U69190:U69190 Homo sapiens cDNA /clone=27655 /gb=U69190 /; 33300\_at Cluster Incl. AL031282:dJ283E3.3.1 (Cell Division Cycle 2-Like 2 (PITSL; 35135\_at Cluster Incl. X13956:Human 12S RNA induced by poly(rI), poly(rC) and Ne; 35629\_at Cluster Incl. AL022238:dJ1042K10.3 (novel protein) /cds=(0,731) /gb=AL0; 36881\_at Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein ; 38718\_at Cluster Incl. AL050101:Homo sapiens mRNA; cDNA DKFZp586E1519 (from clon; 38723\_at Cluster Incl.
- 30 AF052137:Homo sapiens clone 23918 mRNA sequence /cds=UNKN; 39747\_at Cluster Incl. U52427:Human RNA polymerase II seventh subunit (rpb-7) ge; 34365\_at Cluster Incl. AF042386:Homo sapiens cyclophilin-33B (CYP-33) mRNA, comp; 35779\_at Cluster Incl. AJ133421:Homo sapiens mRNA for leucocyte vacuolar protein; 35780\_at Cluster Incl. AF035292:Homo sapiens clone 23584 mRNA sequence /cds=UNKN; 36166\_at Cluster Incl.
- 35 AF083190:Homo sapiens SPF31 (SPF31) mRNA, complete cds /c; 36594\_s\_at Cluster Incl. U72263:Human multiple exostoses type II protein EXT2.I ; 36649\_at Cluster Incl. X66113:H.sapiens mRNA for PM/Sc1 100kD nucleolar protein ; 36955\_at Cluster Incl. U10362:Human GP36b glycoprotein mRNA, complete cds /cds=(; 37325\_at Cluster Incl. D14697:Human mRNA for KIAA0003 gene, complete cds /cds=(1; 38373\_g\_at Cluster Incl. U66042:Human clone 191B7

- placenta expressed mRNA from c; 39086\_g\_at Cluster Incl. AA768912:nz82h06.s1 Homo sapiens cDNA /clone=IMAGE-1302; 40905\_s\_at Cluster Incl. AL050369:Homo sapiens mRNA; cDNA DKFZp566J153 (from clo; 2064\_g\_at L20046 /FEATURE= /DEFINITION=HUMERCC5A Human ERCC5 excision repair pro; 745\_at D50495 /FEATURE=mRNA /DEFINITION=HUMTEF Homo sapiens mRNA for transcripti; 465\_at U74667 /FEATURE= /DEFINITION=HSU74667 Human tat interactive protein (TIP6.
- 5 **Metagene** 239; 34242\_at Cluster Incl. AB014581:Homo sapiens mRNA for KIAA0681 protein, partial ; 800\_g\_at X80343 /FEATURE=cds /DEFINITION=HSP35R H.sapiens p35 mRNA for regulator.
- 10 **Metagene** 240; 37113\_at Cluster Incl. AF022795:Homo sapiens TGF beta receptor associated protei. **Metagene** 241; 33694\_at Cluster Incl. L40933:Homo sapiens phosphoglucomutase-related protein (P; 35916\_s\_at Cluster Incl. AA877215:ob15e02.s1 Homo sapiens cDNA, 3 end /clone=IM; 33246\_at Cluster Incl. AA521481:aa69h09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 34184\_at Cluster Incl. AB012162:Homo sapiens mRNA for APCL protein, complete cds; 36489\_at Cluster
- 15 Incl. D00860:Homo sapiens mRNA for phosphoribosyl pyrophosphate; 1649\_at U61836 /FEATURE=mRNA /DEFINITION=HSU61836 Human putative cyclin G1 inter. **Metagene** 242; 36234\_at Cluster Incl. U79273:Human clone 23933 mRNA sequence /cds=UNKNOWN /gb=U; 39301\_at Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpai; 38352\_at Cluster Incl. AF016371:Homo sapiens U-snRNP-associated cyclophilin
- 20 (USA; 34778\_at Cluster Incl. AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35763\_at Cluster Incl. AB011112:Homo sapiens mRNA for KIAA0540 protein, partial ; 39914\_r\_at Cluster Incl. W28976:54e5 Homo sapiens cDNA /gb=W28976 /gi=1308924 /u; 40215\_at Cluster Incl. D50840:Homo sapiens mRNA for ceramide glucosyltransferase; 306\_s\_at J02621 /FEATURE=mRNA /DEFINITION=HUMHMG14 Human non-histone chromosomal.
- 25 **Metagene** 243; 37484\_at Cluster Incl. X68742:H.sapiens mRNA for integrin, alpha subunit /cds=UN; 37805\_at Cluster Incl. AF060567:Homo sapiens sushi-repeat protein (SRPUL) mRNA, ; 38592\_s\_at Cluster Incl. AI828210:wk81e09.x1 Homo sapiens cDNA, 3 end /clone=IM; 39307\_s\_at Cluster Incl. X81637:H.sapiens clathrin light chain b gene /cds=UNKNO; 39631\_at Cluster Incl. U52100:Human XMP mRNA, complete cds /cds=(63,566) /gb=U52; 41107\_at Cluster Incl.
- 30 AB002372:Human mRNA for KIAA0374 gene, complete cds /cds=; 33736\_at Cluster Incl. Y16522:Homo sapiens mRNA for hSLP-1 protein /cds=(44,1228; 35668\_at Cluster Incl. AJ001014:Homo sapiens mRNA encoding RAMP1 /cds=(32,478) /; 35704\_at Cluster Incl. X92814:H.sapiens mRNA for rat HREV107-like protein /cds=(; 36023\_at Cluster Incl. AI864120:wg64a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36025\_at Cluster Incl.
- 35 AB002335:Human mRNA for KIAA0337 gene, complete cds /cds=; 36452\_at Cluster Incl. AB028952:Homo sapiens mRNA for KIAA1029 protein, complete; 36492\_at Cluster Incl. AI347155:tc04c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36540\_at Cluster Incl. AB018260:Homo sapiens mRNA for KIAA0717 protein, partial ; 36811\_at Cluster Incl. U24389:Human lysyl oxidase-like protein gene /cds=(446,21; 37192\_at Cluster Incl. U28389:Human

- dematin 52 kDa subunit mRNA, complete cds /c; 37244\_at Cluster Incl. AA746355:oa56f02.r1  
Homo sapiens cDNA /clone=IMAGE-130898; 38004\_at Cluster Incl. X96753:H.sapiens mRNA for  
melanoma-associated chondroitin; 38609\_at Cluster Incl. L34355:Homo sapiens (clone p4) 50 kD  
dystrophin-associate; 38642\_at Cluster Incl. Y10183:H.sapiens mRNA for MEMD protein  
5 /cds=(0,1748) /gb=; 39031\_at Cluster Incl. AA152406:zo07f01.s1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 39058\_at Cluster Incl. U01147:Human guanine nucleotide regulatory protein (ABR) ;  
39080\_at Cluster Incl. M88458:Human ELP-1 mRNA sequence /cds=UNKNOWN /gb=M88458 ;  
41775\_at Cluster Incl. AF064084:Homo sapiens prenylcysteine carboxyl methyltrans; 33346\_r\_at  
Cluster Incl. M61764:Human gamma-tubulin mRNA, complete cds /cds=(24; 33433\_at Cluster Incl.  
10 AL049943:Homo sapiens mRNA; cDNA DKFZp564F0522 (from clon; 33929\_at Cluster Incl.  
X54232:Human mRNA for heparan sulfate proteoglycan (glypi; 34371\_at Cluster Incl.  
U79267:Human clone 23840 mRNA, partial cds /cds=(0,521) /; 34376\_at Cluster Incl.  
AB019517:Homo sapiens PKIG mRNA for protein kinase inhibi; 34403\_at Cluster Incl.  
U58516:Human breast epithelial antigen BA46 mRNA, complet; 34865\_at Cluster Incl.  
15 AI360249:qy84f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36683\_at Cluster Incl.  
AI953789:wx69d10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36989\_at Cluster Incl.  
L19711:Human dystroglycan (DAG1) mRNA, complete cds /cds=; 39842\_at Cluster Incl.  
AF059293:Homo sapiens cytokine-like factor-1 precursor (C; 40196\_at Cluster Incl. D88153:Homo  
sapiens mRNA for HYA22, complete cds /cds=(14; 40587\_s\_at Cluster Incl. AF054186:Homo  
20 sapiens p18 protein mRNA, complete cds /c; 32523\_at Cluster Incl. M20470:Human lymphocyte  
clathrin light-chain B mRNA, comp; 32610\_at Cluster Incl. X93510:H.sapiens mRNA for 37 kDa  
LIM domain protein /cds=; 33128\_s\_at Cluster Incl. W68521:zd36f07.r1 Homo sapiens cDNA, 5 end  
/clone=IMAG; 2058\_s\_at M35011 /FEATURE= /DEFINITION=HUMIBSUB Human integrin beta-  
5 subunit mR; 1597\_at L13720 /FEATURE= /DEFINITION=HUMGAS Homo sapiens growth-  
25 arrest-specific ; 1598\_g\_at L13720 /FEATURE= /DEFINITION=HUMGAS Homo sapiens growth-  
arrest-specifi; 1447\_at D00761 /FEATURE= /DEFINITION=HUMPSC5 Human mRNA for  
proteasome subunit H; 1314\_at D44466 /FEATURE= /DEFINITION=D44466 Homo sapiens mRNA  
for proteasome sub; 1016\_s\_at U70981 /FEATURE= /DEFINITION=HSU70981 Human interleukin-  
13 receptor mR; 956\_at Tubulin, Beta 2 ; 336\_at D38081 /FEATURE= /DEFINITION=HUMHTAR  
30 Human mRNA for thromboxane A2 recept.  
**Metagene** 244; 31685\_at Cluster Incl. Y08976:H.sapiens mRNA for FEV protein /cds=(584,1300)  
/gb; 32282\_at Cluster Incl. U66047:Human clone Z3-1 placenta expressed mRNA from chro;  
32888\_at Cluster Incl. X52213:H.sapiens Itk mRNA /cds=(258,1652) /gb=X52213 /gi=; 33463\_at  
Cluster Incl. U39487:Human xanthine dehydrogenase/oxidase mRNA, complet; 34972\_s\_at Cluster  
35 Incl. AJ000522:Homo sapiens mRNA for dynein heavy chain /cds=; 35955\_at Cluster Incl.  
S80864:cytochrome c-like polypeptide [human, lung adenoca; 37415\_at Cluster Incl.  
AB018258:Homo sapiens mRNA for KIAA0715 protein, partial ; 31818\_at Cluster Incl.  
AI024916:ov35a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39445\_at Cluster Incl.  
AF038661:Homo sapiens chromosome 1q21-1q23 beta-1,4-galac; 40507\_at Cluster Incl.

- K03195:Human (HepG2) glucose transporter gene mRNA, compl; 32816\_at Cluster Incl.  
 AL050156:Homo sapiens mRNA; cDNA DKFZp586N1020 (from clon; 32837\_at Cluster Incl.  
 U56418:Human lysophosphatidic acid acyltransferase-beta m; 33935\_at Cluster Incl.  
 AL035305:H.sapiens gene from PAC 102G20 /cds=(117,803) /g; 39122\_at Cluster Incl.
- 5 K03515:Human neuroleukin mRNA, complete cds /cds=(15,1691; 39866\_at Cluster Incl.  
 AB028986:Homo sapiens mRNA for KIAA1063 protein, partial ; 39899\_at Cluster Incl.  
 AC005525:Homo sapiens chromosome 19, cosmid F22162 /cds=(; 40170\_at Cluster Incl.  
 AI687306:tp86a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40254\_s\_at Cluster Incl.  
 AI922937:wn66d06.x1 Homo sapiens cDNA, 3 end /clone=IM; 41281\_s\_at Cluster Incl.
- 10 AF060502:Homo sapiens peroxisome assembly protein PEX10; 41331\_at Cluster Incl.  
 R93981:yt73d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 41496\_at Cluster Incl.  
 AL050189:Homo sapiens mRNA; cDNA DKFZp586B0323 (from clon; 41500\_at Cluster Incl.  
 AI761818:wi62g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32550\_r\_at Cluster Incl.  
 Y11525:H.sapiens mRNA for CCAAT/enhancer binding protei; 33134\_at Cluster Incl.
- 15 AB011083:Homo sapiens mRNA for KIAA0511 protein, partial ; 1992\_at U46922 /FEATURE=  
 /DEFINITION=HSU46922 Human FHIT mRNA, complete cds ; 1966\_i\_at U18334 /FEATURE=cds  
 /DEFINITION=HSUNOSIIC1 Human nitric oxide synthase; 1760\_s\_at D11327 /FEATURE=  
 /DEFINITION=HUMLCPTP Human mRNA for protein-tyrosine ; 1141\_at L27080 /FEATURE=cds  
 /DEFINITION=HUMMC5R Human melanocortin 5 receptor (M; 916\_at L18983
- 20 /FEATURE=mRNA /DEFINITION=HUMTYROPHO Homo sapiens tyrosine phospho; 736\_f\_at  
 D87002 /FEATURE=cds#2 /DEFINITION=D87002 Homo sapiens immunoglobulin Ia; 648\_at  
 L37112 /FEATURE=mRNA /DEFINITION=HUMVVR Homo sapiens vasopressin V3 recep;  
 414\_at X59373 /FEATURE=mRNA /DEFINITION=HSHOX4D Human HOX4D mRNA for a  
 homeobox ; 170\_at U51096 /FEATURE= /DEFINITION=HSU51096 Human homeobox protein
- 25 Cdx2 mRNA, c.  
**Metagene** 245; 31499\_s\_at Cluster Incl. X16863:Human Fc-gamma RIII-1 cDNA for Fc-gamma  
 receptor; 33092\_at Cluster Incl. AC005946:Homo sapiens chromosome 19, cosmid R28782 /cds=(;  
 34609\_g\_at Cluster Incl. M24194:Human MHC protein homologous to chicken B comple;  
 32307\_s\_at Cluster Incl. V00503:Human mRNA encoding Pro-alpha-2 chain of type I ; 32941\_at
- 30 Cluster Incl. M91196:Homo sapiens DNA-binding protein mRNA, complete cd; 34978\_g\_at Cluster  
 Incl. AJ007395:Homo sapiens mRNA for QA79 membrane protein /c; 35474\_s\_at Cluster Incl.  
 Y15915:Homo sapiens mRNA for chimaeric transcript of co; 36770\_at Cluster Incl. U18671:Human  
 Stat2 gene, complete cds /cds=(57,2612) /gb=; 38201\_at Cluster Incl. U21551:Human ECA39  
 mRNA, complete cds /cds=(0,1154) /gb=U; 38598\_at Cluster Incl. AI679353:tu73f03.x1 Homo
- 35 sapiens cDNA, 3 end /clone=IMAG; 40369\_f\_at Cluster Incl. AL022723:dJ377H14.1 (major  
 histocompatibility complex, ; 40370\_f\_at Cluster Incl. M90683:Human lymphocyte antigen (HLA-  
 G1) mRNA, complete; 34666\_at Cluster Incl. X07834:Human mRNA for manganese superoxide  
 dismutase (EC ; 40519\_at Cluster Incl. Y00638:Human mRNA for leukocyte common antigen  
 (T200) /cd; 36151\_at Cluster Incl. U60644:Human HU-K4 mRNA, complete cds /cds=(487,1800)

- /gb; 38077\_at Cluster Incl. X52022:H.sapiens RNA for type VI collagen alpha3 chain /c; 2024\_s\_at M79321 /FEATURE= /DEFINITION=HUMLYNTK Human Lyn B protein mRNA, comple;
- 1991\_s\_at U43784 /FEATURE= /DEFINITION=HSU43784 Human mitogen activated protein ;
- 1984\_s\_at X69549 /FEATURE=cds /DEFINITION=HSRHO2 H.sapiens mRNA for rho GDP-diss;
- 5 1146\_at Cd4 Antigen ; 1150\_at Tyrosine Phosphatase, Epsilon ; 834\_at U40462 /FEATURE= /DEFINITION=HSU40462 Human Ikaros/LyF-1 homolog (hIk-1) ; 428\_s\_at V00567 /FEATURE=cds /DEFINITION=HSMGLO Human messenger RNA fragment for; 201\_s\_at S82297 /FEATURE= /DEFINITION=S82297 beta 2-microglobulin {11bp deleted ; 184\_at U03642 /FEATURE=cds /DEFINITION=HSU03642 Human G protein-coupled receptor; 129\_g\_at X82153
- 10 /FEATURE=cds /DEFINITION=HSOC2RNA H.sapiens mRNA for cathepsin O; 160041\_at X79568 /FEATURE=cds /DEFINITION=HSBDP1 H.sapiens BDP1 mRNA for protein.
- Metagene** 246; 38855\_s\_at Cluster Incl. D82343:Homo sapiens mRNA for AMY, complete cds /cds=(28; 38957\_at Cluster Incl. AB002367:Human mRNA for KIAA0369 gene, complete cds /cds=; 41665\_at Cluster Incl. AB020631:Homo sapiens mRNA for KIAA0824 protein, partial ; 32084\_at
- 15 Cluster Incl. AF057164:Homo sapiens organic cation transporter OCTN2 (O; 37983\_at Cluster Incl. S77410:type 1 angiotensin II receptor [human, liver, mRNA; 40155\_at Cluster Incl. D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(2; 35277\_at Cluster Incl. AB018305:Homo sapiens mRNA for KIAA0762 protein, partial ; 37729\_at Cluster Incl. Y08614:Homo sapiens mRNA for CRM1 protein /cds=(38,3253) ; 38026\_at Cluster Incl. U01244:Human fibulin-1D mRNA, complete
- 20 cds /cds=(10,2121); 39550\_at Cluster Incl. AB011156:Homo sapiens mRNA for KIAA0584 protein, partial ; 40239\_g\_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IM; 40240\_at Cluster Incl. AC004131:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-; 41839\_at Cluster Incl. L13698:Human gas1 gene, complete cds /cds=(410,1447) /gb=; 962\_at X83107 /FEATURE=cds /DEFINITION=HSBMXGENE H.sapiens Bmx mRNA for cytoplas;
- 25 661\_at L13698 /FEATURE= /DEFINITION=HUMGAS1A Human gas1 gene, complete cds ; 615\_s\_at M24351 /FEATURE=expanded\_cds /DEFINITION=HUMPTHL4 Human parathyroid hor; 160030\_at X06562 /FEATURE=cds /DEFINITION=HSGHR Human mRNA for growth hormone re.
- Metagene** 247; 31693\_f\_at Cluster Incl. Z80776:H.sapiens H2A/g gene /cds=(0,392) /gb=Z80776 /gi; 41053\_at Cluster Incl. AJ245433:Homo sapiens mRNA for G4 protein (G4 gene, locat; 41636\_at
- 30 Cluster Incl. AB014565:Homo sapiens mRNA for KIAA0665 protein, complete; 32655\_s\_at Cluster Incl. X87613:H.sapiens mRNA for skeletal muscle abundant prot; 33289\_f\_at Cluster Incl. D88827:Homo sapiens mRNA for zinc finger protein FPM315; 36040\_at Cluster Incl. AI337192:qx88h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38007\_at Cluster Incl. L11353:Human moesin-ezrin-radixin-like protein mRNA, comp; 38260\_at Cluster Incl.
- 35 AL050306:Human DNA sequence from clone 475B7 on chromosom; 33350\_s\_at Cluster Incl. Z78315:HSZ78315 Homo sapiens cDNA /clone=2.120-(CEPH) /; 34300\_at Cluster Incl. AI352450:qt16g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37326\_at Cluster Incl. U93305:Homo sapiens A4 differentiation-dependent protein ; 33165\_at Cluster Incl. AL041879:DKFZp434H0419\_r1 Homo sapiens cDNA, 5 end /clon; 992\_at X52221

- /FEATURE=mRNA /DEFINITION=HSERCC25 H.sapiens ERCC2 gene, exons 1 &.
- Metagene** 248; 32363\_at Cluster Incl. AF059214:Homo sapiens cholesterol 25-hydroxylase mRNA, co; 39310\_at Cluster Incl. X86163:H.sapiens mRNA for B2-bradykinin receptor, 3 /cds=; 40659\_at Cluster Incl. U12767:Human mitogen induced nuclear orphan receptor (MIN; 40662\_g\_at Cluster
- 5 Incl. D78579:Homo sapiens mRNA for neuron derived orphan rece; 41386\_i\_at Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds; 41387\_r\_at Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds; 37187\_at Cluster Incl. M36820:Human cytokine (GRO-beta) mRNA, complete cds /cds=; 38299\_at Cluster Incl. X04430:Human IFN-beta 2a mRNA for interferon-beta-2 /cds=; 39402\_at Cluster Incl.
- 10 M15330:Human interleukin 1-beta (IL1B) mRNA, complete cds; 41779\_at Cluster Incl. U70426:Homo sapiens A28-RGS14p mRNA, complete cds /cds=(9; 32786\_at Cluster Incl. X51345:Human jun-B mRNA for JUN-B protein /cds=(253,1296); 36097\_at Cluster Incl. M62831:Human transcription factor ETR101 mRNA, complete c; 36979\_at Cluster Incl. M20681:Human glucose transporter-like protein-III (GLUT3); 37701\_at Cluster Incl.
- 15 L13463:Human helix-loop-helix basic phosphoprotein (G0S8); 37724\_at Cluster Incl. V00568:Human mRNA encoding the c-myc oncogene /cds=(558,1; 39143\_at Cluster Incl. U08015:Human NF-ATc mRNA, complete cds /cds=(239,2389) /g; 2049\_s\_at M29039 /FEATURE=cds /DEFINITION=HUMJUNCAA Human transactivator (jun-B); 1973\_s\_at V00568 /FEATURE=cds /DEFINITION=HSMYC1 Human mRNA encoding the c-myc o; 1779\_s\_at
- 20 M16750 /FEATURE= /DEFINITION=HUMPIM1 Human pim-1 oncogene mRNA, comple; 1520\_s\_at X04500 /FEATURE=expanded\_cds /DEFINITION=HSIL1B Human gene for prointe; 1334\_s\_at X03656 /FEATURE=mRNA /DEFINITION=HSGCSFG Human gene for granulocyte co; 529\_at U15932 /FEATURE= /DEFINITION=HSU15932 Human dual-specificity protein phos; 265\_s\_at M24736 /FEATURE= /DEFINITION=HUMELAM1A Human endothelial leukocyte adhe;
- 25 190\_at U12767 /FEATURE= /DEFINITION=HSU12767 Human mitogen induced nuclear orpha. **Metagene** 249; 41860\_at Cluster Incl. AF070559:Homo sapiens clone 24463 mRNA sequence /cds=UNKN; 39039\_s\_at Cluster Incl. AI557497:Pt2.1\_16\_A04.r Homo sapiens cDNA, 3 end /clon; 40874\_at Cluster Incl. AJ005259:Homo sapiens mRNA for EDF-1 protein /cds=(34,480; 41193\_at Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(; 33821\_at Cluster
- 30 Incl. AL034374:Human DNA sequence from clone 483K16 on chromoso; 36578\_at Cluster Incl. U37547:Human IAP homolog B (MIHB) mRNA, complete cds /cds; 37757\_at Cluster Incl. L23959:Homo sapiens E2F-related transcription factor (DP-; 38374\_at Cluster Incl. AF050110:Homo sapiens TGFb inducible early protein and ea; 39092\_at Cluster Incl. AW007731:wt68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39174\_at Cluster Incl.
- 35 X77548:H. sapiens cDNA for RFG /cds=(76,1920) /gb=X77548 ; 39181\_at Cluster Incl. U00928:Human clone CE29 4.1 (CAC)n/(GTG)n repeat-containi; 1670\_at L23959 /FEATURE= /DEFINITION=HUMDP1A Homo sapiens E2F-related transcript; 1466\_s\_at S81661 /FEATURE= /DEFINITION=S81661 Keratinocyte growth factor [human; 843\_at U48296 /FEATURE= /DEFINITION=HSU48296 Homo sapiens protein tyrosine phosph.

- Metagene 250;** 37877\_at Cluster Incl. AL050269:Homo sapiens mRNA; cDNA DKFZp564C103 (from clone; 38594\_i\_at Cluster Incl. AB006622:Homo sapiens mRNA for KIAA0284 gene, partial c; 34289\_f\_at Cluster Incl. D50920:Human mRNA for KIAA0130 gene, complete cds /cds=; 34702\_f\_at Cluster Incl. M27826:Human endogenous retroviral protease mRNA, compl; 35617\_at
- 5 Cluster Incl. U29725:Human BMK1 alpha kinase mRNA, complete cds /cds=(2; 36005\_at Cluster Incl. AF042800:Homo sapiens suppressor of white apricot homolog; 37269\_at Cluster Incl. D38496:Human mRNA for LZTR-1, complete cds /cds=(862,2520; 37910\_at Cluster Incl. U52112:host cell factor 1 /cds=(344,6451) /gb=U52112 /gi=; 40123\_at Cluster Incl. D87435:Human mRNA for KIAA0248 gene, partial cds /cds=(0; 32801\_at Cluster Incl. AB002315:Human mRNA
- 10 for KIAA0317 gene, complete cds /cds=; 33909\_at Cluster Incl. L35013:Human spliceosomal protein (SAP 49) gene, complete; 34404\_at Cluster Incl. W28167:43a1 Homo sapiens cDNA /gb=W28167 /gi=1308115 /ug=; 35771\_at Cluster Incl. AF049460:Homo sapiens nuclear DEAF-1 related transcriptio; 36940\_at Cluster Incl. D86970:Human mRNA for KIAA0216 gene, complete cds /cds=(4; 38043\_at Cluster Incl. X55448:H.sapiens G6PD gene for glucose-6-phosphate dehydr;
- 15 38829\_r\_at Cluster Incl. AA628946:af28f05.s1 Homo sapiens cDNA, 3 end /clone=IM; 40263\_at Cluster Incl. AF001891:Homo sapiens clone lambda MEN1 region unknown pr; 41836\_at Cluster Incl. U94836:Human ERPROT 213-21 mRNA, complete cds /cds=(88,27; 1181\_at Guanine Nucleotide-Binding Protein Hsr1 ; 1162\_g\_at Guanine Nucleotide-Binding Protein Hsr1 .
- Metagene 251;** 31688\_at Cluster Incl. AF005080:Homo sapiens skin-specific protein (xp5) mRNA, c; 35022\_at Cluster Incl. S83308:SOX5=Sry-related HMG box gene {alternatively splic; 39615\_at
- 20 Cluster Incl. AB028949:Homo sapiens mRNA for KIAA1026 protein, partial ; 35217\_at Cluster Incl. AL049404:Homo sapiens mRNA; cDNA DKFZp586F0219 (from clon; 41345\_at Cluster Incl. AI223140:qg53a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 514\_at U26710 /FEATURE= /DEFINITION=HSU26710 Human cbl-b mRNA, complete cds .
- 25 **Metagene 252;** 34636\_at Cluster Incl. M23892:Human 15-lipoxygenase mRNA, complete cds /cds=(3,1; 38932\_at Cluster Incl. M29580:Human zinc-finger protein 7 (ZFP7) mRNA, complete ; 39638\_at Cluster Incl. S73885:AP-4=basic helix-loop-helix DNA-binding protein [h; 41639\_at Cluster Incl. D38553:Human mRNA for KIAA0074 gene, partial cds /cds=(0; 35145\_at Cluster Incl. X96401:H.sapiens mRNA for ROX protein /cds=(212,1960) /gb.
- 30 **Metagene 253;** 36264\_at Cluster Incl. S75168:Matk=megakaryocyte-associated tyrosine kinase [hum; 37149\_s\_at Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (c; 41063\_g\_at Cluster Incl. AA037278:zc52c04.r1 Homo sapiens cDNA, 5 end /clone=IM; 32560\_s\_at Cluster Incl. W30959:zc65h10.r1 Homo sapiens cDNA, 5 end /clone=IMAG.
- Metagene 254;** 31413\_at Cluster Incl. AF000990:Homo sapiens testis-specific Testis Transcript Y; 32428\_at Cluster Incl. AF026564:Homo sapiens RNA binding protein II (RBMII) gene; 32924\_at
- 35 Cluster Incl. AB021227:Homo sapiens mRNA for membrane-type-5 matrix met; 34522\_at Cluster Incl. AF070625:Homo sapiens clone 24734 mRNA sequence /cds=UNKN; 38158\_at Cluster Incl. D79987:Human mRNA for KIAA0165 gene, complete cds /cds=(1; 33784\_at Cluster Incl. U12597:Human tumor necrosis factor type 2 receptor associ; 1004\_at X68149 /FEATURE=exon#2

- /DEFINITION=HSBLR1A Homo sapiens BLR1 gene for Bu.
- Metagene 255;** 31510\_s\_at Cluster Incl. Z48950:H.sapiens hH3.3B gene for histone H3.3 /cds=(10,; 36347\_f\_at Cluster Incl. AA873858:oh79b10.s1 Homo sapiens cDNA, 3 end /clone=IM; 33226\_at Cluster Incl. AB020683:Homo sapiens mRNA for KIAA0876 protein, partial ; 35672\_at Cluster Incl.
- 5 AL080144:Homo sapiens mRNA; cDNA DKFZp434N093 (from clone; 39435\_at Cluster Incl. D45333:HUMHG7879 Homo sapiens cDNA /gb=D45333 /gi=1136736; 41183\_at Cluster Incl. U15782:Human cleavage stimulation factor 77kDa subunit mR; 842\_at U48251 /FEATURE= /DEFINITION=HSU48251 Homo sapiens protein kinase C-bindi.
- Metagene 256;** 33997\_at Cluster Incl. AL049449:Homo sapiens mRNA; cDNA DKFZp586B1722
- 10 (from clon; 34981\_at Cluster Incl. M55513:Human potassium channel (HPCN1) mRNA, complete cds; 41430\_at Cluster Incl. AB011113:Homo sapiens mRNA for KIAA0541 protein, partial ; 41463\_at Cluster Incl. AL042729:DKFZp434B0222\_s1 Homo sapiens cDNA, 3 end /clon; 32686\_at Cluster Incl. D86096:Human DNA for prostaglandin E receptor EP3 subtype; 33787\_at Cluster Incl. AB011109:Homo sapiens mRNA for KIAA0537 protein, complete; 35168\_f\_at Cluster Incl.
- 15 M92642:Homo sapiens alpha-1 type XVI collagen (COL16A1); 37259\_at Cluster Incl. Z81326:H.sapiens mRNA for protease inhibitor 12 (PI12; ne; 37279\_at Cluster Incl. U10550:Human Gem GTPase (gem) mRNA, complete cds /cds=(21; 37602\_at Cluster Incl. Z49878:H.sapiens mRNA for guanidinoacetate N-methyltransf; 38711\_at Cluster Incl. AB014527:Homo sapiens mRNA for KIAA0627 protein, partial ; 39754\_at Cluster Incl. X53002:Human mRNA for integrin
- 20 beta-5 subunit /cds=(336,2; 40446\_at Cluster Incl. AL021366:cICK0721Q.4.1 (PHD finger protein 2) (isoform 2); 41742\_s\_at Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRN; 33358\_at Cluster Incl. W29087:56b8 Homo sapiens cDNA /gb=W29087 /gi=1309053 /ug=; 33380\_at Cluster Incl. AB005754:Homo sapiens mRNA for LAK-1, complete cds /cds=(; 33408\_at Cluster Incl. AB023151:Homo sapiens mRNA for KIAA0934 protein, partial ; 37338\_at Cluster Incl.
- 25 D61391:Human mRNA for phosphoribosylpyrophosphate syntheta; 37406\_at Cluster Incl. X94232:H.sapiens mRNA for novel T-cell activation protein; 38431\_at Cluster Incl. U09759:Human protein kinase (JNK2) mRNA, complete cds /cd; 38803\_at Cluster Incl. AF052142:Homo sapiens clone 24665 mRNA sequence /cds=UNKN; 33169\_at Cluster Incl. U61262:Human neogenin mRNA, complete cds /cds=(136,4521) ; 1861\_at U66879 /FEATURE= /DEFINITION=HSU66879 Human
- 30 Bcl-2 binding component 6 (b.
- Metagene 257;** 31742\_at Cluster Incl. AF064090:Homo sapiens ligand for herpesvirus entry mediat; 32135\_at Cluster Incl. U00968:Human SREBP-1 mRNA, complete cds /cds=(166,3609) /; 38672\_at Cluster Incl. Y13247:Homo sapiens fb19 mRNA /cds=(539,3361) /gb=Y13247 ; 32783\_at Cluster Incl. X82494:H.sapiens mRNA for fibulin-2 /cds=(69,3623) /gb=X8; 36933\_at Cluster Incl.
- 35 D87953:Human mRNA for RTP, complete cds /cds=(122,1306) /; 37761\_at Cluster Incl. AB015020:Homo sapiens mRNA for BAP2-beta protein, complet; 1563\_s\_at M58286 /FEATURE= /DEFINITION=HUMTNFRB Homo sapiens tumor necrosis fact; 675\_at J04164 /FEATURE= /DEFINITION=HUM927A Human interferon-inducible protein 9; 195\_s\_at U28014 /FEATURE= /DEFINITION=HSU28014 Human cysteine protease (ICRel-I.



- Metagene 258;** 34239\_at Cluster Incl. AL049787:Novel human gene mapping to chromosome 13 /cds=(5; 38634\_at Cluster Incl. M11433:Human cellular retinol-binding protein mRNA, compl; 39710\_at Cluster Incl. U30521:Human P311 HUM (3.1) mRNA, complete cds /cds=(202,; 34296\_at Cluster Incl. AF041210:Homo sapiens midline 1 fetal kidney isoform 3 (M; 37657\_at Cluster Incl.
- 5 Y16270:Homo sapiens PALM gene, exon 1 and joined CDS /cds; 38072\_at Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso; 38479\_at Cluster Incl. Y07969:H.sapiens mRNA for APRIL protein /cds=(230,979) /g; 1975\_s\_at X03563 /FEATURE=cds /DEFINITION=HSIGF1G1 Human gene for insulin-like g; 1761\_at D37965 /FEATURE= /DEFINITION=HUMPRLTS Human mRNA for PDGF receptor beta-; 1709\_g\_at U07620
- 10 /FEATURE= /DEFINITION=HSU07620 Human MAP kinase mRNA, complete ; 1246\_at U35234 /FEATURE= /DEFINITION=HSU35234 Human protein tyrosine phosphatase.
- Metagene 259;** 39610\_at Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148; 36091\_at Cluster Incl. AF051323:Homo sapiens Src-associated adaptor protein (SAP; 37618\_at Cluster Incl. M16937:Human homeo box c1 protein, mRNA, complete cds /cd; 38294\_at Cluster Incl. X17360:Human HOX 5.1 gene for HOX 5.1 protein /cds=(1243,; 37015\_at Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) ; 39840\_at Cluster Incl. AI037867:oy02f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33203\_s\_at Cluster Incl. U59831:Human transcription factor, forkhead related act; 873\_at M26679 /FEATURE=expanded\_cds /DEFINITION=HUMHOX13G Homo sapiens homeobox ; 444\_g\_at
- 20 X17360 /FEATURE=mRNA /DEFINITION=HSHOX51 Human HOX 5.1 gene for HOX 5.1.
- Metagene 260;** 31544\_at Cluster Incl. L13203:Human HNF-3/fork-head homolog-3 HFH-3 mRNA, comple; 35045\_r\_at Cluster Incl. X60655:H.sapiens EVX1 mRNA /cds=(228,1451) /gb=X60655 /; 36016\_at Cluster Incl. AF013252:Homo sapiens preprocartistatin (Cort) mRNA, comp; 1092\_at M65199 /FEATURE= /DEFINITION=HUMET2A Human endothelin 2 (ET2) mRNA, comp.
- 25 **Metagene 261;** 32001\_s\_at Cluster Incl. M80482:Human subtilisin-like protein (PACE4) mRNA, comp; 36412\_s\_at Cluster Incl. U53831:Homo sapiens interferon regulatory factor 7B mRN; 34974\_at Cluster Incl. Y13323:Homo sapiens mRNA for disintegrin-protease /cds=(6; 41038\_at Cluster Incl. M32011:Human neutrophil oxidase factor (p67-phox) mRNA, c; 41106\_at Cluster Incl. AF022797:Homo sapiens intermediate conductance calcium-ac; 41409\_at Cluster Incl.
- 30 AF044896:Homo sapiens ICB-1 mRNA, complete cds /cds=(128,; 41678\_at Cluster Incl. AF025304:Homo sapiens protein-tyrosine kinase EPHB2v (EPH; 31891\_at Cluster Incl. U58515:Human chitinase (HUMTCHIT) mRNA, exon 1b form, par; 33227\_at Cluster Incl. AI984234:wz57e04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33731\_at Cluster Incl. AJ130718:Homo sapiens mRNA for glycoprotein-associated am; 33752\_at Cluster Incl.
- 35 AB020657:Homo sapiens mRNA for KIAA0850 protein, complete; 34749\_at Cluster Incl. U83461:Human putative copper uptake protein (hCTR2) mRNA,; 37542\_at Cluster Incl. D86961:Human mRNA for KIAA0206 gene, partial cds /cds=(0,; 37922\_at Cluster Incl. L02648:Homo sapiens (clone V6) transcobalamin II (TCN2) m; 39774\_at Cluster Incl. X80695:H.sapiens OXA1Hs mRNA /cds=(6,1313) /gb=X80695 /gi; 40049\_at Cluster Incl.

- X76104:H.sapiens DAP-kinase mRNA /cds=(336,4631) /gb=X761; 40432\_at Cluster Incl.  
 AA522891:ni41b12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41209\_at Cluster Incl.  
 M15856:Human lipoprotein lipase mRNA, complete cds /cds=U; 36963\_at Cluster Incl.  
 U30255:Human phosphogluconate dehydrogenase (hPGDH) gene;; 37021\_at Cluster Incl.
- 5 X16832:Human mRNA for cathepsin H (EC 3.4.22.16) /cds=(34; 37025\_at Cluster Incl.  
 AL120815:DKFZp762F172\_r1 Homo sapiens cDNA, 5 end /clone; 37343\_at Cluster Incl.  
 U01062:Human type 3 inositol 1,4,5-trisphosphate receptor; 1647\_at U51903 /FEATURE=  
 /DEFINITION=HSU51903 Human RasGAP-related protein (IQGA; 1085\_s\_at M37238  
 /FEATURE=mRNA /DEFINITION=HUMPLC Human phospholipase C mRNA, co.
- 10 **Metagene** 262; 31974\_at Cluster Incl. AJ132445:Homo sapiens CLDN14 gene /cds=(0,719)  
 /gb=AJ1324; 33124\_at Cluster Incl. AB000450:Homo sapiens mRNA for VRK2, complete cds  
 /cds=(1; 1591\_s\_at J03242 /FEATURE= /DEFINITION=HUMGFIL2 Human insulin-like growth  
 factor .  
**Metagene** 263; 37578\_at Cluster Incl. D25248:Homo sapiens mRNA, clone-RES4-4
- 15 /cds=UNKNOWN /gb=D; 37584\_at Cluster Incl. AJ007669:Homo sapiens mRNA for Fanconi  
 anemia group G /cd; 34782\_at Cluster Incl. AL021938:Homo sapiens DNA sequence from PAC  
 232K4 on chro; 37037\_at Cluster Incl. M24486:Human prolyl 4-hydroxylase alpha subunit mRNA,  
 com; 37295\_at Cluster Incl. X63469:H.sapiens mRNA for transcription factor TFIIE beta;  
 39468\_r\_at Cluster Incl. W27081:22g5 Homo sapiens cDNA /gb=W27081 /gi=1306660 /u; 41264\_at
- 20 Cluster Incl. AL050172:Homo sapiens mRNA; cDNA DKFZp586F1322 (from clon; 2088\_s\_at  
 D31661 /FEATURE= /DEFINITION=HUMERKA Human mRNA for tyrosine kinase, c; 1767\_s\_at  
 X14885 /FEATURE=mRNA /DEFINITION=HSTGF31 H.sapiens gene for transformi; 1711\_at  
 U09477 /FEATURE= /DEFINITION=HSU09477 Human clone 53BP1 p53-binding prot; 1688\_s\_at  
 X87843 /FEATURE=cds /DEFINITION=HSCYCHASS H.sapiens mRNA for cyclin H ; 1374\_g\_at
- 25 M31523 /FEATURE= /DEFINITION=HUMTFAA Human transcription factor (E2A) ; 224\_at  
 S81439 /FEATURE= /DEFINITION=S81439 EGR alpha=early growth response gene .  
**Metagene** 264; 36396\_at Cluster Incl. AL049443:Homo sapiens mRNA; cDNA DKFZp586N2020  
 (from clon; 37816\_at Cluster Incl. M57729:Human complement component C5 mRNA, complete cds  
 /; 40704\_at Cluster Incl. Z29090:H.sapiens mRNA for phosphatidylinositol 3-kinase /; 32676\_at
- 30 Cluster Incl. M93405:Human methylmalonate semialdehyde dehydrogenase ge; 32697\_at Cluster  
 Incl. AF042729:Homo sapiens lithium-sensitive myo-inositol mono; 34261\_at Cluster Incl.  
 D84307:Homo sapiens mRNA for phosphoethanolamine cytidily; 35987\_g\_at Cluster Incl.  
 AL050395:Homo sapiens mRNA; cDNA DKFZp586D1020 (from cl; 36860\_at Cluster Incl.  
 AB028987:Homo sapiens mRNA for KIAA1064 protein, partial ; 37249\_at Cluster Incl.
- 35 AF079529:Homo sapiens cAMP-specific phosphodiesterase 8B ; 37251\_s\_at Cluster Incl.  
 AF016004:Homo sapiens m6b1 mRNA, complete cds /cds=(254; 38351\_at Cluster Incl.  
 AL050154:Homo sapiens mRNA; cDNA DKFZp586L0120 (from clon; 39377\_at Cluster Incl.  
 D87453:Human mRNA for KIAA0264 gene, partial cds /cds=(0; 39422\_at Cluster Incl.  
 AB007923:Homo sapiens mRNA for KIAA0454 protein, partial ; 39746\_at Cluster Incl.

- X63563:H.sapiens mRNA for RNA polymerase II 140 kDa subun; 40161\_at Cluster Incl.  
 L32137:Human germline oligomeric matrix protein (COMP) mR; 40834\_at Cluster Incl.  
 AB002298:Human mRNA for KIAA0300 gene, partial cds /cds=(; 32253\_at Cluster Incl.  
 AB007927:Homo sapiens mRNA for KIAA0458 protein, complete; 33446\_at Cluster Incl.
- 5 W26407:29b8 Homo sapiens cDNA /gb=W26407 /gi=1307106 /ug=; 34372\_at Cluster Incl.  
 AB002310:Human mRNA for KIAA0312 gene, partial cds /cds=(; 35342\_at Cluster Incl.  
 AF052159:Homo sapiens clone 24416 mRNA sequence /cds=UNKN; 35795\_at Cluster Incl.  
 AJ011972:Homo sapiens mRNA for histone deacetylase-like p; 38105\_at Cluster Incl.  
 W26521:32g11 Homo sapiens cDNA /gb=W26521 /gi=1307382 /ug; 41249\_at Cluster Incl.
- 10 AL031282:dJ283E3.6.1 (PUTATIVE novel protein similar to m; 1171\_s\_at Transcription Factor  
 Oct-1a/1b, Alt. Splice 2, Oct-1b; 1058\_at S69790 /FEATURE= /DEFINITION=S69790 Brush-  
 1=tumor suppressor {3 region}; 819\_at U76456 /FEATURE= /DEFINITION=HSU76456 Homo  
 sapiens tissue inhibitor of me; 218\_at S74221 /FEATURE= /DEFINITION=S74221 IK=IK factor  
 [human, leukemic cells K.
- 15 **Metagene** 265; 38923\_at Cluster Incl. L76159:Homo sapiens FRG1 mRNA, complete cds  
 /cds=(191,967; 40036\_at Cluster Incl. AF035940:Homo sapiens MAGOH mRNA, complete cds  
 /cds=(65,5; 31822\_at Cluster Incl. L12579:Human alternatively spliced CUTL1 mRNA, complete c;  
 35218\_at Cluster Incl. AF022385:Homo sapiens apoptosis-related protein TFAR15 (T; 35224\_at  
 Cluster Incl. AF070569:Homo sapiens clone 24659 mRNA sequence /cds=UNKN; 36013\_at Cluster
- 20 Incl. AF006621:Homo sapiens embryonic lung protein (HUEL) mRNA,; 39743\_at Cluster Incl.  
 AI862521:wj15a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39767\_at Cluster Incl.  
 D13627:Human mRNA for KIAA0002 gene, complete cds /cds=(2; 40076\_at Cluster Incl.  
 AF004430:Homo sapiens hD54+ins2 isoform (hD54) mRNA, comp; 40410\_at Cluster Incl.  
 W26651:34c5 Homo sapiens cDNA /gb=W26651 /gi=1307494 /ug=; 33343\_at Cluster Incl.
- 25 AB022663:Homo sapiens HFB30 mRNA, complete cds /cds=(236; 34305\_at Cluster Incl.  
 Z29505:H.sapiens mRNA for nucleic acid binding protein su; 34893\_at Cluster Incl.  
 AI557064:PT2.1\_13\_A12.r Homo sapiens cDNA, 3 end /clone; 35349\_at Cluster Incl.  
 AF031647:Homo sapiens JAB1-containing signalosome subunit; 35744\_at Cluster Incl.  
 D50931:Human mRNA for KIAA0141 gene, complete cds /cds=(8; 36122\_at Cluster Incl.
- 30 X59417:H.sapiens PROS-27 mRNA /cds=(62,802) /gb=X59417 /g; 36687\_at Cluster Incl.  
 N50520:yy89b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 37381\_g\_at Cluster Incl.  
 X59268:Human mRNA for general transcription factor IIB; 37403\_at Cluster Incl. X05908:Human  
 mRNA for lipocortin /cds=(74,1114) /gb=X0590; 37659\_at Cluster Incl. L42572:Homo sapiens  
 p87/89 gene, complete cds /cds=(92,23; 38068\_at Cluster Incl. M63175:Human autocrine motility
- 35 factor receptor mRNA /cds; 38399\_at Cluster Incl. AL034428:Human DNA sequence from clone  
 705D16 on chromoso; 38450\_at Cluster Incl. X69804:H.sapiens mRNA for La/SS-B protein  
 /cds=UNKNOWN /g; 38744\_at Cluster Incl. N95406:zb80g12.s1 Homo sapiens cDNA, 3 end  
 /clone=IMAGE-; 38801\_at Cluster Incl. AI742846:wg46h09.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 40903\_at Cluster Incl. AL049929:Homo sapiens mRNA; cDNA DKFZp547O0510

- (from clone; 41510\_s\_at Cluster Incl. L15189:Homo sapiens mitochondrial HSP75 mRNA, complete ; 1825\_at L33075 /FEATURE= /DEFINITION=HUMIQGA Homo sapiens ras GTPase-activating-; 1399\_at L34587 /FEATURE= /DEFINITION=HUMRPIE Homo sapiens RNA polymerase II clone; 924\_s\_at J03805 /FEATURE= /DEFINITION=HUMALPHLB Human phosphatase 2A mRNA, parti; 781\_at X98001 /FEATURE=cds /DEFINITION=HSGGII H.sapiens mRNA for geranylgeranyl .
- 5 **Metagene** 266; 34022\_at Cluster Incl. M36821:Human cytokine (GRO-gamma) mRNA, complete cds /cds; 40672\_at Cluster Incl. U57721:Human L-kynurenine hydrolase mRNA, complete cds /c; 32640\_at Cluster Incl. M24283:Human major group rhinovirus receptor (HRV) mRNA, ; 38631\_at
- 10 Cluster Incl. M92357:Homo sapiens B94 protein mRNA, complete cds /cds=(; 1369\_s\_at M28130 /FEATURE=mRNA /DEFINITION=HUMIL8A Human interleukin 8 (IL8) gen; 595\_at M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha ind; 408\_at X54489 /FEATURE=mRNA /DEFINITION=HSMGSAG Human gene for melanoma growth s.
- Metagene** 267; 37163\_at Cluster Incl. AL050374:Homo sapiens mRNA; cDNA DKFZp586C1619
- 15 (from clone; 33770\_at Cluster Incl. AF009225:Homo sapiens Ikb kinase alpha subunit (IKK alpha; 35238\_at Cluster Incl. AB000509:Homo sapiens mRNA for TRAF5, complete cds /cds=(; 36505\_at Cluster Incl. D55655:Homo sapiens mRNA for cardiac calsequestrin, compl; 37254\_at Cluster Incl. U09366:Human zinc finger protein ZNF133 /cds=(445,2409) /; 40080\_at Cluster Incl. D42044:Human mRNA for KIAA0090 gene, partial cds /cds=(0,; 32858\_at Cluster Incl.
- 20 AI341565:qq94g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33392\_at Cluster Incl. AL080155:Homo sapiens mRNA; cDNA DKFZp434J154 (from clone; 35297\_at Cluster Incl. AC002400:Human Chromosome 16 BAC clone CIT987SK-A-735G6 /; 35765\_at Cluster Incl. X91504:H.sapiens mRNA for ARP1 protein /cds=(11,616) /gb=; 36676\_at Cluster Incl. AL031659:dJ343K2.2.1 (ribophorin II (isoform I)) /cds=(28; 38115\_at Cluster Incl.
- 25 AF055479:Homo sapiens lung cancer candidate FUS1 (FUS1) m; 38456\_s\_at Cluster Incl. AL049650:dJ734P14.2.2 (snRNP (small nuclear ribonucleop; 38484\_at Cluster Incl. D21267:Homo sapiens mRNA, complete cds /cds=(205,825) /gb; 40593\_at Cluster Incl. X66975:H.sapiens mRNA for heterogeneous nuclear ribonucle; 549\_at S80343 /FEATURE= /DEFINITION=S80343 ArgRS=arginyI-tRNA synthetase [human,.
- 30 **Metagene** 268; 31451\_at Cluster Incl. U62794:Human CDC42 GAP-related protein mRNA, partial cds ; 31536\_at Cluster Incl. AB020693:Homo sapiens mRNA for KIAA0886 protein, complete; 34642\_at Cluster Incl. U28964:Homo sapiens 14-3-3 protein mRNA, complete cds /cd; 33989\_f\_at Cluster Incl. W28869:53h2 Homo sapiens cDNA /gb=W28869 /gi=1308880 /u; 34953\_i\_at Cluster Incl. D89094:Homo sapiens mRNA for 3,5 -cyclic GMP phosphodi; 35968\_s\_at Cluster Incl.
- 35 AF001307:Homo sapiens aryl hydrocarbon receptor nuclear; 36262\_at Cluster Incl. Z12173:H.sapiens GNS mRNA encoding glucosamine-6-sulphata; 36263\_g\_at Cluster Incl. Z12173:H.sapiens GNS mRNA encoding glucosamine-6-sulpha; 37488\_at Cluster Incl. L00635:Human farnesyl-protein transferase beta-subunit mR; 38526\_at Cluster Incl. U02882:Human rolipram-sensitive 3,5 -cyclic AMP phosphodi; 39277\_at Cluster Incl. U60805:Human oncostatin-M

- specific receptor beta subunit ; 39933\_at Cluster Incl. X93921:H.sapiens mRNA for protein-tyrosine-phosphatase (t; 40696\_at Cluster Incl. U50062:Homo sapiens RIP protein kinase mRNA, complete cds; 41061\_at Cluster Incl. AF052288:untitled /cds=(0,2988) /gb=AF052288 /gi=3510692 ; 31829\_r\_at Cluster Incl. AF027515:Homo sapiens trans-golgi network glycoprotein ; 33801\_at
- 5 Cluster Incl. AF104222:Homo sapiens CD2 cytoplasmic domain binding prot; 34691\_f\_at Cluster Incl. AF006087:Homo sapiens Arp2/3 protein complex subunit p2; 40126\_at Cluster Incl. Z97200:Homo sapiens DNA sequence from PAC 79C4 on chromos; 40433\_at Cluster Incl. W25921:15a11 Homo sapiens cDNA /gb=W25921 /gi=1306044 /ug; 40493\_at Cluster Incl. L05424:Human hyaluronate receptor (CD44) gene /cds=(136,2; 33823\_at Cluster Incl.
- 10 D12676:Human mRNA for lysosomal sialoglycoprotein, comple; 34389\_at Cluster Incl. M64108:Human udulin 1 mRNA, 3 end /cds=(0,2531) /gb=M641; 34890\_at Cluster Incl. L09235:Human vacuolar ATPase (isoform VA68) mRNA, complet; 35737\_at Cluster Incl. U90549:Human non-histone chromosomal protein (NHC) mRNA, ; 35806\_at Cluster Incl. W26854:17b4 Homo sapiens cDNA /gb=W26854 /gi=1306217 /ug=; 38401\_s\_at Cluster Incl.
- 15 W27594:34h4 Homo sapiens cDNA /gb=W27594 /gi=1307542 /u; 39901\_at Cluster Incl. U70312:Homo sapiens integrin binding protein Del-1 (Del1); 40608\_at Cluster Incl. AA013087:ze27c09.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 40962\_s\_at Cluster Incl. D26155:Human mRNA for transcriptional activator hSNF2a; 41300\_s\_at Cluster Incl. AA477898:zu34f08.r1 Homo sapiens cDNA, 5 end /clone=IM; 32571\_at Cluster Incl.
- 20 X68836:H.sapiens mRNA for S-adenosylmethionine synthetase; 1903\_at Ras-Related Protein Rap1b ; 1870\_at D13540 /FEATURE= /DEFINITION=HUMSHPTP3 Homo sapiens SH-PTP3 mRNA for pro; 1694\_s\_at D13413 /FEATURE=mRNA /DEFINITION=HUMTA120 Human mRNA for tumor-associia; 1656\_s\_at U07563 /FEATURE=cds#1 /DEFINITION=HSABLGR3 Human proto-oncogene tyrosi; 1648\_at U60805 /FEATURE= /DEFINITION=HSU60805 Human oncostatin-M specific
- 25 recept; 953\_g\_at Fk506-Binding Protein, Alt. Splice 2 ; 757\_at D28364 /FEATURE= /DEFINITION=HUMAI23 Human mRNA for annexin II, 5 UTR (se; 600\_at M28215 /FEATURE= /DEFINITION=HUMRAB5A Homo sapiens GTP-binding protein (R; 370\_at Z35102 /FEATURE=cds /DEFINITION=HSPROKINX H.sapiens mRNA for Ndr protein ; 351\_f\_at D28423 /FEATURE= /DEFINITION=HUMPSF82 Human mRNA for pre-mRNA splicing ; 289\_at L29277
- 30 /FEATURE= /DEFINITION=HUMAPRF Homo sapiens DNA-binding protein (AP. **Metagene** 269; 33494\_at Cluster Incl. S69232:electron transfer flavoprotein-ubiquinone oxidored; 37452\_at Cluster Incl. M15881:Human uromodulin (Tamm-Horsfall glycoprotein) mRNA; 37520\_at Cluster Incl. AJ006591:Homo sapiens mRNA for cysteine-rich protein /cds; 41040\_at Cluster Incl. U77664:Human RNaseP protein p38 (RPP38) mRNA, complete cd; 41439\_at Cluster Incl.
- 35 AJ001381:Homo sapiens incomplete cDNA for a mutated allele; 31866\_at Cluster Incl. AC005239:Homo sapiens chromosome 19, cosmid F23149 /cds=(; 34253\_at Cluster Incl. D83781:Human mRNA for KIAA0197 gene, partial cds /cds=(0; 35166\_at Cluster Incl. D87343:Homo sapiens mRNA for DCRA, complete cds /cds=(239; 36090\_at Cluster Incl. AL080162:Homo sapiens mRNA; cDNA DKFZp434N024 (from clone; 37569\_at Cluster Incl.

- AF035606:Homo sapiens calcium binding protein (ALG-2) mRNA; 37642\_at Cluster Incl.  
 D63877:Human mRNA for KIAA0157 gene, partial cds /cds=(0,; 37991\_at Cluster Incl.  
 L38961:Human putative transmembrane protein precursor (B5; 38989\_at Cluster Incl.  
 AF035296:Homo sapiens clone 23837 mRNA sequence /cds=UNKN; 32262\_at Cluster Incl.
- 5 AL049669:Human gene from PAC 612B18, chromosome 1 /cds=(2; 34369\_at Cluster Incl.  
 D86987:Homo sapiens mRNA for KIAA0214 protein, complete c; 34787\_at Cluster Incl.  
 X93209:H.sapiens mRNA for NRD1 convertase /cds=UNKNOWN /g; 35329\_at Cluster Incl.  
 AF091084:Homo sapiens clone 638 unknown mRNA, complete se; 36177\_at Cluster Incl.  
 X78627:H.sapiens mRNA for translin /cds=(81,767) /gb=X786; 36597\_at Cluster Incl.
- 10 D21262:Human mRNA for KIAA0035 gene, partial cds /cds=(0,; 36603\_at Cluster Incl.  
 D86973:Human mRNA for KIAA0219 gene, partial cds /cds=(0,; 36612\_at Cluster Incl.  
 D87470:Human mRNA for KIAA0280 gene, partial cds /cds=(0,; 38372\_at Cluster Incl.  
 U66042:Human clone 191B7 placenta expressed mRNA from chr; 38773\_at Cluster Incl.  
 AB003151:Homo sapiens DNA, chromosome 21q22.2, PAC clone ; 39116\_at Cluster Incl.
- 15 AF070626:Homo sapiens clone 24483 unknown mRNA, parital c; 39884\_g\_at Cluster Incl.  
 AF091078:Homo sapiens clone 559 unknown mRNA, complete ; 40224\_s\_at Cluster Incl.  
 AB014585:Homo sapiens mRNA for KIAA0685 protein, comple; 40629\_at Cluster Incl.  
 L19783:Human GPI-H mRNA, complete cds /cds=(60,626) /gb=L; 41242\_at Cluster Incl.  
 AB011004:Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosa; 41278\_at Cluster Incl.
- 20 AF041474:Homo sapiens BAF53a (BAF53a) mRNA, complete cds ; 41595\_at Cluster Incl.  
 AB023164:Homo sapiens mRNA for KIAA0947 protein, partial ; 32595\_at Cluster Incl.  
 U07231:Homo sapiens G-rich sequence factor-1 (GRSF-1) mRNA; 1371\_s\_at M29874 /FEATURE=  
 /DEFINITION=HUMCYP2BB Human cytochrome P450-IIIB (hIIB; 155\_s\_at U61397 /FEATURE=  
 /DEFINITION=HSU61397 Human ubiquitin-homology domain p.
- 25 **Metagene 270**; 34003\_at Cluster Incl. U47924:Human chromosome 12p13 sequence  
 /cds=(373,1122) /g; 37466\_at Cluster Incl. D84488:Homo sapiens mRNA for small GTP-binding  
 protein, c; 41037\_at Cluster Incl. U63824:Human transcription factor RTEF-1 (RTEF1) mRNA, co;  
 31886\_at Cluster Incl. X55740:Human placental cDNA coding for 5nucleotidase (EC ; 34177\_at  
 Cluster Incl. AF038660:Homo sapiens chromosome 1p33-p34 beta-1,4-galact; 34230\_r\_at Cluster
- 30 Incl. D84454:Human mRNA for UDP-galactose translocator, compl; 34272\_at Cluster Incl.  
 U27768:Human RGP4 mRNA, complete cds /cds=(97,714) /gb=U2; 35275\_at Cluster Incl.  
 AL050025:Homo sapiens mRNA; cDNA DKFZp564D066 (from clone; 35832\_at Cluster Incl.  
 AB029000:Homo sapiens mRNA for KIAA1077 protein, partial ; 36188\_at Cluster Incl.  
 D32257:Human GTF3A mRNA for Xenopus transcription factor ; 36582\_g\_at Cluster Incl.
- 35 U09510:Human glycyl-tRNA synthetase mRNA, complete cds ; 36965\_at Cluster Incl.  
 U13616:Human ankyrin G (ANK-3) mRNA, complete cds /cds=(1; 37048\_at Cluster Incl.  
 U58970:Human putative outer mitochondrial membrane 34 kDa; 38422\_s\_at Cluster Incl.  
 U29332:Homo sapiens heart protein (FHL-2) mRNA, complet; 38435\_at Cluster Incl.  
 U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cd; 38783\_at Cluster Incl.

- J05581:Human polymorphic epithelial mucin (PEM) mRNA, com; 40237\_at Cluster Incl.  
 AF035444:Homo sapiens p17-Beckwith-Wiedemann region 1 C (; 41531\_at Cluster Incl.  
 AI445461:tj34g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33213\_g\_at Cluster Incl.  
 AF006751:Homo sapiens ES/130 mRNA, complete cds /cds=(7; 700\_s\_at Mucin 1, Epithelial, Alt.  
 5 Splice 9 ; 658\_at L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSP Human  
 thrombospondin 2 (THBS2); 659\_g\_at L12350 /FEATURE=mRNA /DEFINITION=HUMTHRSP  
 Human thrombospondin 2 (THBS).  
**Metagene** 271; 31700\_at Cluster Incl. AF027957:Homo sapiens G protein-coupled receptor  
 (GPR35) ; 31719\_at Cluster Incl. X02761:Human mRNA for fibronectin (FN precursor) /cds=(0;;  
 10 34060\_g\_at Cluster Incl. AA586695:nn42h06.s1 Homo sapiens cDNA, 3 end /clone=IM; 34147\_g\_at  
 Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, pa; 32269\_at Cluster Incl.  
 W26805:13a12 Homo sapiens cDNA /gb=W26805 /gi=1305889 /ug; 32352\_at Cluster Incl.  
 X52730:Human gene for phenylethanolamine N-methylase (PNM; 34415\_at Cluster Incl.  
 Z22536:Homo sapiens ALK-4 mRNA, complete CDS /cds=(0,1517; 34469\_at Cluster Incl.  
 15 X84746:H.sapiens Histo-blood group AB0 gene, exon 1 /cds=; 35910\_f\_at Cluster Incl.  
 AJ003147:Homo sapiens complete genomic sequence between; 36218\_g\_at Cluster Incl.  
 Z35102:H.sapiens mRNA for Ndr protein kinase /cds=(595;; 37475\_at Cluster Incl.  
 AC004144:Homo sapiens chromosome 19, overlapping cosmids ; 37853\_at Cluster Incl.  
 AI857458:w157e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37885\_at Cluster Incl.  
 20 AF038169:Homo sapiens clone 23790 unknown protein mRNA, c; 38530\_at Cluster Incl.  
 W26021:18c10 Homo sapiens cDNA /gb=W26021 /gi=1306306 /ug; 39281\_at Cluster Incl.  
 AB002378:Human mRNA for KIAA0380 gene, complete cds /cds=; 40299\_at Cluster Incl.  
 AF091890:Homo sapiens G-protein coupled receptor RE2 mRNA; 40359\_at Cluster Incl.  
 M91083:Human DNA-binding protein (HRC1) mRNA, complete cd; 41074\_at Cluster Incl.  
 25 AF062006:Homo sapiens orphan G protein-coupled receptor H; 31846\_at Cluster Incl.  
 AW003733:ws16b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33794\_g\_at Cluster Incl.  
 U19345:Homo sapiens AR1 (TCF20) mRNA, partial cds /cds=; 35986\_at Cluster Incl.  
 AL050395:Homo sapiens mRNA; cDNA DKFZp586D1020 (from clon; 35996\_at Cluster Incl.  
 X98261:H.sapiens mRNA for M-phase phosphoprotein, mpp5 /c; 37285\_at Cluster Incl.  
 30 X60364:Human ALAS mRNA for 5-aminolevulinate synthase pre; 34832\_s\_at Cluster Incl.  
 AB018306:Homo sapiens mRNA for KIAA0763 protein, comple; 35827\_at Cluster Incl.  
 AB020712:Homo sapiens mRNA for KIAA0905 protein, complete; 36615\_at Cluster Incl.  
 M83751:Human arginine-rich protein (ARP) gene, complete c; 39128\_r\_at Cluster Incl.  
 X73478:H.sapiens hPTPA mRNA /cds=(189,1160) /gb=X73478 ; 39473\_r\_at Cluster Incl.  
 35 W29065:56g2 Homo sapiens cDNA /gb=W29065 /gi=1309094 /u; 39854\_r\_at Cluster Incl.  
 AF055000:Homo sapiens clone 24519 unknown mRNA, partial; 39868\_at Cluster Incl.  
 AL046394:DKFZp434M217\_r1 Homo sapiens cDNA, 5 end /clone; 40539\_at Cluster Incl.  
 U42391:Human myosin-IXb mRNA, complete cds /cds=(0,6068) ; 32525\_r\_at Cluster Incl.  
 W29012:55a6 Homo sapiens cDNA /gb=W29012 /gi=1308969 /u; 1415\_at D26561

- /FEATURE=cds#3 /DEFINITION=D26561 Homo sapiens cellular DNA conta; 887\_at M62302  
 /FEATURE= /DEFINITION=HUMGDF1 Human growth/differentiation factor ; 689\_at L02867  
 /FEATURE= /DEFINITION=HUMPPA Homo sapiens 62 kDa paraneoplastic an; 552\_at U02570  
 /FEATURE= /DEFINITION=HSU02570 Human CDC42 GTPase-activating prote; 420\_at X65633  
 5 /FEATURE=cds /DEFINITION=HSACTHR H.sapiens ACTH-R gene for adrenoc; 396\_f\_at X97671  
 /FEATURE=cds /DEFINITION=HSERYTHR H.sapiens mRNA for erythropoie; 259\_s\_at M16441  
 /FEATURE=cds#2 /DEFINITION=HUMTNFAB Human tumor necrosis factor ; 179\_at U38980  
 /FEATURE= /DEFINITION=U38980 Human PMS2 related (hPMSR6) mRNA, co; 121\_at X69699  
 /FEATURE= /DEFINITION=HSPAX8A H.sapiens Pax8 mRNA .
- 10 **Metagene** 272; 37826\_at Cluster Incl. AF020761:Homo sapiens stimulator of Fe transport mRNA,  
 co; 38142\_at Cluster Incl. U38904:Human zinc finger protein C2H2-25 mRNA, complete c;  
 38599\_s\_at Cluster Incl. AD001530:Homo sapiens XAP-5 mRNA, complete cds /cds=(75; 40756\_at  
 Cluster Incl. AF081280:Homo sapiens nucleoplasmin-3 (NPM3) mRNA, comple; 41632\_at Cluster  
 Incl. D38550:Human mRNA for KIAA0075 gene, partial cds /cds=(0; 34768\_at Cluster Incl.
- 15 AL080080:Homo sapiens mRNA; cDNA DKFZp564E1962 (from clon; 40469\_at Cluster Incl.  
 AB011144:Homo sapiens mRNA for KIAA0572 protein, partial ; 40473\_at Cluster Incl.  
 AF024636:Homo sapiens STE20-like kinase 3 (mst-3) mRNA, c; 40865\_at Cluster Incl.  
 U51166:Human G/T mismatch-specific thymine DNA glycosylas; 41755\_at Cluster Incl.  
 AB023194:Homo sapiens mRNA for KIAA0977 protein, complete; 32784\_at Cluster Incl.
- 20 AB011108:Homo sapiens mRNA for KIAA0536 protein, partial ; 35296\_at Cluster Incl.  
 AB019036:Homo sapiens mRNA for geranylgeranyl pyrophospha; 35824\_at Cluster Incl.  
 AJ223321:Homo sapiens RP58 gene, complete CDS /cds=(523,2; 36190\_at Cluster Incl.  
 M63256:Human major Yo paraneoplastic antigen (CDR2) mRNA,; 36970\_at Cluster Incl.  
 D80004:Human mRNA for KIAA0182 gene, partial cds /cds=(0; 37409\_at Cluster Incl.
- 25 U88666:Homo sapiens serine kinase SRPK2 mRNA, complete cd; 38767\_at Cluster Incl.  
 AF041037:Homo sapiens novel antagonist of FGF signaling (; 38824\_at Cluster Incl.  
 AF039103:Homo sapiens Tat-interacting protein TIP30 mRNA,; 41248\_at Cluster Incl.  
 AB014589:Homo sapiens mRNA for KIAA0689 protein, partial ; 41601\_at Cluster Incl.  
 AA142964:zl43a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1987\_at X76079
- 30 /FEATURE=exon#5 /DEFINITION=HSPDGF H.sapiens mRNA for platelet de; 1228\_s\_at U73682  
 /FEATURE= /DEFINITION=HSU73682 Human meningioma-expressed antig.  
**Metagene** 273; 36422\_s\_at Cluster Incl. AF038198:Homo sapiens clone 23928 mRNA sequence  
 /cds=UN; 37811\_at Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subun;  
 32033\_at Cluster Incl. AL096780:Novel human gene mapping to chromosome 22p13.33 s; 35638\_at
- 35 Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(4; 37908\_at Cluster  
 Incl. U31384:Human G protein gamma-11 subunit mRNA, complete cd; 35333\_r\_at Cluster Incl.  
 AB024518:Homo sapiens mRNA for DVS27-related protein, c; 36681\_at Cluster Incl.  
 J02611:Human apolipoprotein D mRNA, complete cds /cds=(61; 1433\_g\_at U68019 /FEATURE=  
 /DEFINITION=HSU68019 Homo sapiens mad protein homolog; 1336\_s\_at X06318



- /FEATURE=cds /DEFINITION=HSPKCB1A Human mRNA for protein kinase.
- Metagene 274;** 35469\_at Cluster Incl. X57830:H.sapiens serotonin 5-HT2 receptor mRNA
- /cds=(145,; 38911\_at Cluster Incl. U41815:Human nucleoporin 98 (NUP98) mRNA, complete cds
- /c; 40308\_at Cluster Incl. AI830496:wh51h03.x1 Homo sapiens cDNA, 3 end /clone=IMAG;
- 5 40655\_at Cluster Incl. U94190:Homo sapiens Duo mRNA, complete cds /cds=(100,5091; 31884\_at Cluster Incl. L40399:Homo sapiens (clone S240ii117/zap112) mRNA, comple; 32060\_at Cluster Incl. U15173:Homo sapiens BCL2/adenovirus E1B 19kD-interacting ; 34278\_at Cluster Incl. L18960:Human protein synthesis factor (eIF-4C) mRNA, comp; 35180\_at Cluster Incl. AL050205:Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone; 35213\_at Cluster Incl.
- 10 AF071185:Homo sapiens formin binding protein 21 mRNA, com; 35632\_at Cluster Incl. U26710:Human cbl-b mRNA, complete cds /cds=(322,3270) /gb; 37615\_at Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(7; 37915\_at Cluster Incl. AL080173:Homo sapiens mRNA; cDNA DKFZp434H071 (from clone; 38263\_at Cluster Incl. X98330:H.sapiens mRNA for ryanodine receptor 2 /cds=(121,; 38277\_at Cluster Incl.
- 15 M29550:Human calcineurin A1 mRNA, complete cds /cds=(107,; 38978\_at Cluster Incl. AF013758:Homo sapiens polyadenylate binding protein-inter; 39083\_at Cluster Incl. U39318:Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH; 39727\_at Cluster Incl. AF023917:Homo sapiens protein tyrosine phosphatase PIR1 m; 39792\_at Cluster Incl. AF000364:Homo sapiens heterogeneous nuclear ribonucleopro; 41133\_at Cluster Incl.
- 20 U32519:Human GAP SH3 binding protein mRNA, complete cds /; 32788\_at Cluster Incl. D42063:Human mRNA for RanBP2 (Ran-binding protein 2), com; 33354\_at Cluster Incl. AA630312:ac08f05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35805\_at Cluster Incl. AA447263:zw93f01.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 36685\_at Cluster Incl. W63793:zc55a10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 36942\_at Cluster Incl.
- 25 D79996:Human mRNA for KIAA0174 gene, complete cds /cds=(6; 37385\_at Cluster Incl. U40763:Human Clk-associated RS cyclophilin CARS-Cyp mRNA,; 38073\_at Cluster Incl. AB007858:Homo sapiens KIAA0398 mRNA, complete cds /cds=(1; 39507\_at Cluster Incl. AL050366:Homo sapiens mRNA; cDNA DKFZp564A126 (from clone; 40236\_at Cluster Incl. D29990:Human mRNA for cationic amino acid transporter 2, ; 40931\_at Cluster Incl.
- 30 AL080084:Homo sapiens mRNA; cDNA DKFZp564G2362 (from clone; 33150\_at Cluster Incl. AI126004:qc50e12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1094\_g\_at M65254 /FEATURE= /DEFINITION=HUMP2B Protein phosphatase 2A 65 kDa regu; 831\_at U28042 /FEATURE= /DEFINITION=HSU28042 Human DEAD box RNA helicase-like pr; 663\_at L18960 /FEATURE= /DEFINITION=HUMEIF4C Human protein synthesis factor (eIF.
- 35 **Metagene 275;** 31522\_f\_at Cluster Incl. Z80779:H.sapiens H2B/g gene /cds=(0,380) /gb=Z80779 /gi; 31942\_at Cluster Incl. AF045583:Homo sapiens tubby like protein 3 (TULP3) mRNA, ; 1687\_s\_at X84213 /FEATURE=cds /DEFINITION=HSCEBP1 H.sapiens BAK mRNA for BCL-2 h. **Metagene 276;** 36308\_at Cluster Incl. D76435:Homo sapiens mRNA for Zic protein, complete cds /c; 40674\_s\_at Cluster Incl. S82986:HOXC6=homeodomain-containing protein {clone 211};

- 39753\_at Cluster Incl. X06256:Human mRNA for integrin alpha 5 subunit /cds=(23,3; 38404\_at Cluster Incl. M55153:Human transglutaminase (TGase) mRNA, complete cds ; 647\_at L35545 /FEATURE=mRNA /DEFINITION=HUMECPC Homo sapiens endothelial cell pr.
- Metagene** 277; 34529\_at Cluster Incl. W26760:12d6 Homo sapiens cDNA /gb=W26760
- 5 /gi=1305844 /ug=; 36281\_at Cluster Incl. M96739:Human NSCL-1 mRNA sequence /cds=UNKNOWN /gb=M96739; 36743\_at Cluster Incl. AL096739:Homo sapiens mRNA; cDNA DKFZp586H0623 (from clon; 37126\_at Cluster Incl. M62800:Human 52-kD SS-A/Ro autoantigen mRNA, complete cds; 39239\_at Cluster Incl. X13444:Human mRNA for CD8 beta-chain glycoprotein (CD8 be; 39318\_at Cluster Incl. X82240:H.sapiens mRNA for Tcell
- 10 leukemia/lymphoma 1 /cds=; 37935\_at Cluster Incl. AF016369:Homo sapiens U4/U6 small nuclear ribonucleoprote; 38067\_at Cluster Incl. D86957:Human mRNA for KIAA0202 gene, partial cds /cds=(0,; 33170\_at Cluster Incl. AB023179:Homo sapiens mRNA for KIAA0962 protein, partial .
- Metagene** 278; 35112\_at Cluster Incl. AF071476:Homo sapiens regulator of G-protein signaling 9L; 36278\_at Cluster Incl. X90846:H.sapiens mRNA for mixed lineage kinase 2 /cds=(28; 39930\_at
- 15 Cluster Incl. D83492:Homo sapiens mRNA for Eph-family protein, complete; 39967\_at Cluster Incl. AB019527:Homo sapiens mRNA for LDOC1 protein, complete cd; 33756\_at Cluster Incl. U39447:Human placenta copper monamine oxidase mRNA, compl; 34231\_at Cluster Incl. AF074606:Homo sapiens histone acetyltransferase (HBO1) mR; 35678\_at Cluster Incl. AB006757:Homo sapiens mRNA for PCDH7 (BH-Pcdh)c, complete; 37265\_at Cluster Incl.
- 20 D87074:Human mRNA for KIAA0237 gene, complete cds /cds=(4; 40776\_at Cluster Incl. M63391:Human desmin gene, complete cds /cds=(80,1489) /gb; 34388\_at Cluster Incl. Y11710:H.sapiens mRNA for extracellular matrix protein co; 36096\_at Cluster Incl. AL080222:Homo sapiens mRNA; cDNA DKFZp566D1146 (from clon; 37765\_at Cluster Incl. X54162:Human mRNA for a 64 Kd autoantigen expressed in th; 38474\_at Cluster Incl.
- 25 L00972:Human cystathionine-beta-synthase (CBS) mRNA /cds=; 38836\_at Cluster Incl. AL008583:dJ327J16.2 (human ortholog of rat Neuronal Pentr; 39549\_at Cluster Incl. AI743090:wg87a11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32526\_at Cluster Incl. AA149644:zl39d08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32582\_at Cluster Incl. AF001548:Human Chromosome 16 BAC clone CIT987SK-A-815A9 /; 33123\_at Cluster Incl.
- 30 L10379:Human (clone CTG-B45d) mRNA sequence /cds=UNKNOWN ; 1361\_at U40705 /FEATURE= /DEFINITION=HSU40705 Homo sapiens telomeric repeat bind.
- Metagene** 279; 40180\_at Cluster Incl. AB000732:Homo sapiens gene for insulin receptor substrate; 538\_at S53911 /FEATURE= /DEFINITION=S53911 CD34=glycoprotein expressed in lympho; 381\_s\_at Y10055 /FEATURE=cds /DEFINITION=HSP110DEL H.sapiens mRNA for phosphoino.
- 35 **Metagene** 280; 34505\_at Cluster Incl. AL109725:Homo sapiens mRNA full length insert cDNA clone ; 32094\_at Cluster Incl. AB017915:Homo sapiens mRNA for condoroitin 6-sulfotransfe; 35615\_at Cluster Incl. D50914:Human mRNA for KIAA0124 gene, partial cds /cds=(0,; 35648\_at Cluster Incl. AB007902:Homo sapiens KIAA0442 mRNA, partial cds /cds=(0,; 38977\_at Cluster Incl. U89436:Human tyrosyl-tRNA synthetase mRNA, complete cds /; 39796\_at Cluster Incl.

- U11292:Human Ki nuclear autoantigen mRNA, complete cds /c; 32848\_at Cluster Incl.  
 AF020736:Homo sapiens ATPase homolog mRNA, complete cds /; 34883\_at Cluster Incl.  
 D87451:Human mRNA for KIAA0262 gene, complete cds /cds=(6; 35844\_at Cluster Incl.  
 D79206:Homo sapiens gene for ryudocan core protein, exon1; 38822\_at Cluster Incl.
- 5 AB011420:Homo sapiens mRNA for DRAK1, complete cds /cds=(; 39824\_at Cluster Incl.  
 AI391564:tg16b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 758\_at D38128  
 /FEATURE=expanded\_cds /DEFINITION=HUMIP2 Homo sapiens IP gene for .  
**Metagene** 281; 34990\_at Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein  
 (SEB); 38951\_at Cluster Incl. M59217:Human collagen type XIII alpha-1 mRNA, complete cd;  
 10 38952\_s\_at Cluster Incl. M33653:Human (clones HT-[125,133]) alpha-2 type IV coll; 39665\_at  
 Cluster Incl. U33267:Human glycine receptor beta subunit (GLRB) mRNA, c; 40330\_at Cluster Incl.  
 AL050031:Homo sapiens mRNA; cDNA DKFZp566E0224 (from clon; 40746\_at Cluster Incl.  
 L20814:Human glutamate receptor 2 (HBGR2) mRNA, complete ; 32056\_at Cluster Incl.  
 AF035811:Homo sapiens protein H5 (H5) mRNA, complete cds ; 32689\_s\_at Cluster Incl.
- 15 D86096:Human DNA for prostaglandin E receptor EP3 subty; 36044\_at Cluster Incl.  
 AF022912:Homo sapiens cGMP phosphodiesterase delta subuni; 36925\_at Cluster Incl.  
 L26336:Human heat shock protein HSPA2 gene, complete cds ; 40455\_at Cluster Incl.  
 AB020637:Homo sapiens mRNA for KIAA0830 protein, partial ; 40764\_at Cluster Incl.  
 M22632:Human mitochondrial aspartate aminotransferase mRNA; 36990\_at Cluster Incl.
- 20 X04741:Human mRNA for protein gene product (PGP) 9.5 /cds; 38743\_f\_at Cluster Incl.  
 X06409:Human mRNA fragment for activated c-raf-1 (exons; 39160\_at Cluster Incl. D90086:Human  
 pyruvate dehydrogenase (EC 1.2.4.1) beta sub; 1969\_s\_at X77743 /FEATURE=cds  
 /DEFINITION=HSCDKAK H.sapiens CDK activating kinas; 1586\_at M35878  
 /FEATURE=expanded\_cds /DEFINITION=HUMIBP3 Human insulin-like grow; 645\_at L26336
- 25 /FEATURE=cds /DEFINITION=HUMHSPA2A Human heat shock protein HSPA2 .  
**Metagene** 282; 36314\_at Cluster Incl. U04806:Human FLT3/FLK2 ligand mRNA, complete cds  
 /cds=(92; 40646\_at Cluster Incl. U20350:Human G protein-coupled receptor V28 mRNA, complet;  
 41400\_at Cluster Incl. K02581:Human thymidine kinase mRNA, complete cds /cds=(57; 41475\_at  
 Cluster Incl. U91512:Human adhesion molecule ninjurin mRNA, complete cd; 37268\_at Cluster Incl.
- 30 U43368:Human VEGF related factor isoform VRF186 precursor; 37600\_at Cluster Incl.  
 U68186:Human extracellular matrix protein 1 mRNA, complet; 37963\_at Cluster Incl.  
 X52151:Homo sapiens arylsulphatase A mRNA, complete cds /; 39014\_at Cluster Incl.  
 D84239:Homo sapiens mRNA for IgG Fc binding protein, comp; 39326\_at Cluster Incl.  
 Z71460:H.sapiens mRNA for vacuolar-type H(+)-ATPase 115 k; 41725\_at Cluster Incl.
- 35 U89896:Homo sapiens casein kinase I gamma 2 mRNA, complet; 34412\_s\_at Cluster Incl.  
 U59632:Homo sapiens H5 mRNA, partial cds; and platelet ; 36993\_at Cluster Incl. M33210:Human  
 colony stimulating factor 1 receptor (CSF1R); 37360\_at Cluster Incl. U66711:Human Ly-6-related  
 protein (9804) gene, complete c; 39541\_at Cluster Incl. W52003:zc92e10.r1 Homo sapiens cDNA, 5  
 end /clone=IMAGE-; 40906\_at Cluster Incl. AC002310:Human Chromosome 16 BAC clone

- CIT987SK-A-635H12 ; 1771\_s\_at J03278 /FEATURE= /DEFINITION=HUMPDGFRA Human platelet-derived growth f; 1505\_at D00596 /FEATURE=cds /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate; 1242\_at U15655 /FEATURE= /DEFINITION=HSU15655 Human ets domain protein ERF mRNA,; 1087\_at M60459 /FEATURE= /DEFINITION=HUMERYTH Human erythropoietin receptor mRNA.
- 5 **Metagene** 283; 31323\_r\_at Cluster Incl. S83374:glutamate transporter II variant B/HBGT IIB {5 r; 31531\_g\_at Cluster Incl. U89344:Human acetyl-CoA carboxylase (ACC2) mRNA, comple; 31564\_at Cluster Incl. S65761:anti-colorectal carcinoma heavy chain=glycoprotein; 31775\_at Cluster Incl. X65018:H.sapiens mRNA for lung surfactant protein D /cds=; 33027\_at Cluster Incl.
- 10 W27906:39d11 Homo sapiens cDNA /gb=W27906 /gi=1307854 /ug; 32353\_at Cluster Incl. M13143:Nucleotide sequence of the cDNA insert of lambda P; 35004\_at Cluster Incl. U31875:Human Hep27 protein mRNA, complete cds /cds=(433,1; 37486\_f\_at Cluster Incl. U68385:Human Meis1-related protein 2 (MRG2), mRNA, part; 37771\_at Cluster Incl. AB020688:Homo sapiens mRNA for KIAA0881 protein, complete; 38203\_at Cluster Incl.
- 15 U69883:Human calcium-activated potassium channel hSK1 (SK; 40739\_at Cluster Incl. M83670:Human carbonic anhydrase IV mRNA, complete cds /cd; 41614\_at Cluster Incl. AB014608:Homo sapiens mRNA for KIAA0708 protein, partial ; 31835\_at Cluster Incl. M13149:Human histidine-rich glycoprotein mRNA, complete c; 32054\_at Cluster Incl. AF048732:Homo sapiens cyclin T2b mRNA, complete cds /cds=; 36530\_g\_at Cluster Incl.
- 20 AI885381:wl93b01.x1 Homo sapiens cDNA, 3 end /clone=IM; 40769\_r\_at Cluster Incl. D14689:Human mRNA for KIAA0023 gene, complete cds /cds=; 33869\_at Cluster Incl. AL080218:Homo sapiens mRNA; cDNA DKFZp586N1323 (from clon; 36148\_at Cluster Incl. U48437:Human amyloid precursor-like protein 1 mRNA, compl; 39877\_at Cluster Incl. AI832082:td12c04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41491\_s\_at Cluster Incl.
- 25 AB028944:Homo sapiens mRNA for KIAA1021 protein, partia; 898\_s\_at L37360 /FEATURE= /DEFINITION=HUMEFL2 Homo sapiens (clone hEHK1-L) EHK1 ; 740\_at D49394 /FEATURE= /DEFINITION=HUMS5HT3RA Human mRNA for serotonin 5-HT3 re.
- Metagene** 284; 31440\_at Cluster Incl. Z47363:H.sapiens TCF-1 mRNA for T cell factor 1 splice fo; 33685\_at Cluster Incl. AC004755:Homo sapiens chromosome 19, fosmid 37502 /cds=(0; 32918\_at
- 30 Cluster Incl. AL080182:Homo sapiens mRNA; cDNA DKFZp434O151 (from clone; 37332\_r\_at Cluster Incl. U24267:Human pyrroline-5-carboxylate dehydrogenase (P5C; 38461\_at Cluster Incl. X83957:H.sapiens mRNA for nebulin /cds=(440,20449) /gb=X8; 39511\_at Cluster Incl. AB011399:Homo sapiens gene for AF-6, complete cds /cds=(0.
- Metagene** 285; 36745\_at Cluster Incl. AF035308:Homo sapiens clone 23798 and 23825 mRNA
- 35 sequence; 1007\_s\_at U48705 /FEATURE=mRNA /DEFINITION=HSU48705 Human receptor tyrosine kina.
- Metagene** 286; 39283\_at Cluster Incl. X83543:H.sapiens APXL mRNA /cds=(90,4940) /gb=X83543 /gi=; 37213\_at Cluster Incl. X90392:H.sapiens mRNA for DNase X gene /cds=(794,1702) /g; 435\_g\_at X03473 /FEATURE=cds /DEFINITION=HSHIS10G Human gene for histone H1(0) .

- Metagene** 287; 31344\_at Cluster Incl. AF063725:Homo sapiens clone BCSynL38 immunoglobulin lambd; 38683\_s\_at Cluster Incl. AB029008:Homo sapiens mRNA for KIAA1085 protein, partial; 40481\_r\_at Cluster Incl. M14333:Homo sapiens c-syn protooncogene mRNA, complete ; 37721\_at Cluster Incl. U79262:Human deoxyhypusine synthase mRNA, complete cds /c; 39837\_s\_at Cluster
- 5 Incl. AC004877:Homo sapiens PAC clone DJ0751H13 from 7q35-qte; 41314\_at Cluster Incl. AF047042:Homo sapiens citrate synthase mRNA, complete cds; 33182\_at Cluster Incl. AI018523:ou47d07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1397\_at L32976 /FEATURE= /DEFINITION=HUMMLK3A Human protein kinase (MLK-3) mRNA,; 1117\_at L27943 /FEATURE=mRNA /DEFINITION=HUMCYDE Homo sapiens cytidine deaminase; 560\_s\_at
- 10 M63589 /FEATURE=mRNA#5 /DEFINITION=HUMSCL7 Human stem cell leukemia gen. **Metagene** 288; 32452\_at Cluster Incl. X66357:H.sapiens mRNA cdk3 for serine/threonine protein k; 34558\_at Cluster Incl. U30185:Human orphan opioid receptor mRNA, complete cds /c; 35091\_at Cluster Incl. AA706226:ah28a07.s1 Homo sapiens cDNA, 3 end /clone=1240; 35597\_at Cluster Incl. AJ000480:Homo sapiens mRNA for C8FW phosphoprotein /cds=(; 36361\_at Cluster Incl.
- 15 U34051:Human cyclin-dependent kinase 5 activator isoform ; 32909\_at Cluster Incl. U46569:Human aquaporin-5 (AQP5) gene /cds=(0,797) /gb=U46; 37088\_at Cluster Incl. AF059681:Homo sapiens serine/threonine kinase 13 (STK13) ; 37129\_at Cluster Incl. AI936758:wp69b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38254\_at Cluster Incl. AB020689:Homo sapiens mRNA for KIAA0882 protein, partial ; 38716\_at Cluster Incl. AB018330:Homo sapiens mRNA for KIAA0787 protein, partial ; 41190\_at Cluster Incl. U83598:Human death domain receptor 3 soluble form (DDR3) ; 38058\_at Cluster Incl. Z22865:H.sapiens dermatopontin mRNA, complete CDS /cds=(1; 40622\_r\_at Cluster Incl. AL096740:Homo sapiens mRNA; cDNA DKFZp586K2123 (from cl; 40919\_at Cluster Incl. M81830:Human somatostatin receptor isoform 2 (SSTR2) gene; 40935\_at Cluster Incl. W28516:47h7 Homo sapiens cDNA /gb=W28516 /gi=1308464 /ug=; 41817\_g\_at Cluster Incl.
- 25 AL049851:Human DNA sequence from clone 889J22B on chrom; 1118\_at L28175 /FEATURE= /DEFINITION=HUMPERE Homo sapiens prostaglandin E2 recep; 908\_at M14660 /FEATURE=cds /DEFINITION=HUMISG2 Human ISG-54K gene (interferon st; 598\_at M60299 /FEATURE=cds /DEFINITION=HUMCOLII Human alpha-1 collagen type II g; 160038\_s\_at J00268 /FEATURE=gene /DEFINITION=HUMINS02 Human insulin gene: repeti.
- 30 **Metagene** 289; 37127\_at Cluster Incl. AB023143:Homo sapiens mRNA for KIAA0926 protein, complete; 37511\_at Cluster Incl. AB030506:Homo sapiens mRNA for B9, complete cds /cds=(158; 41375\_at Cluster Incl. AJ245416:Homo sapiens mRNA for G7b protein (G7b gene, loc; 35161\_at Cluster Incl. AB020667:Homo sapiens mRNA for KIAA0860 protein, complete; 35206\_at Cluster Incl. AF049105:Homo sapiens centrosomal Nek2-associated protein; 36009\_at Cluster Incl.
- 35 AF091092:Homo sapiens clone 683 unknown mRNA, complete se; 36500\_at Cluster Incl. AF027974:Homo sapiens clone LM1955 H105e3 gene, partial c; 36812\_at Cluster Incl. U92715:Homo sapiens breast cancer antiestrogen resistance; 40225\_at Cluster Incl. D88435:Homo sapiens mRNA for HsGAK, complete cds /cds=(0; 40244\_s\_at Cluster Incl. AI743654:wg41d01.x1 Homo sapiens cDNA, 3 end /clone=IM; 40997\_at Cluster Incl. AI660963:wf20e04.x1 Homo sapiens

- cDNA, 3 end /clone=IMAG.
- Metagene 290**; 31446\_s\_at Cluster Incl. D89501:Human PBI gene, complete cds /cds=(14,418) /gb=D; 32956\_at Cluster Incl. AC002550:Human Chromosome 16 BAC clone CIT987SK-A-101F10 ; 38529\_at Cluster Incl. X68968:H.sapiens mRNA for acetyl-CoA carboxylase /cds=(0,; 33258\_g\_at
- 5 Cluster Incl. D26535:Human gene for dihydrolipoamide succinyltransfer; 34200\_at Cluster Incl. X83378:H.sapiens mRNA for putative chloride channel /cds=; 37262\_at Cluster Incl. AF061324:untitled /cds=(0,4649) /gb=AF061324 /gi=3127174 ; 39715\_at Cluster Incl. W28214:45f7 Homo sapiens cDNA /gb=W28214 /gi=1308297 /ug=; 33852\_at Cluster Incl. M77142:Human polyadenylate binding protein (TIA-1) mRNA, ; 34364\_at Cluster Incl. AF042385:Homo sapiens cyclophilin-33A (CYP-33) mRNA, comp; 39101\_at Cluster Incl. S73840:Homo sapiens type IIA myosin heavy chain mRNA, par; 40242\_at Cluster Incl. L36529:Human (clone N5-4) protein p84 mRNA, complete cds ; 1533\_at U63139 /FEATURE= /DEFINITION=HSU63139 Homo sapiens Rad50 (Rad50) mRNA, c; 871\_s\_at M95585 /FEATURE=mRNA /DEFINITION=HUMHLF Human hepatic leukemia factor (; 639\_s\_at L47345 /FEATURE= /DEFINITION=HUMELONA Homo
- 10 sapiens elongin A mRNA, comp; 394\_at X92106 /FEATURE=cds /DEFINITION=HSBLEO H.sapiens mRNA for bleomycin hydro; 108\_g\_at Z95624 /FEATURE=cds /DEFINITION=HSU237H1 Human DNA sequence from cosmid.
- Metagene 291**; 33943\_at Cluster Incl. L20941:Human ferritin heavy chain mRNA, complete cds /cds; 34530\_at Cluster Incl. W73822:zd52f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-;
- 20 37147\_at Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin p; 38237\_at Cluster Incl. M64099:Human gamma-glutmyl transpeptidase-related protein; 33308\_at Cluster Incl. M15182:Human beta-glucuronidase mRNA, complete cds /cds=(; 34670\_at Cluster Incl. U60899:Human lysosomal alpha-mannosidase (manB) gene /cds; 34689\_at Cluster Incl. AJ243797:Homo sapiens mRNA for deoxyribonuclease III (drn; 36529\_at Cluster Incl.
- 25 AI885381:wl93b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36902\_at Cluster Incl. X61587:H.sapiens rhoG mRNA for GTPase /cds=(129,704) /gb=; 37181\_at Cluster Incl. X76538:H.sapiens Mpv17 mRNA /cds=(29,559) /gb=X76538 /gi=; 38003\_s\_at Cluster Incl. U94905:Human diacylglycerol kinase zeta mRNA, alternati; 39007\_at Cluster Incl. M55593:Human collagenase type IV (CLG4) gene /cds=(289,22; 39062\_at Cluster Incl. AL008726:dJ337O18.2
- 30 (Lysosomal Protective Protein precurs; 39340\_at Cluster Incl. M16424:Human beta-hexosaminidase alpha chain (HEXA) gene ; 39798\_at Cluster Incl. R87876:yo45h01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 41140\_at Cluster Incl. U05875:Human clone pSK1 interferon gamma receptor accesso; 32203\_at Cluster Incl. AA160708:zo72c02.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 34361\_at Cluster Incl. U33849:Human lymphoma proprotein convertase (LPC) mRNA, c; 35770\_at
- 35 Cluster Incl. D16469:Human mRNA for ORF, Xq terminal portion /cds=(1353; 37754\_at Cluster Incl. L13210:Human Mac-2 binding protein mRNA, complete cds /cd; 38487\_at Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,; 39170\_at Cluster Incl. AL049957:Homo sapiens mRNA; cDNA DKFZp564J0323 (from clon; 39918\_at Cluster Incl. AF042379:Homo sapiens spindle pole body protein spc97 hom; 40274\_at Cluster Incl.

- U48213:Human D-site binding protein gene, promoter region; 1976\_s\_at X06292  
 /FEATURE=mRNA /DEFINITION=HSFESFPS Human c-fes/fps proto-oncogene; 1398\_g\_at L32976  
 /FEATURE= /DEFINITION=HUMMLK3A Human protein kinase (MLK-3) mRNA; 906\_at L78440  
 /FEATURE=mRNA /DEFINITION=HUMSTAT4R Homo sapiens STAT4 mRNA, compl; 816\_g\_at  
 5 U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok ; 464\_s\_at  
 U72882 /FEATURE= /DEFINITION=HSU72882 Human interferon-induced leucine ; 384\_at  
 X71874 /FEATURE=cds#1 /DEFINITION=HSPROSCHY H.sapiens genes for proteasom.  
**Metagene** 292; 36835\_at Cluster Incl. U33052:Human lipid-activated, protein kinase PRK2 mRNA,  
 c; 41192\_at Cluster Incl. AF091090:Homo sapiens clone 669 unknown mRNA, complete se;  
 10 37680\_at Cluster Incl. U81607:Homo sapiens gravin mRNA, complete cds /cds=(191,5.  
**Metagene** 293; 34466\_at Cluster Incl. Y12505:H.sapiens mRNA for serotonin receptor 5-HT4B,  
 spli; 1717\_s\_at U45878 /FEATURE= /DEFINITION=HSU45878 Human inhibitor of apoptosis pro.  
**Metagene** 294; 32728\_at Cluster Incl. X81438:H.sapiens mRNA for amphiphysin /cds=(74,2161)  
 /gb=; 33244\_at Cluster Incl. U07223:Human beta2-chimaerin mRNA, complete cds /cds=(444;  
 15 37283\_at Cluster Incl. X82209:H.sapiens MN1 mRNA /cds=(887,4915) /gb=X82209 /gi=;  
 39026\_r\_at Cluster Incl. AF052114:Homo sapiens clone 23887 mRNA sequence /cds=UN; 39350\_at  
 Cluster Incl. U50410:Human heparan sulphate proteoglycan (OCI5) mRNA, c; 34820\_at Cluster Incl.  
 M57399:Human nerve growth factor (HBNF-1) mRNA, complete ; 35324\_at Cluster Incl.  
 AB011538:Homo sapiens mRNA for MEGF5, partial cds /cds=(0; 35354\_at Cluster Incl.  
 20 AL022326:dJ333H23.2.2 (Synaptogyrin 1A (SYNGR1A)) /cds=(4; 37669\_s\_at Cluster Incl.  
 U16799:Human Na,K-ATPase beta-1 subunit mRNA, complete ; 38086\_at Cluster Incl.  
 AB007935:Homo sapiens mRNA for KIAA0466 protein, partial ; 40199\_at Cluster Incl.  
 M97676:Homo sapiens (region 7) homeobox protein (HOX7) mR; 41245\_at Cluster Incl.  
 D49493:Human gene for human bone morphogenetic protein-3b; 32612\_at Cluster Incl.  
 25 X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=; 1290\_g\_at L02321 /FEATURE=  
 /DEFINITION=HUMGSTM5 Human glutathione S-transferase ; 234\_s\_at M57399 /FEATURE=  
 /DEFINITION=HUMHBNF1 Human nerve growth factor (HBNF-1; 214\_at M97676 /FEATURE=  
 /DEFINITION=HUMHOX7 Homo sapiens (region 7) homeobox pro.  
**Metagene** 295; 41866\_s\_at Cluster Incl. AF022728:Homo sapiens beta-dystrobrevin (BDTN)  
 30 mRNA, co; 33382\_at Cluster Incl. M92449:Human LTR mRNA, 3 end of coding region and 3 fla;  
 41583\_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (B;  
 796\_i\_at X66358 /FEATURE=cds#2 /DEFINITION=HSSTHPKB H.sapiens mRNA KKIALRE for  
 s.  
**Metagene** 296; 31477\_at Cluster Incl. L08044:Human intestinal trefoil factor mRNA, complete cds;  
 35 35934\_at Cluster Incl. L19161:Human translation initiation factor eIF-2 gamma su; 36732\_at Cluster  
 Incl. AI004207:ot94g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37139\_at Cluster Incl.  
 AF040628:Homo sapiens ectodysplasin-A (EDA) mRNA, complet; 37472\_at Cluster Incl.  
 U60337:Homo sapiens beta-mannosidase mRNA, complete cds /; 39271\_at Cluster Incl.  
 AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 40512\_at Cluster Incl.

- X51408:Human mRNA for n-chimaerin /cds=(552,1451) /gb=X51; 40835\_at Cluster Incl.  
 AB012922:Homo sapiens MTA1-L1 gene, complete cds /cds=(72; 37686\_s\_at Cluster Incl.  
 Y09008:H.sapiens mRNA for uracil-DNA glycosylase /cds=(; 1272\_at L19161 /FEATURE=  
 /DEFINITION=HUMIEF2G Human translation initiation facto; 577\_at M94250  
 5 /FEATURE=expanded\_cds /DEFINITION=HUMMKXX Human retinoic acid indu.  
**Metagene** 297; 31471\_at Cluster Incl. AL031393:Human DNA sequence from clone 733D15 on  
 chromoso; 31567\_at Cluster Incl. S82769:GABAA receptor gamma 3 subunit [human, fetal brain;  
 38582\_at Cluster Incl. AI961220:wt15b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41404\_at  
 Cluster Incl. AJ010119:Homo sapiens mRNA for Ribosomal protein kinase B; 32622\_at Cluster Incl.  
 10 L36983:Homo sapiens dynamin (DNM) mRNA, complete cds /cds; 33750\_at Cluster Incl.  
 X97198:H.sapiens mRNA for receptor phosphate PCP-2 /cds=(; 34769\_at Cluster Incl.  
 U82535:Human fatty acid amide hydrolase mRNA, complete cd; 35243\_at Cluster Incl.  
 AA535884:nf90d04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38703\_at Cluster Incl.  
 AF005050:Homo sapiens aspartyl aminopeptidase mRNA, compl; 39700\_at Cluster Incl.  
 15 AI961929:wt39g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40821\_at Cluster Incl.  
 M61832:Human S-adenosylhomocysteine hydrolase (AHCY) mRNA; 33438\_at Cluster Incl.  
 AL049981:Homo sapiens mRNA; cDNA DKFZp564D012 (from clone; 36179\_at Cluster Incl.  
 U12779:Human MAP kinase activated protein kinase 2 mRNA, ; 37753\_at Cluster Incl.  
 U66617:Human SWI/SNF complex 60 KDa subunit (BAF60a) mRNA; 40596\_at Cluster Incl.  
 20 U76366:Human Treacher Collins syndrome (TCOF1) mRNA, comp; 40925\_at Cluster Incl.  
 AA554945:ni36d11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1564\_at M63167 /FEATURE=  
 /DEFINITION=HUMRACPC Human rac protein kinase alpha mRN; 1225\_g\_at X66363  
 /FEATURE=cds /DEFINITION=HSSTHPKD H.sapiens mRNA PCTAIRE-1 for ; 247\_s\_at M26856  
 /FEATURE=cds /DEFINITION=HUMCP21OH Human 21-hydroxylase B gene, .  
 25 **Metagene** 298; 32406\_at Cluster Incl. AB020696:Homo sapiens mRNA for KIAA0889 protein,  
 complete; 37476\_at Cluster Incl. AA650210:ns88b12.s1 Homo sapiens cDNA /clone=IMAGE-  
 119068; 38175\_at Cluster Incl. AB014567:Homo sapiens mRNA for KIAA0667 protein, partial ;  
 39925\_at Cluster Incl. M95610:Human alpha 2 type IX collagen (COL9A2) mRNA, part; 40301\_at  
 Cluster Incl. AI703188:wd92g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41055\_at Cluster  
 30 Incl. AB002361:Human mRNA for KIAA0363 gene, partial cds /cds=(; 31875\_at Cluster Incl.  
 AF055024:Homo sapiens clone 24763 mRNA sequence /cds=UNKN; 38625\_g\_at Cluster Incl.  
 AF054506:Homo sapiens erythroid K-CI cotransporter spli; 40848\_g\_at Cluster Incl.  
 AB018293:Homo sapiens mRNA for KIAA0750 protein, comple; 41235\_at Cluster Incl.  
 AL022312:dJ1104E15.2 (activating transcription factor 4 (; 33430\_at Cluster Incl.  
 35 AA143321:zo37d01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36120\_at Cluster Incl.  
 X63657:H.sapiens fvt1 mRNA /cds=(107,1105) /gb=X63657 /gi; 38433\_at Cluster Incl.  
 M76125:Human tyrosine kinase receptor (axl) mRNA, complet; 39175\_at Cluster Incl.  
 D25328:Human mRNA for platelet-type phosphofructokinase, ; 40231\_at Cluster Incl.  
 AI193899:qe80f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1881\_at Oncogene Aml1-Evi-1,



- Fusion Activated ; 1363\_at M87770 /FEATURE= /DEFINITION=HUMKSAMI Human fibroblast growth factor rec.
- Metagene** 299; 34914\_at Cluster Incl. U94778:Human PEST phosphatase interacting protein homolog; 34193\_at Cluster Incl. AF002246:Homo sapiens neural cell adhesion molecule (CALL; 32819\_at Cluster Incl. AJ223352:Homo sapiens mRNA for histone H2B, clone pjG; 33387\_at Cluster Incl. AB007854:Homo sapiens KIAA0394 mRNA, complete cds /cds=(1; 37018\_at Cluster Incl. AI189287:qd05c04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1186\_at D49493 /FEATURE=\_expandedcds /DEFINITION=D49493 Human gene for human bon; 820\_at U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione.
- 10 **Metagene** 300; 33029\_at Cluster Incl. AF038461:Homo sapiens 12R-lipoxygenase mRNA, complete cds; 40815\_g\_at Cluster Incl. L40586:Homo sapiens iduronate-2-sulphatase (IDS) mRNA, ; 37022\_at Cluster Incl. U41344:Human prolargin (PRELP) gene, 5 flanking sequence ; 1663\_at Retinoic Acid Receptor, Gamma 2 .
- Metagene** 301; 31589\_at Cluster Incl. AL031983:dJ271M21.2 (hs6M1-12 (7 transmembrane receptor ( ; 32397\_r\_at Cluster Incl. AA079018:zm94e12.s1 Homo sapiens cDNA, 3 end /clone=IM; 35068\_at Cluster Incl. U88063:Human Agouti related protein (Art) mRNA, complete ; 35104\_r\_at Cluster Incl. M26682:Human T-cell translocation gene 1 (Ttg-1) mRNA, ; 36429\_at Cluster Incl. Y13583:Homo sapiens mRNA for G-protein coupled receptor /; 33469\_r\_at Cluster Incl. X68679:H. sapiens mRNA for DOWN 16 /cds=(23,1018) /gb=X; 37165\_f\_at Cluster Incl. X54534:Human mRNA for erythrocyte membrane protein Rh30; 38882\_r\_at Cluster Incl. AF096870:Homo sapiens estrogen-responsive B box protein; 41034\_s\_at Cluster Incl. U92315:Homo sapiens hydroxysteroid sulfotransferase SUL; 35691\_r\_at Cluster Incl. U18760:Human nuclear factor I (NFI) mRNA, clone AT2, pa; 37629\_at Cluster Incl. M55268:Human casein kinase II alpha subunit mRNA, complet; 39689\_at Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40412\_at Cluster Incl. AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41125\_r\_at Cluster Incl. D45421:Human mRNA for phosphodiesterase I alpha, comple; 36094\_at Cluster Incl. M21984:Human (clone PWHITnT16) skeletal muscle Troponin T ; 36123\_at Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds; 37335\_at Cluster Incl. U41668:Human deoxyguanosine kinase mRNA, complete cds /cd; 39198\_s\_at Cluster Incl.
- 20 W27763:37c8 Homo sapiens cDNA /gb=W27763 /gi=1307711 /u; 39815\_at Cluster Incl. AA883101:am24d05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40883\_at Cluster Incl. W28230:43h12 Homo sapiens cDNA /gb=W28230 /gi=1308178 /ug; 41305\_at Cluster Incl. M95549:Homo sapiens sodium/glucose cotransporter-like pro; 41546\_at Cluster Incl. AI738463:wi32b08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32538\_at Cluster Incl.
- 30 S95936:transferrin [human, liver, mRNA, 2347 nt] /cds=(79; 32594\_at Cluster Incl. AF026291:Homo sapiens chaperonin containing t-complex pol; 2030\_at N95031 /FEATURE= /DEFINITION=N95031 zb32b01.s1 Soares\_parathyroid\_tumor\_ ; 1742\_at S61953 /FEATURE= /DEFINITION=S61953 c-erbB3=receptor tyrosine kinase {a1; 1707\_g\_at U01337 /FEATURE=expanded\_cds /DEFINITION=HSU01337 Human Ser/Thr protei; 1569\_r\_at L42243
- 35

- /FEATURE=exon#3 /DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8; 778\_s\_at D16827  
 /FEATURE=cds /DEFINITION=HUMSSTR5 Human gene for fifth somatosta; 441\_s\_at X13967  
 /FEATURE=cds /DEFINITION=HSLIF Human mRNA for leukaemia inhibito; 403\_s\_at X69878  
 /FEATURE=cds /DEFINITION=HSFLT4X H.sapiens Flt4 mRNA for transme; 225\_at M31328
- 5 /FEATURE=mRNA /DEFINITION=HUMGNBPB3 Human guanine nucleotide-bind.  
**Metagene** 302; 31608\_g\_at Cluster Incl. AJ002428:Homo sapiens VDAC1 pseudogene /cds=(0,853)  
 /gb; 31682\_s\_at Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), compl;  
 31951\_s\_at Cluster Incl. Z48501:H.sapiens mRNA for polyadenylate binding protein; 34648\_at  
 Cluster Incl. Z12830:H.sapiens mRNA for SSR alpha subunit /cds=(29,889); 35099\_at Cluster Incl.
- 10 AF019225:Homo sapiens apolipoprotein L mRNA, complete cds; 36383\_at Cluster Incl.  
 M17254:Human erg2 gene encoding erg2 protein, complete cd; 32892\_at Cluster Incl.  
 X85106:H.sapiens mRNA for ribosomal S6 kinase /cds=(174,2; 34017\_s\_at Cluster Incl.  
 AF022853:untitled /cds=(0,4370) /gb=AF022853 /gi=258577; 35967\_at Cluster Incl.  
 M69238:Human aryl hydrocarbon receptor nuclear translocat; 38580\_at Cluster Incl. U43083:Human
- 15 G alpha-q (Gaq) mRNA, complete cds /cds=(220; 41390\_at Cluster Incl. X69086:H.sapiens mRNA  
 for utrophin /cds=(0,10301) /gb=X69; 37531\_at Cluster Incl. D86965:Human mRNA for KIAA0210  
 gene, complete cds /cds=(1; 40096\_at Cluster Incl. D14710:Human mRNA for ATP synthase alpha  
 subunit, complet; 40440\_at Cluster Incl. AL080119:Homo sapiens mRNA; cDNA DKFZp564M2423  
 (from clon; 41144\_g\_at Cluster Incl. U12022:Human calmodulin (CALM1) gene /cds=(199,648)
- 20 /gb; 33372\_at Cluster Incl. AI189226:qd04h11.x1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 34339\_at Cluster Incl. AB009282:Homo sapiens mRNA for cytochrome b5, partial cds; 34855\_at  
 Cluster Incl. X76770:H.sapiens PAP mRNA /cds=UNKNOWN /gb=X76770 /gi=556; 35784\_at  
 Cluster Incl. U64520:Human synaptobrevin-3 mRNA, complete cds /cds=(24,; 40618\_at Cluster Incl.  
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- 25 /DEFINITION=HSU34994 Homo sapiens DNA dependent prote; 1920\_s\_at X77794  
 /FEATURE=cds /DEFINITION=HSCYCG1 H.sapiens mRNA for cyclin G1 ; 1839\_at Ras-Like  
 Protein Tc4 ; 1844\_s\_at L05624 /FEATURE= /DEFINITION=HUMMKK Homo sapiens MAP  
 kinase kinase mRN; 1824\_s\_at J05614 /FEATURE=mRNA /DEFINITION=HUMPCNAPRM  
 Human proliferating cell n; 622\_at M28212 /FEATURE= /DEFINITION=HUMRAB6A Homo
- 30 sapiens GTP-binding protein (R; 504\_at U39318 /FEATURE= /DEFINITION=HSU39318 Human  
 E2 ubiquitin conjugating enzy; 475\_at U50062 /FEATURE= /DEFINITION=HSU50062 Homo  
 sapiens RIP protein kinase mRN; 466\_at U77948 /FEATURE= /DEFINITION=HSU77948 Human  
 Bruton s tyrosine kinase-asso; 398\_at X98743 /FEATURE=cds /DEFINITION=HSRNAHELC  
 H.sapiens mRNA for RNA helicase; 353\_at D30037 /FEATURE= /DEFINITION=HUMPITPB
- 35 Human mRNA for phosphatidylinositol; 263\_g\_at M21154 /FEATURE=mRNA  
 /DEFINITION=HUMAMD Human S-adenosylmethionine deca; 228\_at M35416  
 /FEATURE=mRNA /DEFINITION=HUMRALBA Human GTP-binding protein (RALB; 167\_at  
 U49436 /FEATURE= /DEFINITION=HSU49436 Human translation initiation factor.  
**Metagene** 303; 34525\_at Cluster Incl. AB018563:Homo sapiens TML1 mRNA, complete cds

- /cds=(30,41; 38578\_at Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA; 38859\_at Cluster Incl. AL080141:Homo sapiens mRNA; cDNA DKFZp434M183 (from clone; 40396\_at Cluster Incl. U49395:Human ionotropic ATP receptor P2X5a mRNA, complete; 38968\_at Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, compl; 38760\_f\_at Cluster
- 5 Incl. U90546:Human butyrophilin (BTF4) mRNA, complete cds /cd; 38786\_at Cluster Incl. AL079279:Homo sapiens mRNA full length insert cDNA clone ; 406\_at X53587 /FEATURE=mRNA /DEFINITION=HSINTB4R Human mRNA for integrin beta 4 .  
**Metagene** 304; 35067\_at Cluster Incl. AI925946:wh12f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35450\_s\_at Cluster Incl. AF015553:Homo sapiens TFII-I protein (TFII-I) mRNA, com; 35949\_at Cluster Incl. AB018317:Homo sapiens mRNA for KIAA0774 protein, partial ; 36258\_at Cluster Incl. Y07512:Human mRNA for type I beta cGMP-dependent protein ; 36791\_g\_at Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1; 41454\_at Cluster Incl. W27949:39h3 Homo sapiens cDNA /gb=W27949 /gi=1307897 /ug=; 31867\_at Cluster Incl. AF052174:Homo sapiens clone 24630 mRNA sequence /cds=UNKN; 32078\_at Cluster Incl.
- 15 D42055:Human mRNA for KIAA0093 gene, partial cds /cds=(0; 33800\_at Cluster Incl. AF036927:Homo sapiens adenylyl cyclase type IX mRNA, comp; 34202\_at Cluster Incl. AL050071:Homo sapiens mRNA; cDNA DKFZp566B0846 (from clon; 34719\_at Cluster Incl. AB020645:Homo sapiens mRNA for KIAA0838 protein, complete; 36029\_at Cluster Incl. U57911:Human fetal brain (239FB) mRNA, from the WAGR regi; 36894\_at Cluster Incl.
- 20 AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,84; 37225\_at Cluster Incl. D79994:Human mRNA for KIAA0172 gene, partial cds /cds=(0; 37253\_at Cluster Incl. X92493:H.sapiens mRNA for STM-7 protein /cds=(419,2041) /; 37981\_at Cluster Incl. D17530:Homo sapiens mRNA for drebrin E, complete cds /cds; 38656\_s\_at Cluster Incl. W27939:39g3 Homo sapiens cDNA /gb=W27939 /gi=1307887 /u; 39038\_at Cluster Incl.
- 25 AF093118:Homo sapiens UP50 mRNA, complete cds /cds=(168,1; 39388\_at Cluster Incl. AA902713:ok71f11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40064\_at Cluster Incl. AB011121:Homo sapiens mRNA for KIAA0549 protein, partial ; 41744\_at Cluster Incl. AF070533:Homo sapiens clone 24619 mRNA sequence /cds=UNKN; 33404\_at Cluster Incl. U02390:Human adenylyl cyclase-associated protein homolog ; 33405\_at Cluster Incl.
- 30 N90755:zb22c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 34356\_at Cluster Incl. U52960:Human RNA polymerase II complex component SRB7 mRN; 34803\_at Cluster Incl. AF022789:Homo sapiens ubiquitin hydrolyzing enzyme I (UBH; 35831\_at Cluster Incl. AB014511:Homo sapiens mRNA for KIAA0611 protein, partial ; 37655\_at Cluster Incl. X75304:H.sapiens giantin mRNA /cds=(126,9905) /gb=X75304 ; 38032\_at Cluster Incl.
- 35 AB018279:Homo sapiens mRNA for KIAA0736 protein, complete; 38465\_at Cluster Incl. M37721:Human peptidylglycine alpha-amidating monooxygenas; 38839\_at Cluster Incl. AL096719:Homo sapiens mRNA; cDNA DKFZp566N043 (from clone; 38840\_s\_at Cluster Incl. L10678:Human profilin II mRNA, complete cds /cds=(13,43; 39178\_at Cluster Incl. L10333:Homo sapiens neuroendocrine-specific protein A (NS; 39544\_at Cluster Incl. AB002351:Human mRNA for

- KIAA0353 gene, partial cds /cds=(; 40966\_at Cluster Incl. AF099989:Homo sapiens Ste-20 related kinase SPAK mRNA, co; 32531\_at Cluster Incl. X52947:Human mRNA for cardiac gap junction protein /cds=(.
- Metagene** 305; 31667\_r\_at Cluster Incl. W27698:36f8 Homo sapiens cDNA /gb=W27698
- 5 /gi=1307664 /u; 31671\_at Cluster Incl. D82351:Human retropseudogene MSSP-1 DNA, complete cds /cd; 32336\_at Cluster Incl. X05236:Human fibroblast mRNA for aldolase A /cds=(146,124; 32929\_at Cluster Incl. R56605:yg94a11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 38921\_at Cluster Incl. U86078:Homo sapiens calmodulin-stimulated phosphodiesterase; 39276\_g\_at Cluster Incl. M76558:Human neuronal DHP-sensitive, voltage-dependent; 33311\_at Cluster Incl.
- 10 U05569:Human alphaA-crystallin (CRYA1) mRNA, complete cds; 36008\_at Cluster Incl. AF041434:Homo sapiens potentially prenylated protein tyro; 37267\_at Cluster Incl. Z50115:H.sapiens mRNA for thimet oligopeptidase (metallop; 38726\_at Cluster Incl. W80399:zh49e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 38997\_at Cluster Incl. X96924:H.sapiens gene encoding mitochondrial citrate tran; 39406\_at Cluster Incl. U50330:Human
- 15 procollagen C-proteinase (pCP-2) mRNA, compl; 40116\_at Cluster Incl. X15573:Human liver-type 1-phosphofructokinase (PFKL) mRNA; 32844\_at Cluster Incl. AF104913:Homo sapiens eukaryotic protein synthesis initia; 33913\_at Cluster Incl. M33509:Human HLA-B-associated transcript 2 (BAT2) mRNA, c; 37719\_at Cluster Incl. AF070539:Homo sapiens clone 24433 myelodysplasia/myeloid ; 41310\_f\_at Cluster Incl. X12794:Human v-erbA related ear-2 gene
- 20 /cds=(0,1211) /g; 33129\_at Cluster Incl. N80906:zb07c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 1444\_at AB003177 /FEATURE= /DEFINITION=AB003177 Homo sapiens mRNA for proteasome; 1395\_at L25081 /FEATURE= /DEFINITION=HUMRHOCa Homo sapiens GTPase (rhoC) mRNA, c; 1306\_at D12686 /FEATURE= /DEFINITION=HUMEIF4G Human mRNA for eukaryotic initiati; 1312\_at D38047 /FEATURE= /DEFINITION=HUMPSP31 Human
- 25 mRNA for 26S proteasome subu; 884\_at M59911 /FEATURE= /DEFINITION=HUMINTA3A Human integrin alpha-3 chain mRNA,; 848\_at U19261 /FEATURE= /DEFINITION=HSU19261 Homo sapiens Epstein-Barr virus-ind; 806\_at U56998 /FEATURE= /DEFINITION=HSU56998 Human putative serine/threonine pro.
- Metagene** 306; 38177\_at Cluster Incl. AJ001015:Homo sapiens mRNA encoding RAMP2
- 30 /cds=(68,595) /; 31904\_at Cluster Incl. U67733:Human cGMP-stimulated 3,5 -cyclic nucleotide phosph; 33295\_at Cluster Incl. X85785:H.sapiens DARC gene /cds=(494,1510) /gb=X85785 /gi; 33790\_at Cluster Incl. AI720438:as81g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34235\_at Cluster Incl. AB018301:Homo sapiens mRNA for KIAA0758 protein, partial ; 35147\_at Cluster Incl. AB002360:Human mRNA for KIAA0362 gene, partial cds /cds=(; 37961\_at Cluster Incl.
- 35 U90907:Human clone 23907 mRNA sequence /cds=UNKNOWN /gb=U; 36174\_at Cluster Incl. X70326:H.sapiens MacMarcks mRNA /cds=(13,600) /gb=X70326 ; 37042\_at Cluster Incl. U09577:Homo sapiens lysosomal hyaluronidase (LUCA2/HYAL2); 37394\_at Cluster Incl. J03507:Human complement protein component C7 mRNA, comple; 37397\_at Cluster Incl. L34657:Homo sapiens platelet/endothelial cell adhesion mo; 37398\_at Cluster Incl.

- AA100961:zn40b06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38453\_at Cluster Incl.  
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 AB018310:Homo sapiens mRNA for KIAA0767 protein, partial ; 41266\_at Cluster Incl.  
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 10 /cds=UNKNOWN /gb=U; 33577\_at Cluster Incl. AC004079:Homo sapiens PAC clone DJ0167F23  
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 cds /cds=(; 40354\_at Cluster Incl. AB023421:Homo sapiens mRNA for heat shock protein apg-1, ;  
 41049\_at Cluster Incl. S62539:insulin receptor substrate-1 [human, skeletal musc; 41476\_at Cluster  
 15 Incl. N36926:yy38e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 41649\_at Cluster Incl.  
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 D13635:Human mRNA for KIAA0010 gene, complete cds /cds=(3; 34180\_at Cluster Incl.  
 AB002292:Human mRNA for KIAA0294 gene, complete cds /cds=; 35202\_at Cluster Incl.  
 20 AF025654:Homo sapiens mRNA capping enzyme (HCE) mRNA, com; 35697\_at Cluster Incl.  
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 AF000416:Homo sapiens EXT-like protein 2 (EXTL2) mRNA, co; 36544\_at Cluster Incl.  
 AF038193:Homo sapiens clone 23608 mRNA sequence /cds=UNKN; 36554\_at Cluster Incl.  
 25 Y15521:Homo sapiens ASMTL gene /cds=(0,1889) /gb=Y15521 /; 36864\_at Cluster Incl.  
 AJ001625:Homo sapiens mRNA for Pex3 protein /cds=(63,1184; 38335\_at Cluster Incl.  
 U88620:Human 8-hydroxyguanine glycosylase (hMMH) mRNA, co; 38692\_at Cluster Incl.  
 AF045451:Homo sapiens transcriptional regulatory protein ; 39380\_at Cluster Incl.  
 AB014597:Homo sapiens mRNA for KIAA0697 protein, partial ; 39405\_at Cluster Incl.  
 30 D87455:Human mRNA for KIAA0266 gene, complete cds /cds=(7; 39701\_at Cluster Incl.  
 AB006625:Homo sapiens mRNA for KIAA0287 gene, partial cds; 40111\_g\_at Cluster Incl.  
 U49283:Human NAD<sup>+</sup>-specific isocitrate dehydrogenase bet; 40838\_at Cluster Incl.  
 AB011102:Homo sapiens mRNA for KIAA0530 protein, partial ; 32842\_at Cluster Incl.  
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 35 AL049381:Homo sapiens mRNA; cDNA DKFZp586J2118 (from clon; 33357\_at Cluster Incl.  
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- U41654:Human adenovirus protein E3-14.7k interacting prot; 35787\_at Cluster Incl.
- AI986201:wr81a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36196\_at Cluster Incl.
- U24183:Human phosphofructokinase (PFKM) mRNA, complete cd; 40537\_at Cluster Incl.
- AB018284:Homo sapiens mRNA for KIAA0741 protein, complete; 41338\_at Cluster Incl.
- 5 AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33186\_i\_at Cluster Incl.
- AL046961:DKFZp586J0417\_r1 Homo sapiens cDNA, 5 end /cl; 1828\_s\_at M27968
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- /FEATURE=mRNA /DEFINITION=HSPOLAR Human mRNA for DNA polymerase al; 202\_at
- M65217 /FEATURE= /DEFINITION=HUMHSF2 Human heat shock factor 2 (HSF2) mRNA; 185\_at
- 10 U04840 /FEATURE= /DEFINITION=HSU04840 Human onconeural ventral antigen-1 .
- Metagene** 308; 31979\_at Cluster Incl. D49818:Homo sapiens mRNA for 6-phosphofructo-2-kinase/fru; 34041\_at Cluster Incl. U83171:Human macrophage-derived chemokine precursor (MDC); 39977\_at Cluster Incl. U69274:Human zinc finger protein mRNA, complete cds /cds=;
- 41752\_at Cluster Incl. W28190:43c6 Homo sapiens cDNA /gb=W28190 /gi=1308138 /ug=;
- 15 35302\_at Cluster Incl. AJ132712:Homo sapiens mRNA for tip associating protein (T; 40944\_at Cluster Incl. AF028008:Homo sapiens SP1-like zinc finger transcription ; 1909\_at M14745
- /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA .
- Metagene** 309; 36393\_at Cluster Incl. U43843:Human h-neuro-d4 protein mRNA, complete cds /cds=;
- 36310\_at Cluster Incl. X86570:Homo sapiens mRNA for acidic hair keratin 1 /cds=;
- 20 33707\_at Cluster Incl. AF058921:Homo sapiens cytosolic phospholipase A2-gamma mR; 37186\_s\_at Cluster Incl. U11863:Human clone HP-DAO2 diamine oxidase, copper/topa; 37226\_at Cluster Incl. U15172:Homo sapiens BCL2/adenovirus E1B 19kD-interacting ; 41130\_at Cluster Incl. Y08698:H.sapiens mRNA for RanBP3 (59 kDa) /cds=(20,1708) ; 34847\_s\_at Cluster Incl. AF112471:Homo sapiens calcium/calmodulin-dependent prot; 36184\_at Cluster Incl. L06419:Homo sapiens lysyl hydroxylase (PLOD) mRNA, comple; 40219\_at Cluster Incl. AI796944:we25b03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 847\_at U17969 /FEATURE=exons#1-6 /DEFINITION=HSU17969 Human initiation factor eI.
- Metagene** 310; 32394\_s\_at Cluster Incl. X55954:Human mRNA for HL23 ribosomal protein homologue ; 33458\_r\_at Cluster Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IM;
- 30 37119\_at Cluster Incl. AL035296:H.sapiens gene from PAC 560B9 /cds=(139,564) /gb; 39260\_at Cluster Incl. U59185:Human putative monocarboxylate transporter (MCT) m; 31850\_at Cluster Incl. M90656:Human gamma-glutamylcysteine synthetase (GCS) mRNA; 31869\_at Cluster Incl. AB014540:Homo sapiens mRNA for KIAA0640 protein, partial ; 32624\_at Cluster Incl. AL050050:Homo sapiens mRNA; cDNA DKFZp566D133 (from clone; 34657\_at Cluster Incl.
- 35 AB014529:Homo sapiens mRNA for KIAA0629 protein, partial ; 34688\_at Cluster Incl. AB029001:Homo sapiens mRNA for KIAA1078 protein, partial ; 34752\_at Cluster Incl. AL080111:Homo sapiens mRNA; cDNA DKFZp586G2222 (from clon; 34753\_at Cluster Incl. X92396:H.sapiens mRNA for novel gene in Xq28 region /cds=; 34761\_r\_at Cluster Incl. U41766:Human metalloprotease/disintegrin/cysteine-rich ; 34763\_at Cluster Incl. AF020043:Homo

- sapiens chromosome-associated polypeptide (; 35187\_at Cluster Incl. AL080216:Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone; 36913\_at Cluster Incl. U75679:Human histone stem-loop binding protein (SLBP) mRNA; 37638\_at Cluster Incl. D50857:Human DOCK180 protein mRNA, complete cds /cds=(23,; 37962\_r\_at Cluster Incl. D63506:Homo sapiens mRNA for unc-
- 5 18homologue, complete ; 37973\_at Cluster Incl. AB018256:Homo sapiens mRNA for KIAA0713 protein, partial ; 37994\_at Cluster Incl. X69962:H.sapiens FMR-1 mRNA /cds=(219,2117) /gb=X69962 /g; 38654\_at Cluster Incl. X65488:H.sapiens U21.1 mRNA /cds=(41,2461) /gb=X65488 /gi; 38992\_at Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=3; 38993\_r\_at Cluster Incl. W27522:32a12 Homo sapiens cDNA /gb=W27522 /gi=1307326 /; 39028\_at
- 10 Cluster Incl. Y08890:H.sapiens mRNA for Ran\_GTP binding protein 5 /cds=; 39046\_at Cluster Incl. AL049324:Homo sapiens mRNA; cDNA DKFZp564D246 (from clone; 39071\_at Cluster Incl. M14648:Human cell adhesion protein (vitronectin) receptor; 39344\_at Cluster Incl. U53209:Human transformer-2 alpha (htra-2 alpha) mRNA, com; 39389\_at Cluster Incl. M38690:Human CD9 antigen mRNA, complete cds /cds=(51,737); 39714\_at Cluster Incl. AF042081:Homo sapiens SH3 domain
- 15 binding glutamic acid-ri; 40048\_at Cluster Incl. D43951:Human mRNA for KIAA0099 gene, complete cds /cds=(5; 40125\_at Cluster Incl. L10284:Homo sapiens integral membrane protein, calnexin, ; 40509\_at Cluster Incl. J04058:Human electron transfer flavoprotein alpha-subunit; 41132\_r\_at Cluster Incl. U01923:Human BTK region clone ftp-3 mRNA /cds=UNKNOWN /; 41738\_at Cluster Incl. M64110:Human caldesmon mRNA, complete cds /cds=(111,1727); 32175\_at
- 20 Cluster Incl. S72008:hCDC10=CDC10 homolog [human, fetal lung, mRNA, 231; 32219\_at Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1; 32778\_at Cluster Incl. D26070:Human mRNA for type 1 inositol 1,4,5-trisphosphate; 32803\_at Cluster Incl. AF104398:Homo sapiens cornichon mRNA, complete cds /cds=(; 32841\_at Cluster Incl. U19765:Human nucleic acid binding protein gene, complete ; 32850\_at Cluster Incl.
- 25 Z25535:H.sapiens mRNA for nuclear pore complex protein hn; 33443\_at Cluster Incl. Z99129:Human DNA sequence from clone 425C14 on chromosome; 33859\_at Cluster Incl. U96915:Homo sapiens sin3 associated polypeptide p18 (SAP1; 34306\_at Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1; 34326\_at Cluster Incl. X82103:H.sapiens mRNA for beta-COP /cds=(0,911) /gb=X8210; 34329\_at Cluster Incl.
- 30 N25547:yx76e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 34368\_at Cluster Incl. U31814:Human transcriptional regulator homolog RPD3 mRNA,; 34402\_at Cluster Incl. AB024327:Homo sapiens pt-wd mRNA for WD-40 repeat protein; 34793\_s\_at Cluster Incl. M22299:Human T-plastin polypeptide mRNA, complete cds, ; 34814\_at Cluster Incl. AL041443:DKFZp434D0717\_s1 Homo sapiens cDNA, 3 end /clone; 34850\_at Cluster Incl.
- 35 AB017644:Homo sapiens mRNA for ubiquitin-conjugating enzy; 34887\_at Cluster Incl. N92548:zb29g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35747\_at Cluster Incl. AF035287:Homo sapiens clone 23742 mRNA, partial cds /cds=; 35754\_at Cluster Incl. L40391:Homo sapiens (clone s153) mRNA fragment /cds=UNKNO; 35790\_at Cluster Incl. AF054179:Homo sapiens H beta 58 homolog mRNA, complete cd; 35814\_at Cluster Incl.

- AF064603:Homo sapiens GA17 protein mRNA, complete cds /cd; 36107\_at Cluster Incl.  
 AA845575:ak04e09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36112\_r\_at Cluster Incl.  
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 U29185:Homo sapiens prion protein (PrP) gene, complete ; 36163\_at Cluster Incl. L13761:Human  
 5 dihydrolipoamide dehydrogenase gene /cds=(20; 36606\_at Cluster Incl. X51405:Human mRNA for  
 carboxypeptidase E (EC 3.4.17.10) /; 36631\_at Cluster Incl. D49396:Human mRNA for  
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 protein mRNA /cds=(155,1180) /gb=; 36688\_at Cluster Incl. U11313:Human sterol carrier protein-  
 X/sterol carrier prot; 36971\_at Cluster Incl. D87446:Human mRNA for KIAA0257 gene, partial cds  
 10 /cds=(0; 36980\_at Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,10;  
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 36998\_s\_at Cluster Incl. Y08262:H.sapiens mRNA for SCA2 protein /cds=(0,2746) /g; 37000\_at  
 Cluster Incl. AL035304:H.sapiens gene from PAC 295C6, similar to rat PO; 37358\_at Cluster Incl.  
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 15 M82809:Human annexin IV (ANX4) mRNA, complete cds /cds=(7; 37696\_at Cluster Incl.  
 L06328:Human voltage-dependent anion channel isoform 2 (V; 37708\_r\_at Cluster Incl.  
 M81118:Human alcohol dehydrogenase chi polypeptide (ADH; 37731\_at Cluster Incl.  
 Z29064:H.sapiens AF-1p mRNA /cds=(92,2782) /gb=Z29064 /gi; 37740\_r\_at Cluster Incl.  
 J02683:Human ADP/ATP carrier protein mRNA, complete cds; 38079\_at Cluster Incl.  
 20 AL049367:Homo sapiens mRNA; cDNA DKFZp586B0918 (from clon; 38106\_at Cluster Incl.  
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 Z48042:H.sapiens mRNA encoding GPI-anchored protein p137 ; 41257\_at Cluster Incl.  
 D16217:Human mRNA for calpastatin, complete cds /cds=(162; 32517\_at Cluster Incl.  
 25 AB028639:Homo sapiens CAPN7 mRNA for PalBH, complete cds ; 1848\_at M22995 /FEATURE=  
 /DEFINITION=HUMKREV1A Human ras-related protein (Krev-1; 1659\_s\_at D78132 /FEATURE=  
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 36054\_at Cluster Incl. AB020699:Homo sapiens mRNA for KIAA0892 protein, partial ; 39432\_at  
 35 Cluster Incl. AF038662:Homo sapiens chromosome 3q13 beta-1,4-galactosyl; 40424\_at Cluster Incl.  
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 L40586:Homo sapiens iduronate-2-sulphatase (IDS) mRNA, co; 41201\_at Cluster Incl.  
 AF000430:Homo sapiens dynamin-like protein mRNA, complete; 41766\_at Cluster Incl.  
 D55649:Human mRNA for alpha mannosidase II isozyme, compl; 35781\_g\_at Cluster Incl.



- AF035292:Homo sapiens clone 23584 mRNA sequence /cds=UN; 36659\_at Cluster Incl.  
 X05610:Human mRNA for type IV collagen alpha (2) chain /c; 40957\_at Cluster Incl.  
 D63881:Human mRNA for KIAA0160 gene, partial cds /cds=(0,; 41788\_i\_at Cluster Incl.  
 AB014569:Homo sapiens mRNA for KIAA0669 protein, comple.
- 5 **Metagene** 312; 31506\_s\_at Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /c;  
 38585\_at Cluster Incl. M91036:H.sapiens G-gamma globin and A-gamma globin genes,; 39208\_i\_at  
 Cluster Incl. M54995:Human connective tissue activation peptide III m; 41096\_at Cluster Incl.  
 AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41617\_at Cluster Incl.  
 AI349593:qp73f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG.
- 10 **Metagene** 313; 41858\_at Cluster Incl. AL049261:Homo sapiens mRNA; cDNA DKFZp564E053  
 (from clone; 36036\_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /cds;  
 36081\_s\_at Cluster Incl. AB004848:Homo sapiens mRNA expressed in placenta, clone; 38621\_at  
 Cluster Incl. AJ012008:Homo sapiens genes encoding RNCC protein, DDAH p; 37716\_at Cluster  
 Incl. X05323:Human MRC OX-2 gene signal sequence /cds=(0,824) /; 39103\_s\_at Cluster Incl.
- 15 H98552:yv97h03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 589\_at M32313  
 /FEATURE=mRNA /DEFINITION=HUM5AR Human steroid 5-alpha-reductase m.  
**Metagene** 314; 35071\_s\_at Cluster Incl. AF042377:Homo sapiens GDP-mannose 4,6 dehydratase  
 mRNA,; 32313\_at Cluster Incl. M12125:Human fibroblast muscle-type tropomyosin mRNA, com;  
 32314\_g\_at Cluster Incl. M12125:Human fibroblast muscle-type tropomyosin mRNA, c; 34428\_at
- 20 Cluster Incl. D50312:Human mRNA for uKATP-1, complete cds /cds=(270,154; 38881\_i\_at Cluster  
 Incl. AF096870:Homo sapiens estrogen-responsive B box protein; 40039\_g\_at Cluster Incl.  
 W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41396\_at Cluster Incl.  
 AB006629:Homo sapiens mRNA for KIAA0291 gene, partial cds; 41412\_at Cluster Incl.  
 AL023553:dJ347H13.2 (human ortholog of rat Pippin) /cds=(; 31830\_s\_at Cluster Incl.
- 25 Y13492:Homo sapiens mRNA for smoothelin-B /cds=(219,297; 31831\_at Cluster Incl.  
 AI888563:wn33a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32104\_i\_at Cluster Incl.  
 U66063:Homo sapiens calcium/calmodulin-dependent protei; 32133\_at Cluster Incl.  
 AB011161:Homo sapiens mRNA for KIAA0589 protein, partial ; 32625\_at Cluster Incl.  
 X15357:Human mRNA for natriuretic peptide receptor (ANP-A; 34724\_at Cluster Incl.
- 30 AI670100:wc11g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35146\_at Cluster Incl.  
 AB007836:Homo sapiens mRNA for Hic-5, partial cds /cds=(0; 35239\_at Cluster Incl.  
 X86810:Homo sapiens EDMD gene /cds=(110,874) /gb=X86810 /; 36471\_f\_at Cluster Incl.  
 U46746:Human dystrobrevin-epsilon mRNA, complete cds /c; 36892\_at Cluster Incl.  
 AF032108:Homo sapiens integrin alpha-7 mRNA, complete cds; 36900\_at Cluster Incl.
- 35 U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(; 37256\_at Cluster Incl.  
 AI829890:wj47a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37567\_at Cluster Incl.  
 X98834:H.sapiens mRNA for zinc finger protein, Hsa12 /cds; 38338\_at Cluster Incl.  
 AI201108:qf69g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40109\_at Cluster Incl.  
 J03161:Human serum response factor (SRF) mRNA, complete c; 33883\_at Cluster Incl.

- AB001466:Homo sapiens mRNA for Efs1, complete cds /cds=(6; 33912\_at Cluster Incl.  
 Y13834:Homo sapiens mRNA for farnesylated-proteins conver; 34320\_at Cluster Incl.  
 AL050224:Homo sapiens mRNA; cDNA DKFZp586L2123 (from clone; 34802\_at Cluster Incl.  
 X15882:Human mRNA for collagen VI alpha-2 C-terminal glob; 35336\_at Cluster Incl.
- 5 AL021707:Human DNA sequence from clone 508I15 on chromoso; 35846\_at Cluster Incl.  
 M24899:Human triiodothyronine (ear7) mRNA, complete cds /; 36156\_at Cluster Incl.  
 U41518:Human channel-like integral membrane protein (AQP-; 37300\_at Cluster Incl.  
 AB002323:Human mRNA for KIAA0325 gene, partial cds /cds=(; 38437\_at Cluster Incl.  
 X80199:H.sapiens MLN51 mRNA /cds=(233,1837) /gb=X80199 /g; 39108\_at Cluster Incl.
- 10 U22526:Human 2,3-oxidosqualene-lanosterol cyclase mRNA, c; 39145\_at Cluster Incl.  
 J02854:Human 20-kDa myosin light chain (MLC-2) mRNA, comp; 39548\_at Cluster Incl.  
 U77970:Human neuronal PAS2 (NPAS2) mRNA, complete cds /cd; 40174\_at Cluster Incl.  
 AF026004:Homo sapiens chloride channel protein (CIC-2) mR; 40562\_at Cluster Incl.  
 M69013:Human guanine nucleotide-binding regulatory protei; 41282\_s\_at Cluster Incl.
- 15 AA194159:zr37h01.r1 Homo sapiens cDNA, 5 end /clone=IM; 823\_at U84487 /FEATURE=  
 /DEFINITION=HSU84487 Human CX3C chemokine precursor, mRN; 361\_at Y13620 /FEATURE=  
 /DEFINITION=HSRNABCL9 Homo sapiens mRNA for BCL9 gene .  
**Metagene** 315; 33697\_at Cluster Incl. Y12851:Homo sapiens P2X7 gene, exon 1 and joined CDS  
 /cds; 32329\_at Cluster Incl. X99142:H.sapiens mRNA for hair keratin, hHb6 /cds=(0,1451; 37796\_at
- 20 Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(0,24; 38132\_at Cluster  
 Incl. M88338:Human serum constituent protein (MSE55) mRNA, comp; 40687\_at Cluster Incl.  
 M96789:Homo sapiens connexin 37 (GJA4) mRNA, complete cds; 40733\_f\_at Cluster Incl.  
 D89377:Homo sapiens mRNA for MSX-2, complete cds /cds=(; 41428\_at Cluster Incl.  
 AF104942:Homo sapiens ABC transporter MOAT-C (MOAT-C) mRN; 41856\_at Cluster Incl.
- 25 AL049370:Homo sapiens mRNA; cDNA DKFZp586D0918 (from clone; 34294\_at Cluster Incl.  
 AL041493:DKFZp434F2117\_s1 Homo sapiens cDNA, 3 end /clone; 37281\_at Cluster Incl.  
 D87071:Human mRNA for KIAA0233 gene, complete cds /cds=(2; 37573\_at Cluster Incl.  
 AF007150:Homo sapiens clone 23767 and 23782 mRNA sequence; 41180\_i\_at Cluster Incl.  
 U49785:Human D-dopachrome tautomerase mRNA, complete cd; 32201\_at Cluster Incl.
- 30 Z96932:Homo sapiens mRNA for NA14 protein /cds=(46,405) /; 34885\_at Cluster Incl.  
 AJ002308:Homo sapiens mRNA for synaptogyrin 2 /cds=(29,70; 35256\_at Cluster Incl.  
 AL096737:Homo sapiens mRNA; cDNA DKFZp434F152 (from clone; 35369\_at Cluster Incl.  
 AB023154:Homo sapiens mRNA for KIAA0937 protein, partial ; 36987\_at Cluster Incl.  
 M94362:Human lamin B2 (LAMB2) mRNA, partial cds /cds=(0,1; 37049\_g\_at Cluster Incl.
- 35 U58970:Human putative outer mitochondrial membrane 34 k; 37384\_at Cluster Incl. D13640:Human  
 mRNA for KIAA0015 gene, complete cds /cds=(1; 39166\_s\_at Cluster Incl. D83174:Human mRNA  
 for collagen binding protein 2, compl; 39831\_at Cluster Incl. AI972631:wr41c07.x1 Homo sapiens  
 cDNA, 3 end /clone=IMAG; 40183\_at Cluster Incl. AI660225:we68f05.x1 Homo sapiens cDNA, 3  
 end /clone=IMAG; 1083\_s\_at M35093 /FEATURE=cds /DEFINITION=HUMETMAGA Human

- secreted epithelial tu; 749\_at D78586 /FEATURE= /DEFINITION=HUMMUPCAD Human CAD mRNA for multifunctional.
- Metagene** 316; 33749\_at Cluster Incl. AB007455:Homo sapiens mRNA for P53TG1-A, complete cds /cd; 35631\_at Cluster Incl. U37689:Human RNA polymerase II subunit (hsRPB8) mRNA, com;
- 5 37184\_at Cluster Incl. L37792:Human syntaxin 1A mRNA, complete cds /cds=(1,867) ; 34298\_at Cluster Incl. X69532:H.sapiens gene for inter-alpha-trypsin inhibitor h; 37333\_at Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosin-5)-methyltransfera; 39469\_s\_at Cluster Incl. W25905:14g5 Homo sapiens cDNA /gb=W25905 /gi=1306028 /u; 41361\_at Cluster Incl. W28148:43f2 Homo sapiens cDNA /gb=W28148 /gi=1308159 /ug=; 1833\_at M68520 /FEATURE=
- 10 /DEFINITION=HUMCDC2A Human cdc2-related protein kinase ; 1622\_at D87116 /FEATURE= /DEFINITION=D87116 Human mRNA for MAP kinase kinase 3b .
- Metagene** 317; 35374\_at Cluster Incl. AB007914:Homo sapiens mRNA for KIAA0445 protein, complete; 37836\_at Cluster Incl. AB023215:Homo sapiens mRNA for KIAA0998 protein, partial ; 41120\_at Cluster Incl. D14686:Human gene for glycine cleavage system T-protein /; 41865\_at
- 15 Cluster Incl. AF052185:Homo sapiens clone 24418 mRNA sequence /cds=UNKN; 31801\_at Cluster Incl. AI808712:wf57c05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37555\_at Cluster Incl. X95263:H.sapiens mRNA for PWP2 protein /cds=(31,2790) /gb; 41172\_at Cluster Incl. AA126515:zn85c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 35840\_at Cluster Incl. AL050060:Homo sapiens mRNA; cDNA DKFZp566H073 (from clone; 36935\_at Cluster Incl. M23379:Human GTPase-activating protein ras p21 (RASA) mRN; 38386\_r\_at Cluster Incl. U34683:Human glutathione synthetase mRNA, complete cds ; 33161\_at Cluster Incl. AI018098:ov65b11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1373\_at M31523 /FEATURE=
- 20 /DEFINITION=HUMTFAA Human transcription factor (E2A) mR.
- Metagene** 318; 32405\_at Cluster Incl. AB014607:Homo sapiens mRNA for KIAA0707 protein, partial ; 33993\_at Cluster Incl. M22919:Human nonmuscle/smooth muscle alkali myosin light ; 40752\_at Cluster Incl. AI024359:ov75g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32109\_at Cluster Incl. AA524547:ng45h04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32123\_at Cluster Incl. L02870:Human alpha-1 type VII collagen (COL7A1) mRNA, com; 36480\_at Cluster Incl. X80497:H.sapiens PHKLA mRNA /cds=(126,3833) /gb=X80497 /g; 40451\_at Cluster Incl.
- 30 AL080203:Homo sapiens mRNA; cDNA DKFZp434F222 (from clone; 40862\_i\_at Cluster Incl. X15334:Human gene for creatine kinase B (EC 2.7.3.2) /c; 40863\_r\_at Cluster Incl. X15334:Human gene for creatine kinase B (EC 2.7.3.2) /c; 32169\_at Cluster Incl. AB020682:Homo sapiens mRNA for KIAA0875 protein, partial ; 33822\_at Cluster Incl. Z11584:H.sapiens mRNA for NuMA protein /cds=(258,6563) /g; 34827\_at Cluster Incl. AF045458:Homo sapiens serine/threonine kinase ULK1 (ULK1); 36124\_at Cluster Incl. X59434:Human rohu mRNA for rhodanese /cds=(34,924) /gb=X5; 37330\_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5CDh; 37331\_g\_at Cluster Incl. U24266:Human pyrroline-5-carboxylate dehydrogenase (P5C; 37369\_s\_at Cluster Incl. L41066:Homo sapiens NF-AT3 mRNA, complete cds /cds=(141; 37405\_at Cluster Incl. U29091:Human selenium-binding protein (hSBP) mRNA, comple; 37745\_s\_at Cluster Incl.
- 35

- U15780:Human p82 (ST5) mRNA, alternatively spliced, com; 38063\_at Cluster Incl.
- U00952:Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-contain; 33118\_at Cluster Incl.
- U73167:Homo sapiens cosmid clone LUCA14 from 3p21.3 /cds=; 844\_at U48707 /FEATURE= /DEFINITION=HSU48707 Human protein phosphatase-1 inhibit; 329\_s\_at Nuclear Mitotic
- 5 Apparatus Protein 1, Alt. Splice Form 2 .
- Metagene** 319; 32385\_at Cluster Incl. AL050032:Homo sapiens mRNA; cDNA DKFZp566F1224 (from clon; 36337\_at Cluster Incl. AI760801:wi67f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32921\_at Cluster Incl. X83300:H.sapiens SMA4 mRNA /cds=(66,488) /gb=X83300 /gi=6; 37797\_at Cluster Incl. AJ224326:Homo sapiens mRNA for putative ribulose-5-phosph; 41088\_at Cluster Incl.
- 10 X12433:Human pHS1-2 mRNA with ORF homologous to membrane ; 31853\_at Cluster Incl.
- AF080227:Homo sapiens embryonic ectoderm development prot; 33229\_at Cluster Incl.
- U08316:Human insulin-stimulated protein kinase 1 (ISPK-1); 37537\_at Cluster Incl. L04510:Human nucleotide binding protein mRNA, complete cd; 38637\_at Cluster Incl. L16895:Human lysyl oxidase (LOX) gene, exon 7 /cds=(0,6) ; 1532\_g\_at U50535 /FEATURE= /DEFINITION=HSU50535
- 15 Human BRCA2 region, mRNA sequenc; 877\_at M27691 /FEATURE= /DEFINITION=HUMCREB Human transactivator protein (CREB) .
- Metagene** 320; 34714\_at Cluster Incl. AL050267:Homo sapiens mRNA; cDNA DKFZp564A032 (from clone; 34721\_at Cluster Incl. U42031:Human 54 kDa progesterone receptor-associated immu; 40504\_at Cluster Incl. AF001601:Homo sapiens paraoxonase (PON2) mRNA, complete c; 40522\_at
- 20 Cluster Incl. X59834:Human rearranged mRNA for glutamine synthase /cds=; 36626\_at Cluster Incl. X87176:H.sapiens mRNA for 17-beta-hydroxysteroid dehydrog; 36630\_at Cluster Incl.
- Z50781:H.sapiens mRNA for leucine zipper protein /cds=(13; 1269\_at M61906 /FEATURE= /DEFINITION=HUMP13KIN Human P13-kinase associated p85 m; 723\_s\_at Small Nuclear Ribonucleoprotein, Polypeptide C, Alt. Splice 2 .
- 25 **Metagene** 321; 32497\_s\_at Cluster Incl. S70609:glycine transporter type 1b [human, substantia n; 34652\_at Cluster Incl. U77968:Human neuronal PAS1 (NPAS1) mRNA, complete cds /cd; 35944\_at Cluster Incl. AL031228:dJ1033B10.3 (GalT3 (beta3-Galactosyltransferase); 40843\_at Cluster Incl.
- AF012023:Homo sapiens integrin cytoplasmic domain associa; 856\_at S79267 /FEATURE= /DEFINITION=S79267 CD4 receptor {exons 1 and 2} [human, ; 744\_at D50487 /FEATURE=
- 30 /DEFINITION=HUMHRH1 Human mRNA for RNA helicase (HRH1), ; 453\_at U66616 /FEATURE= /DEFINITION=HSU66616 Human SWI/SNF complex 170 KDa subun.
- Metagene** 322; 41810\_at Cluster Incl. AA203545:zx59a05.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1863\_s\_at U67092 /FEATURE=exon#5 /DEFINITION=HSU67092 Human ataxia-telangiectasi; 1049\_g\_at U38480 /FEATURE= /DEFINITION=HSU38480 Human retinoid X
- 35 receptor-gamma .
- Metagene** 323; 32306\_g\_at Cluster Incl. J03464:Human collagen alpha-2 type I mRNA, complete cds; 34916\_s\_at Cluster Incl. S76792:OX40=cell surface antigen [human, mRNA Partial, ; 35879\_at Cluster Incl. M77140:H.sapiens pro-galanin mRNA, 3 end /cds=(0,323) /g; 36231\_at Cluster Incl. AC002073:Human PAC clone DJ515N1 from 22q11.2-q22 /cds=(0; 41872\_at Cluster Incl.

- AF073308:Homo sapiens nonsyndromic hearing impairment pro; 31859\_at Cluster Incl.  
 J05070:Human type IV collagenase mRNA, complete cds /cds=; 33245\_at Cluster Incl.  
 AF004709:Homo sapiens stress-activated protein kinase 4 m; 37233\_at Cluster Incl.  
 AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003 ; 35816\_at Cluster Incl.
- 5 U46692:Human cystatin B gene, complete cds /cds=(96,392) ; 36575\_at Cluster Incl.  
 S59049:BL34=B cell activation gene [human, mRNA, 1398 nt]; 36657\_at Cluster Incl.  
 AA883870:am26f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38466\_at Cluster Incl.  
 X82153:H.sapiens mRNA for cathepsin O /cds=(129,1118) /gb; 1481\_at L23808 /FEATURE=  
 /DEFINITION=HUMHME Human metalloproteinase (HME) mRNA, ; 1482\_g\_at L23808
- 10 /FEATURE= /DEFINITION=HUMHME Human metalloproteinase (HME) mRNA; 973\_at Y10032  
 /FEATURE=cds /DEFINITION=HSRNASTPK H.sapiens mRNA for putative ser; 980\_at AF002020  
 /FEATURE= /DEFINITION=AF002020 Homo sapiens Niemann-Pick C disea; 649\_s\_at L06797  
 /FEATURE= /DEFINITION=HUMGPCR Human (clone L5) orphan G protein-; 668\_s\_at L22524  
 /FEATURE=expanded\_cds /DEFINITION=HUMMATRY06 Human matrilysin ge; 432\_s\_at
- 15 X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell receptor ; 212\_at  
 M97639 /FEATURE= /DEFINITION=HUMROR2A Human transmembrane receptor (ror2); 128\_at  
 X82153 /FEATURE=cds /DEFINITION=HSOC2RNA H.sapiens mRNA for cathepsin O .  
**Metagene** 324; 33646\_g\_at Cluster Incl. X61094:H.sapiens RNA for GM2-activator protein (clone  
 p; 34506\_at Cluster Incl. M13928:Human delta-aminolevulinate dehydratase mRNA, comp;  
 20 41062\_at Cluster Incl. AA037278:zc52c04.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 520\_at  
 U07358 /FEATURE= /DEFINITION=HSU07358 Human protein kinase (zpk) mRNA, co.  
**Metagene** 325; 31502\_at Cluster Incl. W27953:39h7 Homo sapiens cDNA /gb=W27953  
 /gi=1307901 /ug=; 33069\_f\_at Cluster Incl. U06641:Human UDP glucuronosyltransferase mRNA,  
 partial ; 33080\_s\_at Cluster Incl. AB007943:Homo sapiens mRNA for KIAA0474 protein, comple;  
 25 34634\_s\_at Cluster Incl. U68487:Human 5-hydroxytryptamine7 receptor isoform b mR; 35536\_at  
 Cluster Incl. AB011176:Homo sapiens mRNA for KIAA0604 protein, complete; 32923\_r\_at Cluster  
 Incl. M58378:Human synapsin I (SYN1) gene /cds=(0,2117) /gb=M; 34906\_g\_at Cluster Incl.  
 AA977136:oq24f02.s1 Homo sapiens cDNA, 3 end /clone=IM; 35899\_at Cluster Incl.  
 AF109401:Homo sapiens neurotrophic factor artemin precurs; 41867\_at Cluster Incl.
- 30 AF055009:Homo sapiens clone 24747 mRNA sequence /cds=UNKN; 31861\_at Cluster Incl.  
 L14754:Human DNA-binding protein (SMBP2) mRNA, complete c; 32660\_at Cluster Incl.  
 AB002340:Human mRNA for KIAA0342 gene, complete cds /cds=; 36011\_at Cluster Incl.  
 AF035531:Homo sapiens syntaxin 10 mRNA, complete cds /cds; 36482\_s\_at Cluster Incl.  
 Y15724:Homo sapiens SERCA3 gene, exons 1-7 (and joined ; 36907\_at Cluster Incl. M88468:Homo  
 sapiens mevalonate kinase mRNA, complete cds ; 37939\_at Cluster Incl. AL022318:bK150C2.3  
 35 (PUTATIVE novel protein similar to APO; 39383\_at Cluster Incl. AB007882:Homo sapiens  
 KIAA0422 mRNA, partial cds /cds=(0; 36129\_at Cluster Incl. AB007857:Homo sapiens KIAA0397  
 mRNA, complete cds /cds=(5; 38088\_r\_at Cluster Incl. M80563:Human CAPL protein mRNA,  
 complete cds /cds=(135; 39490\_f\_at Cluster Incl. W26381:29b11 Homo sapiens cDNA

- /gb=W26381 /gi=1307098 /; 39908\_at Cluster Incl. AF069735:Homo sapiens PCAF associated factor 65 alpha mRNA; 40595\_at Cluster Incl. AI345337:tb81g11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1469\_at U12779 /FEATURE= /DEFINITION=HSU12779 Human MAP kinase activated protein; 1392\_at L16862 /FEATURE= /DEFINITION=HUMPROCRKI Homo sapiens G
- 5 protein-coupled r; 1270\_at M64788 /FEATURE= /DEFINITION=HUMRAP1GAP Human GTPase activating protein ; 1032\_at U11872 /FEATURE= /DEFINITION=HSU11872 Human interleukin-8 receptor type ; 882\_at M37435 /FEATURE= /DEFINITION=HUMCSDF1 Human macrophage-specific colony-st; 771\_s\_at D00749 /FEATURE=cds /DEFINITION=HUMCD7G3 Human T cell surface antigen C; 534\_s\_at U20391 /FEATURE=mRNA#1 /DEFINITION=HSU20391 Human
- 10 folate receptor (FOLR.  
**Metagene** 326; 33250\_at Cluster Incl. AL031228:dJ1033B10.2 (WD40 protein BING4 (similar to S. c; 34679\_at Cluster Incl. X02596:Human mRNA for bcr (breakpoint cluster region) gen; 32818\_at Cluster Incl. X78565:H.sapiens mRNA for tenascin-C, 7560bp /cds=(313,69; 36195\_at Cluster Incl. U07681:Human NAD(H)-specific isocitrate dehydrogenase alp; 38797\_at Cluster Incl.
- 15 D31887:Human mRNA for KIAA0062 gene, partial cds /cds=(0; 40198\_at Cluster Incl. L06132:Human voltage-dependent anion channel isoform 1 (V; 41485\_at Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC ; 2031\_s\_at U03106 /FEATURE= /DEFINITION=HSU03106 Human wild-type p53 activated fr; 1333\_f\_at X02596 /FEATURE=cds /DEFINITION=HSBCRR Human mRNA for bcr (breakpoint ; 1199\_at D13748 /FEATURE=
- 20 /DEFINITION=HUM4AI Human mRNA for eukaryotic initiation; 867\_s\_at U12471 /FEATURE=cds#2 /DEFINITION=HSU12471 Human thrombospondin-1 gene.; 537\_f\_at U07000 /FEATURE=cds#3 /DEFINITION=HSU07000 Human breakpoint cluster reg; 430\_at X00737 /FEATURE=cds /DEFINITION=HSPNP Human mRNA for purine nucleoside ph.  
**Metagene** 327; 37430\_at Cluster Incl. U78294:Homo sapiens 15S-lipoxygenase mRNA, complete
- 25 cds /; 38597\_f\_at Cluster Incl. D50402:Human mRNA for NRAMPI, complete cds /cds=(175,18; 40730\_at Cluster Incl. U48263:Human pre-pro-orphanin FQ (OFQ) mRNA, complete cds; 32103\_at Cluster Incl. M20786:Human alpha-2-plasmin inhibitor gene /cds=(4,1479); 40506\_s\_at Cluster Incl. U75686:Homo sapiens polyadenylate binding protein mRNA.; 41778\_at Cluster Incl. U53347:Human neutral amino acid transporter B mRNA, compl; 34378\_at Cluster Incl.
- 30 X97324:H.sapiens mRNA for adipophilin /cds=(0,1313) /gb=X; 34892\_at Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds; 36155\_at Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(3; 1491\_at M31166 /FEATURE=mRNA /DEFINITION=HUMTSG14A Human tumor necrosis factor-i.  
**Metagene** 328; 34494\_at Cluster Incl. AJ003125:Homo sapiens mRNA for procollagen I-N
- 35 proteinase; 41440\_at Cluster Incl. D82061:Homo sapiens mRNA for a member of the short-chain ; 33235\_at Cluster Incl. AB023155:Homo sapiens mRNA for KIAA0938 protein, complete; 36147\_at Cluster Incl. X74104:H.sapiens mRNA for TRAP beta subunit /cds=(50,601); 40257\_at Cluster Incl. AI400011:tg85a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32533\_s\_at Cluster Incl. AF054825:Homo sapiens VAMP5 mRNA, complete cds /cds=(57.

- Metagene** 329; 31675\_s\_at Cluster Incl. AF019083:Homo sapiens phosphatase and tensin homolog 2 ; 31950\_at Cluster Incl. Y00345:Human mRNA for polyA binding protein /cds=(502,240; 37819\_at Cluster Incl. AF007130:Homo sapiens clone 23750 unknown mRNA, partial c; 38924\_s\_at Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4; 39231\_at Cluster Incl.
- 5 AF006513:Homo sapiens CHD1 mRNA, complete cds /cds=(163,5; 39317\_at Cluster Incl. D86324:Homo sapiens mRNA for CMP-N-acetylneuraminic acid ; 39964\_at Cluster Incl. AJ007590:Homo sapiens mRNA for XRP2 protein /cds=(172,122; 41620\_at Cluster Incl. AB018259:Homo sapiens mRNA for KIAA0716 protein, complete; 41621\_i\_at Cluster Incl. AA868898:ak55b08.s1 Homo sapiens cDNA, 3 end /clone=IM; 41651\_at Cluster Incl.
- 10 AB028956:Homo sapiens mRNA for KIAA1033 protein, partial ; 32059\_at Cluster Incl. U79282:Human clone 23801 mRNA sequence /cds=UNKNOWN /gb=U; 36060\_at Cluster Incl. U51920:Human signal recognition particle (SRP54) mRNA, co; 36502\_at Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete; 36550\_at Cluster Incl. AL049538:Human DNA sequence from clone 117516 on chromoso; 36898\_r\_at Cluster Incl.
- 15 X74331:H.sapiens mRNA for DNA primase (subunit p58) /cd; 37255\_at Cluster Incl. U36601:Homo sapiens heparan N-deacetylase/N-sulfotransfer; 37936\_at Cluster Incl. AI184802:qd24g04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37971\_at Cluster Incl. AL050089:Homo sapiens mRNA; cDNA DKFZp586E0518 (from clon; 38291\_at Cluster Incl. J00123:Human enkephalin gene /cds=(0,803) /gb=J00123 /gi=; 38670\_at Cluster Incl. AL031685:dJ963K23.2 (novel protein) /cds=(2,688)
- 20 /gb=AL03; 38972\_at Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKN; 39032\_at Cluster Incl. AJ222700:Homo sapiens mRNA for TSC-22 protein /cds=(191,6; 39396\_at Cluster Incl. AF081281:Homo sapiens lysophospholipase (LPL1) mRNA, comp; 39434\_at Cluster Incl. AB011164:Homo sapiens mRNA for KIAA0592 protein, partial ; 39744\_at Cluster Incl. AF000982:Homo sapiens dead box, X isoform (DBX) mRNA, alt; 40083\_at
- 25 Cluster Incl. AB014525:Homo sapiens mRNA for KIAA0625 protein, partial ; 40088\_at Cluster Incl. X84373:H.sapiens mRNA for nuclear factor RIP140 /cds=(287; 40453\_s\_at Cluster Incl. U30826:Human splicing factor SRp40-1 (SRp40) mRNA, comp; 40767\_at Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor; 40803\_at Cluster Incl. AL050161:Homo sapiens mRNA; cDNA DKFZp586B0222 (from clon; 40878\_f\_at Cluster Incl.
- 30 AF041081:Homo sapiens D15F37 pseudogene, S4 allele, mRN; 41175\_at Cluster Incl. L20298:Homo sapiens transcription factor (CBFB) mRNA, 3 ; 41767\_r\_at Cluster Incl. AB020662:Homo sapiens mRNA for KIAA0855 protein, partia; 32215\_i\_at Cluster Incl. AB020685:Homo sapiens mRNA for KIAA0878 protein, comple; 33893\_r\_at Cluster Incl. AB007939:Homo sapiens mRNA for KIAA0470 protein, comple; 34386\_at Cluster Incl.
- 35 AF072250:Homo sapiens methyl-CpG binding protein MBD4 (MB; 34393\_r\_at Cluster Incl. AL050268:Homo sapiens mRNA; cDNA DKFZp564B163 (from clo; 34876\_at Cluster Incl. U65090:Human carboxypeptidase D mRNA, complete cds /cds=(; 35803\_at Cluster Incl. S82240:RhoE=26 kda GTPase homolog [human, HeLa cell line; 35811\_at Cluster Incl. AF037204:Homo sapiens RING zinc finger protein (RZF) mRNA; 36572\_r\_at Cluster Incl.

- D31885:Human mRNA for KIAA0069 gene, partial cds /cds=(; 37294\_at Cluster Incl.  
 X61123:Human BTG1 mRNA /cds=(308,823) /gb=X61123 /gi=2950; 37651\_at Cluster Incl.  
 D31888:Human mRNA for KIAA0071 gene, partial cds /cds=(0; 37685\_at Cluster Incl.  
 U45976:Human clathrin assembly protein lymphoid myeloid l; 38041\_at Cluster Incl.
- 5 U41514:Human UDP-GalNAc-polypeptide N-acetylgalactosaminy; 38084\_at Cluster Incl.  
 AA648295:ns20e08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38110\_at Cluster Incl.  
 AF000652:Homo sapiens syntenin (sycl) mRNA, complete cds ; 38392\_at Cluster Incl.  
 AF006088:Homo sapiens Arp2/3 protein complex subunit p16-; 38402\_at Cluster Incl.  
 U36336:Human lysosome-associated membrane protein-2b (LAM; 38764\_at Cluster Incl.
- 10 AF007142:Homo sapiens clone 23938 mRNA sequence /cds=UNKN; 38820\_at Cluster Incl.  
 AF051894:Homo sapiens 15 kDa selenoprotein mRNA, complete; 39506\_at Cluster Incl.  
 AA933984:on95f04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32504\_at Cluster Incl.  
 AW024812:wu69c05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1463\_at M93425 /FEATURE=  
 /DEFINITION=HUMPTPPEST Human protein tyrosine phosphata; 1377\_at M58603 /FEATURE=  
 15 /DEFINITION=HUMNFKB Human nuclear factor kappa-B DNA bi; 1038\_s\_at U19247  
 /FEATURE=mRNA /DEFINITION=HSINFGRA7 Homo sapiens interferon-gam; 763\_at AB001106  
 /FEATURE= /DEFINITION=AB001106 Homo sapiens mRNA for glia matura; 377\_g\_at AB000220  
 /FEATURE= /DEFINITION=AB000220 Homo sapiens mRNA for semaphori.  
**Metagene 330**; 31733\_at Cluster Incl. Y07683:H.sapiens mRNA for P2X3 purinoceptor  
 20 /cds=(165,135; 38276\_at Cluster Incl. U91616:Human I kappa B epsilon (IkBe) mRNA, complete  
 cds ; 32514\_s\_at Cluster Incl. AF032906:Homo sapiens cathepsin Z precursor (CTS2) mRNA;  
 652\_g\_at L07493 /FEATURE= /DEFINITION=HUM14RPA Homo sapiens replication protein .  
**Metagene 331**; 31783\_at Cluster Incl. U52112:renin-binding protein /cds=(191,1444) /gb=U52112 /;  
 33641\_g\_at Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /c; 35132\_at  
 25 Cluster Incl. X98411:H.sapiens mRNA for myosin-IE /cds=(0,2348) /gb=X98; 36372\_at Cluster Incl.  
 U51333:Human hexokinase III (HK3) mRNA, complete cds /cds; 34435\_at Cluster Incl.  
 AB008775:Homo sapiens AQP9 mRNA for aquaporin 9, complete; 35926\_s\_at Cluster Incl.  
 AF004230:Homo sapiens monocyte/macrophage Ig-related re; 36781\_at Cluster Incl.  
 X01683:Human mRNA for alpha 1-antitrypsin /cds=(38,1294) ; 37100\_at Cluster Incl.
- 30 AJ008112:Homo sapiens mRNA for C17orf1 protein /cds=(39,1; 38129\_at Cluster Incl.  
 L13943:Human glycerol kinase (GK) mRNA exons 1-4, complet; 38533\_s\_at Cluster Incl.  
 J03925:Human Mac-1 gene encoding complement receptor ty; 39649\_at Cluster Incl.  
 X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X7881; 39950\_at Cluster Incl.  
 Y08136:H.sapiens mRNA for ASM-like phosphodiesterase 3a /; 40698\_at Cluster Incl.
- 35 X96719:H.sapiens mRNA for AICL (activation-induced C-type; 40712\_at Cluster Incl.  
 D26579:Homo sapiens mRNA for transmembrane protein, compl; 40742\_at Cluster Incl.  
 M16591:Human hemopoietic cell protein-tyrosine kinase (HC; 32112\_s\_at Cluster Incl.  
 AI800499:tc11f11.x1 Homo sapiens cDNA, 3 end /clone=IM; 32736\_at Cluster Incl.  
 W68830:zd37g06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 33748\_at Cluster Incl.



- D86976:Human mRNA for KIAA0223 gene, partial cds /cds=(0,; 33802\_at Cluster Incl.  
 Z82244:bK286B10.2 (Heme Oxygenase 1 (HO-1, EC 1.14.99.3)); 34210\_at Cluster Incl.  
 N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 36028\_at Cluster Incl.  
 U45285:Human specific 116-kDa vacuolar proton pump subunit; 36833\_at Cluster Incl.
- 5 U78027:Homo sapiens Brutons tyrosine kinase (BTK), alpha-; 37220\_at Cluster Incl.  
 M63835:Human IgG Fc receptor I gene /cds=(155,1279) /gb=M; 37536\_at Cluster Incl.  
 Z11697:Homo sapiens mRNA for HB15 /cds=(10,627) /gb=Z1169; 37967\_at Cluster Incl.  
 AF000424:Homo sapiens LST1 mRNA, cLST1/C splice variant, ; 38666\_at Cluster Incl.  
 M85169:Human homologue of yeast sec7 mRNA, complete cds /; 38976\_at Cluster Incl.
- 10 D44497:Human mRNA for actin binding protein p57, complete; 39799\_at Cluster Incl.  
 M94856:Human fatty acid binding protein homologue (PA-FAB; 40518\_at Cluster Incl.  
 Y00062:Human mRNA for T200 leukocyte common antigen (CD45; 41169\_at Cluster Incl.  
 X74039:H.sapiens mRNA for urokinase plasminogen activator; 32824\_at Cluster Incl.  
 AF039704:Homo sapiens lysosomal pepstatin insensitive pro; 35261\_at Cluster Incl.
- 15 W07033:za93f08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 36103\_at Cluster Incl.  
 D90144:Homo sapiens gene for LD78 alpha precursor, comple; 36674\_at Cluster Incl.  
 J04130:Human activation (Act-2) mRNA, complete cds /cds=(; 37011\_at Cluster Incl.  
 U49392:Human allograft inflammatory factor-1 (AIF-1) mRNA; 37023\_at Cluster Incl.  
 J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, com; 37688\_f\_at Cluster Incl.
- 20 M31932:Human IgG low affinity Fc fragment receptor (FcR; 38038\_at Cluster Incl. U21128:Human  
 lumican mRNA, complete cds /cds=(84,1100) /g; 41814\_at Cluster Incl. M29877:Human alpha-L-  
 fucosidase, complete cds /cds=UNKNOWN; 32570\_at Cluster Incl. L76465:Homo sapiens NAD+-  
 dependent 15 hydroxyprostaglandi; 33106\_at Cluster Incl. U22662:Human nuclear orphan receptor  
 LXR-alpha mRNA, comp; 2045\_s\_at M16592 /FEATURE=mRNA /DEFINITION=HUMHCKB
- 25 Human hemopoietic cell protei; 2002\_s\_at U27467 /FEATURE= /DEFINITION=HSU27467 Human  
 Bcl-2 related (Bfl-1) mRNA; 1665\_s\_at Endothelial Cell Growth Factor 1 ; 1506\_at D11086  
 /FEATURE= /DEFINITION=HUMIL2RG Human mRNA for interleukin 2 recep; 1402\_at M16038  
 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine k; 1127\_at L07597  
 /FEATURE= /DEFINITION=HUMS6KINA Homo sapiens ribosomal protein S6; 341\_at D10202
- 30 /FEATURE= /DEFINITION=HUMPAFRE Homo sapiens mRNA for platelet-acti; 210\_at M95678  
 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-  
**Metagene** 332; 33670\_at Cluster Incl. X74439:H.sapiens mRNA for estrogen receptor gene  
 5flankin; 32281\_at Cluster Incl. AF070549:Homo sapiens clone 24475 mRNA sequence  
 /cds=UNKN; 35932\_at Cluster Incl. AF081507:untitled /cds=(70,1170) /gb=AF081507
- 35 /gi=3450860; 37157\_at Cluster Incl. X56667:Human mRNA for calretinin /cds=(43,858)  
 /gb=X56667; 33336\_at Cluster Incl. M27819:Human anion exchange protein 1 (AE1, band 3)  
 mRNA,; 39006\_r\_at Cluster Incl. AB018257:Homo sapiens mRNA for KIAA0714 protein, partia;  
 34308\_at Cluster Incl. U90551:Human histone 2A-like protein (H2A/l) mRNA, comple; 35735\_at  
 Cluster Incl. M55542:Human guanylate binding protein isoform I (GBP-2) ; 40974\_at Cluster Incl.

- U63541:Human mRNA expressed in HC/HCC livers and MolT-4 p.
- Metagene** 333; 31661\_at Cluster Incl. AJ243936:Homo sapiens mRNA for G16 protein (G16 gene loca; 33071\_at Cluster Incl. Z98744:histone H2B /cds=(5,382) /gb=W28729 /gi=3080457 /u; 36398\_at Cluster Incl. W28729:50h2 Homo sapiens cDNA /gb=W28729 /gi=1308677 /ug=;
- 5 34457\_at Cluster Incl. U76010:Human putative zinc transporter ZnT-3 (ZnT-3) mRNA; 34527\_r\_at Cluster Incl. AF052108:Homo sapiens clone 23687 mRNA sequence /cds=UN; 35915\_at Cluster Incl. X82540:H.sapiens mRNA for activin beta-C chain /cds=(127,; 36242\_at Cluster Incl. M21539:Human small proline rich protein (sprII) mRNA, clo; 36702\_at Cluster Incl. AJ010277:Homo sapiens mRNA for TBX19 protein /cds=(51,139; 39306\_at Cluster Incl.
- 10 AF052514:Homo sapiens thymus specific serine peptidase mR; 41101\_at Cluster Incl. D87464:Human mRNA for KIAA0274 gene, complete cds /cds=(1; 32717\_at Cluster Incl. AF029729:Homo sapiens neuralized mRNA, complete cds /cds=; 33757\_f\_at Cluster Incl. M69245:Human pregnancy-specific beta-1 glycoprotein (PS; 41227\_at Cluster Incl. AL022162:Homo sapiens DNA sequence from PAC 454M7 on chro; 38008\_at Cluster Incl.
- 15 M98528:Homo sapiens neuron-specific protein gene, last ex; 38024\_at Cluster Incl. AB020678:Homo sapiens mRNA for KIAA0871 protein, complete; 38080\_at Cluster Incl. AI525665:PT1.3\_04\_D06.r Homo sapiens cDNA, 5 end /clone\_ ; 41351\_at Cluster Incl. AA885106:am31h01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41799\_at Cluster Incl. W28595:48h8 Homo sapiens cDNA /gb=W28595 /gi=1308543 /ug=; 2027\_at M87068 /FEATURE=
- 20 /DEFINITION=HUMCAN H.sapiens CaN19 mRNA sequence ; 1792\_g\_at M68520 /FEATURE= /DEFINITION=HUMCDC2A Human cdc2-related protein kinas; 1014\_at U60325 /FEATURE= /DEFINITION=HSU60325 Human DNA polymerase gamma mRNA, n; 866\_at U12471 /FEATURE=cds#1 /DEFINITION=HSU12471 Human thrombospondin-1 gene, p; 732\_f\_at Mucin 3, Intestinal ; 207\_at M86752 /FEATURE= /DEFINITION=HUMIEF Human transformation-sensitive protei.
- 25 **Metagene** 334; 32963\_s\_at Cluster Incl. W27549:32d11 Homo sapiens cDNA /gb=W27549 /gi=1307353 /; 37873\_g\_at Cluster Incl. AF072468:Homo sapiens (JH8) mRNA, partial cds /cds=(0,1; 39566\_at Cluster Incl. X70297:H.sapiens mRNA for neuronal nicotinic acetylcholin; 31863\_at Cluster Incl. D80001:Human mRNA for KIAA0179 gene, partial cds /cds=(0,; 34661\_at
- 30 Cluster Incl. AB002348:Human mRNA for KIAA0350 gene, partial cds /cds=(; 37914\_at Cluster Incl. AB002303:Human mRNA for KIAA0305 gene, complete cds /cds=; 38687\_at Cluster Incl. AL050051:Homo sapiens mRNA; cDNA DKFZp566D193 (from clone; 34337\_s\_at Cluster Incl. AJ010014:Homo sapiens mRNA for M96A protein /cds=(243,2; 34353\_at Cluster Incl. AB014548:Homo sapiens mRNA for KIAA0648 protein, partial ; 38782\_at Cluster Incl.
- 35 M95809:Human basic transcription factor 62kD subunit (BTF). **Metagene** 335; 36354\_at Cluster Incl. AL049689:Novel human mRNA from chromosome 1, similar to T; 34701\_at Cluster Incl. U83192:Homo sapiens post-synaptic density protein 95 (PSD; 36499\_at Cluster Incl. D87469:Human mRNA for KIAA0279 gene, partial cds /cds=(0,; 41357\_at Cluster Incl. W27997:43e3 Homo sapiens cDNA /gb=W27997 /gi=1308152 /ug=.

- Metagene** 336; 35665\_at Cluster Incl. Z46973:H.sapiens mRNA for phosphatidylinositol 3-kinase /; 33395\_at Cluster Incl. AL050028:Homo sapiens mRNA; cDNA DKFZp566C0424 (from clon.
- Metagene** 337; 31521\_f\_at Cluster Incl. X60484:H.sapiens H4/e gene for H4 histone /cds=(0,311) ; 31948\_at Cluster Incl. X79563:H.sapiens 8.2kDa differentiation factor mRNA /cds=; 39953\_i\_at
- 5 Cluster Incl. AB014528:Homo sapiens mRNA for KIAA0628 protein, comple; 32062\_at Cluster Incl. D25216:Human mRNA for KIAA0014 gene, complete cds /cds=(1; 33797\_at Cluster Incl. X98494:H.sapiens mRNA for M phase phosphoprotein 10 /cds=; 35159\_at Cluster Incl. U61232:Human tubulin-folding cofactor E mRNA, complete cd; 35212\_at Cluster Incl. AF064801:Homo sapiens multiple membrane spanning receptor; 36068\_at Cluster Incl.
- 10 AF002210:Homo sapiens copper chaperone for superoxide dis; 36847\_r\_at Cluster Incl. AA121509:zk88c10.s1 Homo sapiens cDNA, 3 end /clone=IM; 36928\_at Cluster Incl. X70394:H.sapiens OZF mRNA /cds=(856,1734) /gb=X70394 /gi=; 37964\_at Cluster Incl. W25793:13e7 Homo sapiens cDNA /gb=W25793 /gi=1305934 /ug=; 40112\_at Cluster Incl. AA522698:ni39d03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40118\_at Cluster Incl.
- 15 X07290:Human HF.12 gene mRNA /cds=(0,589) /gb=X07290 /gi=; 40872\_at Cluster Incl. T57872:ybl9b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 32194\_at Cluster Incl. M37197:Human CCAAT-box-binding factor (CBF) mRNA, complet; 32236\_at Cluster Incl. AF032456:Homo sapiens ubiquitin conjugating enzyme G2 (UB; 33844\_at Cluster Incl. AA160724:zo72h04.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 33861\_at Cluster Incl.
- 20 AI123426:qa49c09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34801\_at Cluster Incl. AB014610:Homo sapiens mRNA for KIAA0710 protein, complete; 34817\_s\_at Cluster Incl. U70671:Human ataxin-2 related protein mRNA, partial cds; 35267\_g\_at Cluster Incl. AL049288:Homo sapiens mRNA; cDNA DKFZp564M053 (from clo; 35739\_at Cluster Incl. AB002369:Human mRNA for KIAA0371 gene, complete cds /cds=; 35776\_at Cluster Incl.
- 25 AF064243:Homo sapiens intersectin short form mRNA, comple; 35783\_at Cluster Incl. H93123:yv05g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 38416\_at Cluster Incl. L27706:Human chaperonin protein (Tc20) gene complete cds; 38774\_at Cluster Incl. U77942:Human syntaxin 7 mRNA, complete cds /cds=(79,864) ; 38778\_at Cluster Incl. AB028969:Homo sapiens mRNA for KIAA1046 protein, complete; 39921\_at Cluster Incl.
- 30 AI526089:DU3.2-7.H07.r Homo sapiens cDNA, 5 end /clone\_e; 40564\_at Cluster Incl. N42007:yw69e06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 40569\_at Cluster Incl. M58297:Human zinc finger protein 42 (MZF-1) mRNA, complet; 41329\_at Cluster Incl. AI458463:tj99b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41512\_at Cluster Incl. AL042733:DKFZp434B2222\_s1 Homo sapiens cDNA, 3 end /clon; 41832\_s\_at Cluster Incl.
- 35 AI535828:jun1.P1.H10 Homo sapiens cDNA, 3 end /clone\_e; 1873\_at D21089 /FEATURE= /DEFINITION=HUMXPCR Human mRNA for XP-C repair compleme; 947\_at D55716 /FEATURE= /DEFINITION=HUMP1CDC47 Human mRNA for P1cdc47, complete ; 782\_at U93867 /FEATURE= /DEFINITION=HSU93867 Human RNA polymerase III subunit (R; 250\_at L41067 /FEATURE= /DEFINITION=HUMHFAT4A Homo sapiens NF-AT4c mRNA, complet.

- Metagene 338;** 32387\_at Cluster Incl. AB017494:Homo sapiens mRNA for LCAT-like lysophospholipase; 41226\_at Cluster Incl. L05147:Human dual specificity phosphatase tyrosine/serine; 41494\_at Cluster Incl. X99802:H.sapiens mRNA for ZYG homologue /cds=(38,2338) /g; 1834\_at D38449 /FEATURE= /DEFINITION=HUMGPCRAA Human mRNA
- 5 for G protein-coupled ; 1750\_at AD000092 /FEATURE=cds#5 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro; 1753\_s\_at AD000092 /FEATURE=cds#7 /DEFINITION=CH19HHR23 Homo sapiens DNA from ch; 1558\_g\_at U24152 /FEATURE= /DEFINITION=HSU24152 Human p21-activated protein kina.
- Metagene 339;** 31621\_s\_at Cluster Incl. M36860:Human elastin mRNA, complete cds
- 10 /cds=(49,2241) ; 40667\_at Cluster Incl. X60992:H.sapiens CD6 mRNA for T cell glycoprotein CD6 /cd; 32189\_g\_at Cluster Incl. M96980:Homo sapiens myelin transcription factor 1 (MTF1; 40600\_at Cluster Incl. AW024467:wu76g06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 2067\_f\_at L22475 /FEATURE= /DEFINITION=HUMBAXG Human Bax gamma mRNA, complete cd; 1517\_at J02906 /FEATURE=mRNA /DEFINITION=HUMCYPIIF Human cytochrome P450IIF1 pro; 671\_at
- 15 J03040 /FEATURE= /DEFINITION=HUMSPARC Human SPARC/osteonectin mRNA, compl.
- Metagene 340;** 36391\_at Cluster Incl. AF048730:Homo sapiens cyclin T1 mRNA, complete cds /cds=(; 34032\_at Cluster Incl. AL109707:Homo sapiens mRNA full length insert cDNA clone ; 34936\_at Cluster Incl. AB012130:Homo sapiens SBC2 mRNA for sodium bicarbonate co; 36225\_s\_at Cluster Incl. W27611:35b9 Homo sapiens cDNA /gb=W27611 /gi=1307559 /u; 38962\_at
- 20 Cluster Incl. AB002296:Human mRNA for KIAA0298 gene, complete cds /cds=; 39286\_at Cluster Incl. D64109:Homo sapiens mRNA for tob family, complete cds /cd; 39634\_at Cluster Incl. AB017168:Homo sapiens mRNA for Slit-2 protein, complete c; 41465\_at Cluster Incl. AJ236885:Homo sapiens mRNA for ZBP-89 protein /cds=(391,2; 34211\_at Cluster Incl. AL079697:DKFZp434E1930\_r1 Homo sapiens cDNA, 5 end /clon; 34676\_at Cluster Incl.
- 25 AB029022:Homo sapiens mRNA for KIAA1099 protein, complete; 37947\_at Cluster Incl. D26362:Human mRNA for KIAA0043 gene, complete cds /cds=(1; 39343\_at Cluster Incl. AW026656:vv15c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33349\_at Cluster Incl. AL049378:Homo sapiens mRNA; cDNA DKFZp586I1518 (from clon; 33862\_at Cluster Incl. AF017786:Homo sapiens phosphatidic acid phosphohydrolase ; 39450\_s\_at Cluster Incl.
- 30 AF050145:Homo sapiens iduronate-2-sulfatase (IDS) mRNA.; 39551\_at Cluster Incl. N98667:yy66d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 40949\_at Cluster Incl. AF035812:Homo sapiens dynein light intermediate chain 2 (; 1602\_at L33881 /FEATURE= /DEFINITION=HUMPKCI Human protein kinase C iota isoform; 1319\_at X74764 /FEATURE=cds /DEFINITION=HSRPTK H.sapiens mRNA for receptor prote; 932\_i\_at L11672 /FEATURE=
- 35 /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger; 462\_at U70862 /FEATURE= /DEFINITION=HSU70862 Human nuclear factor I B3 mRNA, com; 387\_at X80230 /FEATURE=mRNA /DEFINITION=HSSTPKC2K H.sapiens mRNA (clone C-2k) mR.
- Metagene 341;** 36421\_at Cluster Incl. AF038194:Homo sapiens clone 23821 mRNA sequence /cds=UNKN; 36010\_at Cluster Incl. U10492:Human Mox1 protein (MOX1) mRNA, complete cds

- /cds=; 36065\_at Cluster Incl. AF052389:Homo sapiens LIM domain binding protein (LDB1) m;  
37550\_at Cluster Incl. M14113:Human coagulation factor VIII-C mRNA, complete cds; 37919\_at  
Cluster Incl. AF056732:untitled /cds=(83,2014) /gb=AF056732 /gi=3676521; 38994\_at Cluster Incl.  
AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA,; 39048\_at Cluster Incl.
- 5 U95299:Human Notch4 (hNotch4) mRNA, complete cds /cds=(90; 39398\_s\_at Cluster Incl.  
AB023205:Homo sapiens mRNA for KIAA0988 protein, comple; 40458\_at Cluster Incl.  
U43185:Human signal transducer and activator of transcrip; 37709\_at Cluster Incl. M86934:Human  
GS1 (protein of unknown function) mRNA, comp; 37718\_at Cluster Incl. D43636:Human mRNA for  
KIAA0096 gene, partial cds /cds=(0; 525\_g\_at U13695 /FEATURE=cds /DEFINITION=HSU13695
- 10 Human homolog of yeast mutL (h.  
**Metagene** 342; 35235\_at Cluster Incl. AA099265:zk84f07.r1 Homo sapiens cDNA, 5 end  
/clone=IMAG; 38986\_at Cluster Incl. Z49835:H.sapiens mRNA for protein disulfide isomerase /cd;  
38987\_at Cluster Incl. AF052183:Homo sapiens clone 24804 mRNA sequence /cds=UNKN;  
33421\_s\_at Cluster Incl. AB016247:Homo sapiens mRNA for sterol-C5-desaturase, co; 37654\_at
- 15 Cluster Incl. D31764:Human mRNA for KIAA0064 gene, complete cds /cds=(2.  
**Metagene** 343; 38565\_at Cluster Incl. D88667:Homo sapiens mRNA for cerebroside  
sulfotransferase; 32657\_at Cluster Incl. D25278:Human mRNA for KIAA0036 gene, complete cds  
/cds=(1.  
**Metagene** 344; 33631\_at Cluster Incl. AF023612:Homo sapiens Dim1p homolog mRNA, complete
- 20 cds /c; 37114\_at Cluster Incl. L32832:Homo sapiens zinc finger homeodomain protein (ATBF;  
38188\_s\_at Cluster Incl. L28821:Homo sapiens alpha mannosidase II isozyme mRNA, ; 39587\_at  
Cluster Incl. AJ005890:Homo sapiens mRNA for JM1 protein, complete CDS ; 40016\_g\_at Cluster  
Incl. AB002301:Human mRNA for KIAA0303 gene, partial cds /cds; 41010\_at Cluster Incl.  
Y17829:Homo sapiens mRNA for Homer-related protein Syn47 ; 34178\_at Cluster Incl.
- 25 AI884738:w184b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34264\_at Cluster Incl.  
AB026894:Homo sapiens mRNA for NESCA, complete cds /cds=(; 36519\_at Cluster Incl.  
M13194:Human excision repair protein (ERCC1) mRNA, comple; 36562\_at Cluster Incl.  
AB007887:Homo sapiens KIAA0427 mRNA, complete cds /cds=(2; 38257\_at Cluster Incl.  
AF038406:Homo sapiens NADH dehydrogenase-ubiquinone Fe-S ; 40426\_at Cluster Incl.
- 30 X89985:H.sapiens mRNA for BCL7B protein /cds=(37,645) /gb; 40497\_at Cluster Incl.  
AF040707:Homo sapiens candidate tumor suppressor gene 21 ; 40825\_at Cluster Incl.  
AB025186:Homo sapiens mRNA for EB3 protein, complete cds ; 33437\_at Cluster Incl.  
AJ005892:Homo sapiens mRNA for JM23 protein, complete cod; 33901\_at Cluster Incl.  
U81375:Human placental equilibrative nucleoside transport; 35308\_at Cluster Incl. D83200:Homo
- 35 sapiens mRNA expressed in placenta /cds=UNKNO; 36679\_at Cluster Incl. X06272:Human mRNA  
for docking protein (signal recognition; 37768\_at Cluster Incl. M74905:Human 3-alkyladenine DNA  
glycosylase (HAAG) mRNA, ; 38021\_at Cluster Incl. U53204:Human plectin (PLEC1) mRNA,  
complete cds /cds=(51; 38094\_at Cluster Incl. M65028:Human hnRNP type A/B protein mRNA,  
complete cds /c; 38730\_at Cluster Incl. AB020671:Homo sapiens mRNA for KIAA0864 protein,

- partial ; 39088\_at Cluster Incl. Y18007:Homo sapiens mRNA for putative seven transmembrane;  
 32574\_at Cluster Incl. X59960:H.sapiens mRNA for sphingomyelinase /cds=(122,2005; 1241\_at  
 U14603 /FEATURE= /DEFINITION=HSU14603 Human protein-tyrosine phosphatase.
- Metagene** 345; 35584\_s\_at Cluster Incl. AJ224874:Homo sapiens mRNA for L-type calcium  
 5 channel  $\alpha$ ; 35861\_at Cluster Incl. AA018440:ze50a07.s1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 36286\_at Cluster Incl. AF070628:Homo sapiens clone 24803 mRNA sequence /cds=UNKN;  
 37228\_at Cluster Incl. U01038:Human pLK mRNA, complete cds /cds=(63,1874) /gb=U0; 39417\_at  
 Cluster Incl. AB028951:Homo sapiens mRNA for KIAA1028 protein, partial ; 40443\_at Cluster Incl.  
 AF062341:Homo sapiens p120 catenin isoform 1ABC (CTNND1) ; 40232\_at Cluster Incl.
- 10 U75370:Human mitochondrial RNA polymerase mRNA, nuclear g.  
**Metagene** 346; 31755\_at Cluster Incl. AI094859:qa09a09.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 34602\_at Cluster Incl. D63160:Homo sapiens DNA for lectin P35 /cds=(10,951)  
 /gb=; 35544\_at Cluster Incl. Y16280:Homo sapiens mRNA for G protein-coupled receptor E;  
 34905\_at Cluster Incl. AA977136:oq24f02.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36803\_at  
 15 Cluster Incl. L77561:Homo sapiens DGS-D mRNA, 3 end /cds=UNKNOWN /gb=L; 37082\_at  
 Cluster Incl. AB007886:Homo sapiens KIAA0426 mRNA, complete cds /cds=(1; 39650\_s\_at Cluster  
 Incl. AB007895:Homo sapiens KIAA0435 mRNA, complete cds /cds=; 41664\_at Cluster Incl.  
 AF026030:Homo sapiens putative mitochondrial inner membra; 41869\_at Cluster Incl.  
 U78310:Homo sapiens pescadillo mRNA, complete cds /cds=(5; 31839\_at Cluster Incl.
- 20 AC004475:Homo sapiens chromosome 19, cosmid F23858 /cds=(; 32095\_at Cluster Incl.  
 AB018267:Homo sapiens mRNA for KIAA0724 protein, complete; 32122\_at Cluster Incl.  
 L31573:Human sulfite oxidase mRNA, complete cds /cds=(903; 32681\_at Cluster Incl.  
 S68616:Na<sup>+</sup>/H<sup>+</sup> exchanger NHE-1 isoform [human, heart, mRNA; 33225\_at Cluster Incl.  
 AI928387:wo96f10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33307\_at Cluster Incl.
- 25 AL022316:Human DNA sequence from clone 126B4 on chromosom; 35156\_at Cluster Incl.  
 AL050297:Homo sapiens mRNA; cDNA DKFZp564N123 (from clone; 35170\_at Cluster Incl.  
 AF044414:Homo sapiens alpha mannosidase 6A8B (6a8b) mRNA,; 35227\_at Cluster Incl.  
 U72066:Homo sapiens CtBP interacting protein CtIP (CtIP) ; 35620\_at Cluster Incl.  
 AF043250:Homo sapiens mitochondrial outer membrane protei; 35634\_at Cluster Incl.
- 30 U49928:Homo sapiens TAK1 binding protein (TAB1) mRNA, com; 36027\_at Cluster Incl.  
 AA418779:zv98d05.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 36076\_g\_at Cluster Incl.  
 AL037167:DKFZp564P1564\_s1 Homo sapiens cDNA, 3 end /cl; 36475\_at Cluster Incl.  
 Z97630:Human DNA sequence from clone 466N1 on chromosome ; 36870\_at Cluster Incl.  
 AB018347:Homo sapiens mRNA for KIAA0804 protein, partial ; 37992\_s\_at Cluster Incl.
- 35 AI436567:ti03b09.x1 Homo sapiens cDNA, 3 end /clone=IM; 40807\_at Cluster Incl.  
 X86018:H.sapiens mRNA for MUF1 protein /cds=(0,1853) /gb=; 40875\_s\_at Cluster Incl.  
 X06815:Human mRNA for hU1-70K small nuclear RNP protein; 32145\_at Cluster Incl.  
 X58141:Human mRNA for erythrocyte adducin alpha subunit /; 32235\_at Cluster Incl.  
 AB011116:Homo sapiens mRNA for KIAA0544 protein, partial ; 32758\_g\_at Cluster Incl.

- U84720:Homo sapiens mRNA export protein (RAE1) mRNA, co; 33441\_at Cluster Incl.  
 L41143:Homo sapiens expressed pseudo TCTA mRNA at t(1;3) ; 34315\_at Cluster Incl.  
 Y18314:Homo sapiens mRNA for paraplegin-like protein /cds; 35262\_at Cluster Incl.  
 AF022229:Homo sapiens translation initiation factor 6 (eI; 35758\_at Cluster Incl. AB024301:Homo  
 5 sapiens mRNA for RuvB-like DNA helicase TIP; 35826\_at Cluster Incl. AF040253:Homo sapiens  
 transcription factor Tat-CT1 mRNA, ; 36154\_at Cluster Incl. D87452:Human mRNA for KIAA0263  
 gene, complete cds /cds=(3; 36172\_s\_at Cluster Incl. AF002163:Homo sapiens delta-adaptin mRNA,  
 complete cds ; 36194\_at Cluster Incl. M63959:Human alpha-2-macroglobulin receptor-associated pr;  
 36624\_at Cluster Incl. L33842:Homo sapiens (clone FFE-7) type II inosine monopho; 36645\_at  
 10 Cluster Incl. L19067:Human NF-kappa-B transcription factor p65 subunit ; 36973\_at Cluster Incl.  
 U41371:Human spliceosome associated protein (SAP 145) mRNA; 37376\_at Cluster Incl.  
 M68864:Human ORF mRNA, complete cds /cds=(135,1031) /gb=M; 37378\_r\_at Cluster Incl.  
 M13452:Human lamin A mRNA, 3end /cds=(0,1547) /gb=M1345; 38758\_at Cluster Incl.  
 R98910:yr31d04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39089\_at Cluster Incl.  
 15 Y07604:H.sapiens mRNA for nucleoside-diphosphate kinase /; 39130\_at Cluster Incl.  
 AB018313:Homo sapiens mRNA for KIAA0770 protein, partial ; 39149\_at Cluster Incl.  
 X99720:H.sapiens TPRC gene /cds=(212,1687) /gb=X99720 /gi; 39180\_at Cluster Incl.  
 S62140:TLS=translocated in liposarcoma [human, mRNA, 1824; 40182\_s\_at Cluster Incl.  
 AF055027:Homo sapiens clone 24658 mRNA sequence /cds=UN; 40223\_r\_at Cluster Incl.  
 20 AI677689:wd33c06.x1 Homo sapiens cDNA, 3 end /clone=IM; 40264\_g\_at Cluster Incl.  
 AF001891:Homo sapiens clone lambda MEN1 region unknown ; 41316\_s\_at Cluster Incl.  
 U72355:Human Hsp27 ERE-TATA-binding protein (HET) mRNA,; 41527\_f\_at Cluster Incl.  
 W29063:56g11 Homo sapiens cDNA /gb=W29063 /gi=1309092 /; 41590\_at Cluster Incl.  
 AI652660:wb30c10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1310\_at D26599 /FEATURE=  
 25 /DEFINITION=HUMPSH2 Human mRNA for proteasome subunit H; 1000\_at X60188  
 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein seri; 410\_s\_at  
 X57152 /FEATURE=mRNA#1 /DEFINITION=HSCKIIBE Human gene for casein kinas; 162\_at  
 U44839 /FEATURE= /DEFINITION=HSU44839 Human putative ubiquitin C-terminal; 109\_at  
 Z97074 /FEATURE= /DEFINITION=HSRAB9P40 Homo sapiens mRNA for Rab9 effecto.  
 30 **Metagene** 347; 41656\_at Cluster Incl. AF043325:Homo sapiens N-myristoyltransferase 2 mRNA,  
 comp; 41691\_at Cluster Incl. AB018337:Homo sapiens mRNA for KIAA0794 protein, partial ;  
 32143\_at Cluster Incl. AI126171:qd81g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35717\_at  
 Cluster Incl. AB020629:Homo sapiens mRNA for KIAA0822 protein, complete; 37616\_at Cluster  
 Incl. X79888:H.sapiens AUH mRNA /cds=(4,1023) /gb=X79888 /gi=78; 40423\_at Cluster Incl.  
 35 AB020710:Homo sapiens mRNA for KIAA0903 protein, partial ; 40775\_at Cluster Incl.  
 AL021786:Human DNA sequence from PAC 696H22 on chromosome; 41229\_at Cluster Incl.  
 AI222594:qg58g05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32747\_at Cluster Incl.  
 X05409:Human RNA for mitochondrial aldehyde dehydrogenase; 34821\_at Cluster Incl.  
 AL050197:Homo sapiens mRNA; cDNA DKFZp586D0623 (from clon; 35327\_at Cluster Incl.

- U54559:Homo sapiens translation initiation factor eIF3 p4; 37348\_s\_at Cluster Incl.  
 AA845349:ak01g01.s1 Homo sapiens cDNA, 3 end /clone=IM; 38051\_at Cluster Incl.  
 X76220:H.sapiens MAL gene exon 1 (and joined CDS) /cds=(5; 38098\_at Cluster Incl.  
 D80010:Human mRNA for KIAA0188 gene, partial cds /cds=(0; 39110\_at Cluster Incl.
- 5 X55733:H.sapiens initiation factor 4B cDNA /cds=(0,1835) ; 41309\_g\_at Cluster Incl.  
 U37408:Homo sapiens phosphoprotein CtBP mRNA, complete ; 41796\_at Cluster Incl.  
 AB029015:Homo sapiens mRNA for KIAA1092 protein, partial ; 33140\_at Cluster Incl.  
 AF029893:Homo sapiens i-beta-1,3-N-acetylglucosaminyltran; 1897\_at L07594 /FEATURE=  
 /DEFINITION=HUMTGFB3C Human transforming growth factor-; 1787\_at U22398 /FEATURE=  
 10 /DEFINITION=HSU22398 Human Cdk-inhibitor p57KIP2 (KIP2); 103\_at Z19585 /FEATURE=cds  
 /DEFINITION=HSTHROMB4 H.sapiens mRNA for thrombospond.
- Metagene** 348; 35599\_at Cluster Incl. X62250:H.sapiens mRNA for liver glycine methyltransferase;  
 32351\_at Cluster Incl. U66579:Human putative G protein-coupled receptor (GPR20) ; 36729\_g\_at  
 Cluster Incl. M76446:Human alpha-A1-adrenergic receptor mRNA, complet; 37916\_at Cluster Incl.
- 15 AI086057:oz44f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1730\_s\_at M17446  
 /FEATURE=mRNA /DEFINITION=HUMKSGFA Human Kaposi s sarcoma oncog; 910\_at M15205  
 /FEATURE=cds /DEFINITION=HUMTKRA Human thymidine kinase gene, comp.
- Metagene** 349; 31514\_at Cluster Incl. AF034970:Homo sapiens docking protein (DOK-2) mRNA,  
 compl; 31596\_f\_at Cluster Incl. L02326:Homo sapiens (clone Hu lambda-17) lambda-like ge;  
 20 35017\_f\_at Cluster Incl. M80469:Human MHC class I HLA-J gene, exons 1-8 and comp; 33967\_at  
 Cluster Incl. M31525:Human MHC class II lymphocyte antigen (HLA-DNA) ge; 36731\_g\_at Cluster  
 Incl. U66684:HSU66684 Homo sapiens cDNA /gb=U66684 /gi=190656; 37419\_g\_at Cluster Incl.  
 M36653:Human Oct-2 factor mRNA, complete cds /cds=UNKNO; 37421\_f\_at Cluster Incl.  
 AL022723:dJ377H14.9 (major histocompatibility complex, ; 37769\_at Cluster Incl.
- 25 AF011466:Homo sapiens G protein-coupled receptor Edg-4 mR; 37779\_at Cluster Incl.  
 Y08134:H.sapiens mRNA for ASM-like phosphodiesterase 3b /; 37790\_at Cluster Incl.  
 AF068006:Homo sapiens haemopoietic progenitor homeobox HP; 37843\_i\_at Cluster Incl.  
 AF053004:Homo sapiens class I cytokine receptor (WSX1) ; 38149\_at Cluster Incl. D29642:Human  
 mRNA for KIAA0053 gene, complete cds /cds=(1; 38963\_i\_at Cluster Incl. U12707:Human
- 30 Wiskott-Aldrich syndrome protein (WASP) mR; 39568\_g\_at Cluster Incl. AB006190:Homo sapiens  
 mRNA for aquaporin adipose, compl; 40718\_at Cluster Incl. AF013611:Homo sapiens lymphopain  
 mRNA, complete cds /cds=; 41423\_at Cluster Incl. AB018269:Homo sapiens mRNA for KIAA0726  
 protein, complete; 32629\_f\_at Cluster Incl. U90552:Human butyrophilin (BTF5) mRNA, complete  
 cds /cd; 35150\_at Cluster Incl. X60592:Human CDw40 mRNA for nerve growth factor receptor-;  
 35 35197\_at Cluster Incl. AF038188:Homo sapiens clone 23940 mRNA sequence /cds=UNKN;  
 39008\_at Cluster Incl. M13699:Human ceruloplasmin (ferroxidase) mRNA, complete c; 39778\_at  
 Cluster Incl. M55621:Human N-acetylglucosaminyltransferase I (GlcNAc-TI; 40836\_s\_at Cluster  
 Incl. W26677:11f7 Homo sapiens cDNA /gb=W26677 /gi=1305788 /u; 40840\_at Cluster Incl.  
 M80254:H.sapiens cyclophilin isoform (hCyP3) mRNA, comple; 33390\_at Cluster Incl.



- AA203487:zx53d03.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 33448\_at Cluster Incl.
- AB000095:Homo sapiens mRNA for hepatocyte growth factor a; 34835\_at Cluster Incl.
- D87442:Human mRNA for KIAA0253 gene, partial cds /cds=(0,; 35309\_at Cluster Incl.
- U20428:Human SNC19 mRNA sequence /cds=UNKNOWN /gb=U20428 ; 35798\_at Cluster Incl.
- 5 W25936:15b5 Homo sapiens cDNA /gb=W25936 /gi=1306059 /ug=; 37746\_r\_at Cluster Incl.
- U15131:Human p126 (ST5) mRNA, complete cds /cds=(114,35; 38121\_at Cluster Incl.
- X59892:H.sapiens mRNA for IFN-inducible gamma2 protein /c; 38445\_at Cluster Incl.
- Y09160:H.sapiens Sub1.5 mRNA /cds=(435,3044) /gb=Y09160 /; 41565\_at Cluster Incl.
- AF034373:Homo sapiens ataxin-2-like protein A2LP (A2LG) m; 2090\_i\_at H12458 /FEATURE=
- 10 /DEFINITION=H12458 yj12d03.sl Soares placenta Nb2HP H; 1796\_s\_at U05681
- /FEATURE=expanded\_cds /DEFINITION=HSBCL3S2 Human proto-oncogene; 1291\_s\_at L03840
- /FEATURE= /DEFINITION=HUMFGFR4X Human fibroblast growth factor ; 993\_at X54637
- /FEATURE=cds /DEFINITION=HSTYK2 Human tyk2 mRNA for non-receptor p; 810\_at U64105
- /FEATURE= /DEFINITION=HSU64105 Human guanine nucleotide exchange f; 160042\_s\_at
- 15 X58431 /FEATURE=mRNA#1 /DEFINITION=HSHOX22 Human Hox2.2 gene for a h.
- Metagene** 350; 36437\_s\_at Cluster Incl. AF064606:Homo sapiens KB07 protein mRNA, partial cds
- /c; 36213\_at Cluster Incl. AB016816:Homo sapiens MASL1 mRNA, complete cds /cds=(0,31;
- 36238\_at Cluster Incl. Y11284:Homo sapiens AFX1 gene, exon 1 (and joined CDS) /c; 37134\_f\_at
- Cluster Incl. L13266:Homo sapiens N-methyl-d-aspartate receptor (NR1-; 37138\_at Cluster Incl.
- 20 AB018352:Homo sapiens mRNA for KIAA0809 protein, partial ; 37443\_at Cluster Incl.
- AL031588:dJ1163J1.2.1 (novel protein similar to C. elegans; 37445\_at Cluster Incl. AB015633:Homo
- sapiens mRNA for type II membrane protein, ; 38569\_at Cluster Incl. U02683:Human alpha
- palindromic binding protein mRNA, comp; 39246\_at Cluster Incl. Z75330:H.sapiens mRNA for
- nuclear protein SA-1 /cds=(400,; 39266\_at Cluster Incl. AF070632:Homo sapiens clone 24405
- 25 mRNA sequence /cds=UNKN; 31824\_at Cluster Incl. AL049699:dJ747H23.1 (malic enzyme 1,
- soluble (NADP-depend; 33319\_at Cluster Incl. AF009674:Homo sapiens axin (AXIN) mRNA,
- partial cds /cds=; 33791\_at Cluster Incl. Y15227:Homo sapiens mRNA for leukemia associated gene
- 1 /; 37617\_at Cluster Incl. U90912:Human clone 23865 mRNA sequence /cds=UNKNOWN /gb=U;
- 37907\_at Cluster Incl. M34677:Human nested gene protein gene, complete cds /cds=; 38295\_at
- 30 Cluster Incl. X59842:Human PBX2 mRNA /cds=UNKNOWN /gb=X59842 /gi=35312 ; 38662\_at
- Cluster Incl. AL047596:DKFZp586G0421\_s1 Homo sapiens cDNA /clone=DKFZp5; 39337\_at
- Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106; 39708\_at Cluster
- Incl. L29277:Homo sapiens DNA-binding protein (APRF) mRNA, comp; 39719\_at Cluster Incl.
- X56777:H.sapiens mRNA for ZP3 gene /cds=(30,1148) /gb=X56; 39734\_at Cluster Incl.
- 35 U10117:Human endothelial-monocyte activating polypeptide ; 39788\_at Cluster Incl.
- X81889:H.sapiens mRNA for p0071 protein /cds=(141,3776) /; 39791\_at Cluster Incl.
- M23114:Homo sapiens calcium-ATPase (HK1) mRNA, complete c; 40487\_at Cluster Incl.
- W26634:34b10 Homo sapiens cDNA /gb=W26634 /gi=1307477 /ug; 40771\_at Cluster Incl.
- Z98946:Human DNA sequence from clone 376D21 on chromosome; 40813\_at Cluster Incl.

- AI768188:wg82b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40881\_at Cluster Incl.  
 X64330:H.sapiens mRNA for ATP-citrate lyase /cds=(84,3401; 33434\_at Cluster Incl.  
 AF007551:Homo sapiens Bet1p homolog (hbet1) mRNA, complet; 34831\_at Cluster Incl.  
 AF055004:Homo sapiens clone 24640 mRNA sequence /cds=UNKN; 36146\_at Cluster Incl.
- 5 AF057297:Homo sapiens ornithine decarboxylase antizyme 2 ; 36954\_at Cluster Incl.  
 D86972:Human mRNA for KIAA0218 gene, complete cds /cds=(3; 37050\_r\_at Cluster Incl.  
 AI130910:qb81g08.x1 Homo sapiens cDNA, 3 end /clone=IM; 37292\_at Cluster Incl.  
 D83785:Human mRNA for KIAA0200 gene, complete cds /cds=(2; 37393\_at Cluster Incl.  
 L19314:Human HRY gene, complete cds /cds=(0,842) /gb=L193; 38083\_at Cluster Incl.
- 10 AL049386:Homo sapiens mRNA; cDNA DKFZp586M0918 (from clon; 38415\_at Cluster Incl.  
 U14603:Human protein-tyrosine phosphatase (HU-PP-1) mRNA,; 40279\_at Cluster Incl.  
 D50911:Human mRNA for KIAA0121 gene, complete cds /cds=(4; 1674\_at M15990 /FEATURE=  
 /DEFINITION=HUMCYES1 Human c-yes-1 mRNA ; 1507\_s\_at D11151 /FEATURE=\_expandCDS  
 /DEFINITION=HUMETAR8 Human DNA for endothel; 1031\_at U09564 /FEATURE=  
 15 /DEFINITION=HSU09564 Human serine kinase mRNA, complete; 914\_g\_at M21535 /FEATURE=  
 /DEFINITION=HUMERG11 Human erg protein (ets-related ge.  
**Metagene** 351; 32290\_at Cluster Incl. AL049223:Homo sapiens mRNA; cDNA DKFZp564L1916  
 (from clon; 40686\_at Cluster Incl. AI985272:ws06b05.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 36673\_at Cluster Incl. X76057:H.sapiens PM11 mRNA for phosphomannose  
 20 isomerase /; 37353\_g\_at Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA,  
 complet; 39114\_at Cluster Incl. AB022718:Homo sapiens mRNA for DEPP (decidual protein ind;  
 41322\_s\_at Cluster Incl. AI816034:au44e05.x1 Homo sapiens cDNA, 3 end /clone=IM; 1043\_s\_at  
 U27516 /FEATURE= /DEFINITION=HSU27516 Human recombination protein RAD5; 895\_at  
 L19686 /FEATURE=mRNA /DEFINITION=HUMMIF Homo sapiens macrophage migration;  
 25 849\_g\_at U19261 /FEATURE= /DEFINITION=HSU19261 Homo sapiens Epstein-Barr virus-i.  
**Metagene** 352; 34498\_at Cluster Incl. D89974:Homo sapiens mRNA for glycosylphosphatidyl  
 inosito; 37842\_at Cluster Incl. AF054589:Homo sapiens HIC protein mRNA, complete cds /cds;  
 39624\_at Cluster Incl. D89078:Homo sapiens mRNA for leukotriene b4 receptor, com; 36924\_r\_at  
 Cluster Incl. M25756:Human secretogranin II gene, complete cds /cds=(; 41783\_at Cluster Incl.
- 30 M97815:Human retinoic acid-binding protein II (CRABP-II) ; 32250\_at Cluster Incl.  
 X07523:Human mRNA for truncated form of complement factor; 40553\_at Cluster Incl.  
 AI742087:wg38g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40938\_at Cluster Incl.  
 Y13835:Homo sapiens mRNA for farnesylated-proteins conver; 33192\_g\_at Cluster Incl.  
 AW051579:wy87g03.x1 Homo sapiens cDNA, 3 end /clone=IM; 1932\_at U83661 /FEATURE=  
 35 /DEFINITION=HSU83661 Homo sapiens multidrug resistance ; 1573\_at M12783  
 /FEATURE=mRNA /DEFINITION=HUMSISPDG Human c-sis/platelet-derived .  
**Metagene** 353; 36229\_at Cluster Incl. U58917:Homo sapiens IL-17 receptor mRNA, complete cds  
 /cd; 38581\_at Cluster Incl. U40038:Human GTP-binding protein alpha q subunit (GNAQ) m;  
 32178\_r\_at Cluster Incl. AJ011915:Homo sapiens mRNA for synaptosome associated p; 33391\_r\_at

- Cluster Incl. S57235:CD68=110kda transmembrane glycoprotein [human, p; 39525\_at Cluster Incl. AL120687:DKFZp762F2110\_r1 Homo sapiens cDNA, 5 end /clon; 40613\_at Cluster Incl. AL031775:dJ30M3.2 (novel protein) /cds=(0,260) /gb=AL0317; 41809\_at Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAG.
- 5 **Metagene** 354; 39986\_at Cluster Incl. AL050100:Homo sapiens mRNA; cDNA DKFZp586D0919 (from clon; 41389\_s\_at Cluster Incl. U46193:Human renal cell carcinoma antigen RAGE-3 mRNA, ; 41708\_at Cluster Incl. AB028957:Homo sapiens mRNA for KIAA1034 protein, partial ; 36485\_at Cluster Incl. U85647:Homo sapiens small optic lobes homolog (SOLH) mRNA; 36488\_at Cluster Incl. AB011542:Homo sapiens mRNA for MEGF9, partial cds /cds=(0; 38264\_at Cluster Incl.
- 10 U74324:Human guanine nucleotide exchange factor mss4 mRNA; 38272\_at Cluster Incl. AF038844:Homo sapiens MKP-1 like protein tyrosine phosphatase; 38336\_at Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial ; 38988\_at Cluster Incl. AJ007042:Homo sapiens mRNA for TRX5 protein /cds=(762,485; 39695\_at Cluster Incl. M31516:Human decay-accelerating factor mRNA, complete cds; 32174\_at Cluster Incl.
- 15 AF015926:Homo sapiens ezrin-radixin-moesin binding phosphatase; 32807\_at Cluster Incl. AF004292:Homo sapiens clone IMAGE-30181 mRNA sequence /cd; 33917\_at Cluster Incl. AB002336:Human mRNA for KIAA0338 gene, partial cds /cds=(; 40238\_at Cluster Incl. AI674208:wc07f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41816\_at Cluster Incl. AL049851:Human DNA sequence from clone 889J22B on chromosome; 33158\_at Cluster Incl.
- 20 M97252:Homo sapiens Kallmann syndrome (KAL) mRNA, complete.
- Metagene** 355; 31737\_at Cluster Incl. J00068:Human adult skeletal muscle alpha-actin mRNA /cds=; 32432\_f\_at Cluster Incl. L25899:Human ribosomal protein L10 mRNA, complete cds /; 33621\_at Cluster Incl. X71348:Homo sapiens vHNF1-C mRNA /cds=UNKNOWN /gb=X71348 ; 33637\_g\_at Cluster Incl. U87459:Human autoimmunogenic cancer/testis antigen NY-E; 33689\_s\_at
- 25 Cluster Incl. AF012434:untitled /cds=(38,394) /gb=AF012434 /gi=235291; 34085\_at Cluster Incl. Z26876:H.sapiens gene for ribosomal protein L38 /cds=(110; 34618\_at Cluster Incl. L38517:Homo sapiens indian hedgehog protein (IHH) mRNA, 5; 35078\_at Cluster Incl. X93093:H.sapiens LW gene /cds=(9,824) /gb=X93093 /gi=1491; 35471\_g\_at Cluster Incl. AA418537:zv93a09.s1 Homo sapiens cDNA, 3 end /clone=IM; 37529\_at Cluster Incl. AF051946:Homo sapiens T-type calcium
- 30 channel alpha-1 subunit; 38904\_at Cluster Incl. AF077754:Homo sapiens tyrosine kinase pp60c-src (SRC) gene; 40755\_at Cluster Incl. X92841:H.sapiens MICA gene /cds=(39,1196) /gb=X92841 /gi=; 41114\_at Cluster Incl. AB018350:Homo sapiens mRNA for KIAA0807 protein, partial ; 41603\_at Cluster Incl. U02609:Human transducin-like protein mRNA, complete cds /; 32091\_at Cluster Incl. AB007915:Homo sapiens mRNA for KIAA0446 protein, complete; 33337\_at Cluster Incl.
- 35 AF002668:Homo sapiens putative fatty acid desaturase MLD ; 34245\_at Cluster Incl. W25917:14h6 Homo sapiens cDNA /gb=W25917 /gi=1306040 /ug=; 34295\_at Cluster Incl. AB011101:Homo sapiens mRNA for KIAA0529 protein, partial ; 35183\_at Cluster Incl. U78735:Human ABC3 mRNA, complete cds /cds=(559,5673) /gb=; 35653\_at Cluster Incl. U28963:Human Gps2 (GPS2) mRNA, complete cds /cds=(90,1073; 36930\_at Cluster Incl. L05425:Homo sapiens autoantigen

- mRNA, complete cds /cds=(; 37888\_at Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0; 38688\_at Cluster Incl. AB007930:Homo sapiens mRNA for KIAA0461 peroteine, partial; 38695\_at Cluster Incl. AA203303:zx55b01.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 39029\_at Cluster Incl. U11861:Human G10 homolog (edg-2) mRNA, complete cds
- 5 /cds=; 39688\_at Cluster Incl. AF001433:Human requiem (HREQ) mRNA, complete cds /cds=(41; 39723\_at Cluster Incl. AF062536:Homo sapiens cullin 1 mRNA, complete cds /cds=(1; 39800\_s\_at Cluster Incl. U68566:Human HS1 binding protein HAX-1 mRNA, nuclear ge; 40130\_at Cluster Incl. U06863:Human follistatin-related protein precursor mRNA, ; 40870\_g\_at Cluster Incl. AF069517:Homo sapiens RNA binding protein DEF-3 mRNA, c; 33915\_at Cluster Incl.
- 10 W22655:71B9 Homo sapiens cDNA /clone=(not-directional) /g; 34302\_at Cluster Incl. U96074:Human translation initiation factor eIF3 p44 subun; 34325\_at Cluster Incl. AJ005893:Homo sapiens mRNA for JM26 protein, complete CDS; 36093\_at Cluster Incl. AB014514:Homo sapiens mRNA for KIAA0614 protein, partial ; 36185\_at Cluster Incl. D32050:Human mRNA for alanyl-tRNA synthetase, complete cd; 40276\_at Cluster Incl. D50063:Human mRNA for proteasome subunit p40\_ / Mov34 prot; 40609\_at Cluster Incl. AI475497:tj92g12.x1 Homo sapiens cDNA, 3 end
- 15 /clone=IMAG; 40937\_at Cluster Incl. AA160056:zo84f11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41272\_s\_at Cluster Incl. W29031:55c6 Homo sapiens cDNA /gb=W29031 /gi=1308988 /u; 41821\_at Cluster Incl. AA203246:zx54h03.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 32546\_at Cluster Incl. U59309:Human fumarase precursor (FH) mRNA, nuclear gene
- 20 e; 33162\_at Cluster Incl. X02160:Human mRNA for insulin receptor precursor /cds=(48; 1875\_f\_at D38498 /FEATURE= /DEFINITION=HUMPMS1A Human PMS5 mRNA (yeast mismatch ; 1808\_s\_at X89101 /FEATURE=cds /DEFINITION=HSFASMRNA H.sapiens mRNA for Fas (Apo-; 1409\_at J03161 /FEATURE=mRNA /DEFINITION=HUMSRF Human serum response factor (SRF; 541\_g\_at S67070 /FEATURE= /DEFINITION=S67070 heat shock protein HSP72 homolog [h.
- 25 **Metagene** 356; 37471\_at Cluster Incl. U94317:Homo sapiens ribonuclease P protein subunit p40 (R; 38151\_at Cluster Incl. AF002672:Homo sapiens breast cancer suppressor candidate ; 39618\_at Cluster Incl. U43328:Human link protein mRNA, complete cds /cds=(117,11; 39961\_at Cluster Incl. AB011138:Homo sapiens mRNA for KIAA0566 protein, partial ; 41470\_at Cluster Incl. AF027208:Homo sapiens AC133 antigen mRNA, complete cds /c.
- 30 **Metagene** 357; 35075\_at Cluster Incl. AI571208:tn43d09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39619\_at Cluster Incl. AF070551:Homo sapiens clone 24515 mRNA sequence /cds=UNKN; 39940\_at Cluster Incl. AL080094:Homo sapiens mRNA; cDNA DKFZp564O1262 (from clon; 41029\_at Cluster Incl. U44798:Human U1-snRNP binding protein homolog mRNA, compl; 41402\_at Cluster Incl. AL080121:Homo sapiens mRNA; cDNA DKFZp564O0823 (from clon; 36525\_at Cluster Incl. AL049953:Homo sapiens mRNA; cDNA DKFZp564P0622 (from clon; 38975\_at Cluster Incl. AF062534:Homo sapiens genethonin 1 mRNA, complete cds /cd; 39017\_at Cluster Incl. AJ238094:Homo sapiens mRNA for Lsm1 protein /cds=(188,589; 39702\_at Cluster Incl. U77665:Human RNaseP protein p30 (RPP30) mRNA, complete cd; 34400\_at Cluster Incl. AI540957:PEC1.2\_15\_G03.r Homo sapiens cDNA, 5 end /clone; 35288\_at Cluster Incl.
- 35

- AB007884: Homo sapiens KIAA0424 mRNA, partial cds /cds=(80; 37312\_at Cluster Incl.  
D50917: Human mRNA for KIAA0127 gene, complete cds /cds=(2; 869\_at U14193 /FEATURE=  
/DEFINITION=HSU14193 Human TFIIA gamma subunit mRNA, com; 283\_at L16842  
/FEATURE= /DEFINITION=HUMMITCOR Human ubiquinol cytochrome-c redu.
- 5 **Metagene** 358; 35956\_s\_at Cluster Incl. U18467: Human pregnancy-specific beta 1-glycoprotein 7 (;  
37102\_at Cluster Incl. AA203717:zx52f12.r1 Homo sapiens cDNA, 5 end /clone=IMAG;  
39496\_s\_at Cluster Incl. W27595:34h5 Homo sapiens cDNA /gb=W27595 /gi=1307543 /u; 40241\_at  
Cluster Incl. U09850: Human zinc finger protein (ZNF143) mRNA, complete ; 41518\_at Cluster Incl.  
AI925356:wn53b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 601\_s\_at M28439
- 10 /FEATURE=cds /DEFINITION=HUMKER16A8 Human keratin type 16 gene, .  
**Metagene** 359; 32977\_at Cluster Incl. U49187: Human placenta (Diff48) mRNA, complete cds  
/cds=(4; 34898\_at Cluster Incl. M30704: Human amphiregulin (AR) mRNA, complete cds, clones;  
41870\_at Cluster Incl. AF030428: Homo sapiens lung type-I cell membrane-associate; 37544\_at  
Cluster Incl. X64318: H.sapiens E4BP4 gene /cds=(213,1601) /gb=X64318 /g; 38354\_at Cluster Incl.
- 15 X52560: Human gene for nuclear factor NF-IL6 /cds=(0,1037); 39081\_at Cluster Incl.  
AI547258:PN001\_AH\_H08.r Homo sapiens cDNA, 5 end /clone\_ ; 36634\_at Cluster Incl.  
U72649: Human BTG2 (BTG2) mRNA, complete cds /cds=(71,547); 38805\_at Cluster Incl.  
X89750: H.sapiens mRNA for TGIF protein /cds=(311,1129) /g; 39822\_s\_at Cluster Incl.  
AF078077: Homo sapiens growth arrest and DNA-damage-indu; 40268\_at Cluster Incl.
- 20 X16706: Human fra-2 mRNA /cds=(3,983) /gb=X16706 /gi=31464; 33146\_at Cluster Incl.  
L08246: Human myeloid cell differentiation protein (MCL1) ; 1052\_s\_at M83667  
/FEATURE=mRNA /DEFINITION=HUMNFIL6BA Human NF-IL6-beta protein ; 998\_s\_at  
X59770 /FEATURE=mRNA /DEFINITION=HSIL1R2II H.sapiens IL-1R2 mRNA for ty; 277\_at  
L08246 /FEATURE= /DEFINITION=HUMMCLIX Human myeloid cell differentiation .
- 25 **Metagene** 360; 31982\_at Cluster Incl. AB020701: Homo sapiens mRNA for KIAA0894 protein,  
complete; 32986\_s\_at Cluster Incl. D83760: Homo sapiens mRNA for mother against dpp (Mad) r;  
34162\_at Cluster Incl. D84111: Homo sapiens mRNA for RBP-MS/type 5, partial cds /; 34163\_g\_at  
Cluster Incl. D84111: Homo sapiens mRNA for RBP-MS/type 5, partial cds; 36691\_at Cluster Incl.  
X82224: H.sapiens mRNA for glutamine transaminase K /cds=(; 41028\_at Cluster Incl.
- 30 AJ001515: Homo sapiens mRNA for ryanodine receptor 3, comp; 33290\_at Cluster Incl.  
M74161: Human inositol polyphosphate 5-phosphatase (5ptase; 33808\_at Cluster Incl.  
AL022721:dJ109F14.1.1 (Transcriptional Enhancer Factor TE; 34203\_at Cluster Incl. D17408: Homo  
sapiens mRNA for calponin, complete cds /cds=; 35211\_at Cluster Incl. L07590: Human protein  
phosphatase 2A 130 kDa regulatory su; 37580\_at Cluster Incl. AF036271: Homo sapiens EEN-B2-L3  
mRNA, complete cds /cds=(; 38298\_at Cluster Incl. U25138: Human MaxiK potassium channel beta  
subunit mRNA, c; 38984\_at Cluster Incl. AB007896: Homo sapiens KIAA0436 mRNA, partial cds  
/cds=(0; 39730\_at Cluster Incl. X16416: Human c-abl mRNA encoding p150 protein /cds=(147,3;  
41195\_at Cluster Incl. U49957: Human LIM protein (LPP) mRNA, partial cds /cds=(24; 32856\_at  
Cluster Incl. AB020626: Homo sapiens mRNA for KIAA0819 protein, partial ; 35330\_at Cluster Incl.

- AJ012737:Homo sapiens mRNA for filamin, muscle isoform /c; 35359\_at Cluster Incl.
- D87078:Human mRNA for KIAA0235 gene, partial cds /cds=(1,; 37407\_s\_at Cluster Incl.
- AF013570:Homo sapiens smooth muscle myosin heavy chain ; 38048\_at Cluster Incl. D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cds ; 38049\_g\_at Cluster Incl. D84110:Homo sapiens mRNA for RBP-MS/type 4, complete cd; 40165\_at Cluster Incl. AB015345:Homo sapiens HRIHFB2216 mRNA, partial cds /cds=(; 40578\_s\_at Cluster Incl. M77016:Human tropomodulin mRNA, complete cds /cds=(34,1; 1826\_at M12174 /FEATURE= /DEFINITION=HUMRHOA Human ras-related rho mRNA (clone 6; 1635\_at U07563 /FEATURE=Poly\_A\_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogene ; 1297\_at D84110 /FEATURE=
- 10 /DEFINITION=D84110 Homo sapiens mRNA for RBP-MS/type 4,; 1276\_g\_at D84110 /FEATURE= /DEFINITION=D84110 Homo sapiens mRNA for RBP-MS/type ; 1197\_at D00654 /FEATURE=cds /DEFINITION=HUMACTSG7 Homo sapiens gene for enteric ; 343\_s\_at D12485 /FEATURE=cds#1 /DEFINITION=HUMNPP Human mRNA for nucleotide pyro.
- Metagene 361;** 33602\_at Cluster Incl. AJ000479:Homo sapiens mRNA for putative G-protein coupled; 34122\_at Cluster Incl. AF027807:Homo sapiens beta-casein (CSN2) gene, complete c; 35381\_at Cluster Incl. AL080127:Homo sapiens mRNA; cDNA DKFZp434C013 (from clone; 37792\_s\_at Cluster Incl. Y15572:Homo sapiens mRNA for recombination repair prote; 38202\_at Cluster Incl. AB011535:Homo sapiens mRNA for MEGF1, partial cds /cds=(0; 38899\_s\_at Cluster Incl. U95822:Human putative transmembrane GTPase mRNA, partia; 40371\_at Cluster Incl.
- 20 X51362:Human mRNA for dopamine D2 receptor /cds=(165,1496; 35188\_at Cluster Incl. AB018336:Homo sapiens mRNA for KIAA0793 protein, complete; 36479\_at Cluster Incl. AF050078:untitled /cds=(122,1558) /gb=AF050078 /gi=381846; 38623\_at Cluster Incl. AI014538:ou40e01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39738\_at Cluster Incl. Z82215:Homo sapiens DNA sequence from PAC 68O2 on chromos; 41170\_at Cluster Incl.
- 25 AB014563:Homo sapiens mRNA for KIAA0663 protein, complete; 34829\_at Cluster Incl. U59151:Human Cbf5p homolog (CBF5) mRNA, complete cds /cds; 38779\_r\_at Cluster Incl. D16431:Human mRNA for hepatoma-derived growth factor, c; 41262\_at Cluster Incl. AL021707:Human DNA sequence from clone 508I15 on chromoso; 1662\_r\_at Antigen, Prostate Specific, Alt. Splice Form 2 ; 1366\_i\_at M26880 /FEATURE= /DEFINITION=HUMUBI13 Human ubiquitin mRNA, complete c; 258\_at M16441 /FEATURE=cds#1 /DEFINITION=HUMTNFAB Human tumor necrosis factor an.
- 30 **Metagene 362;** 31486\_s\_at Cluster Incl. Z70218:H.sapiens mRNA for MN1 protein (clone ICRFp507I0; 31943\_g\_at Cluster Incl. AF045583:Homo sapiens tubby like protein 3 (TULP3) mRNA; 33533\_at Cluster Incl. U40992:Homo sapiens heat shock protein hsp40 homolog mRNA; 36718\_s\_at Cluster Incl. L42452:Homo sapiens pyruvate dehydrogenase kinase isoen; 36783\_f\_at Cluster Incl. M55422:Human Krueppel-related zinc finger protein (H-pl; 39565\_at Cluster Incl. Z22535:H.sapiens ALK-3 mRNA /cds=(309,1907) /gb=Z22535 /g; 40387\_at Cluster Incl. U80811:Human lysophosphatidic acid receptor homolog mRNA,; 34732\_at Cluster Incl. X65873:H.sapiens mRNA for kinesin (heavy chain) /cds=(313; 34735\_at Cluster Incl.
- 35

- U43195:Human Rho-associated, coiled-coil containing prote; 35221\_at Cluster Incl.  
 X91648:H.sapiens mRNA for pur alpha extended 3untranslate; 36534\_at Cluster Incl.  
 AF070621:Homo sapiens clone 24760 mRNA sequence /cds=UNKN; 37902\_at Cluster Incl.  
 L13278:Homo sapiens zeta-crystallin/quinone reductase mRNA; 39055\_at Cluster Incl.
- 5 M32886:Human sorcin CP-22 mRNA, complete cds /cds=(12,608; 39365\_i\_at Cluster Incl.  
 Y18207:Homo sapiens mRNA for protein phosphatase 1 (PPP; 39724\_s\_at Cluster Incl.  
 U58087:Human Hs-cul-1 mRNA, complete cds /cds=(124,2382; 40119\_at Cluster Incl.  
 AJ006470:Homo sapiens mRNA for cartilage-associated prote; 40441\_g\_at Cluster Incl.  
 AL080119:Homo sapiens mRNA; cDNA DKFZp564M2423 (from cl; 40879\_at Cluster Incl.
- 10 AB014599:Homo sapiens mRNA for KIAA0699 protein, partial ; 41234\_at Cluster Incl.  
 AI540318:tq34f03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41739\_s\_at Cluster Incl.  
 M83216:Human aorta caldesmon mRNA, complete cds /cds=(2; 32179\_s\_at Cluster Incl.  
 Y09568:Homo sapiens mRNA for SNAP23B protein, complete ; 32779\_s\_at Cluster Incl.  
 U23850:Human inositol 1,4,5 trisphosphate receptor type; 33385\_g\_at Cluster Incl. U31346:Human
- 15 calpastatin mRNA, partial cds, long 3UTR /; 34350\_at Cluster Incl. X64838:H.sapiens mRNA for  
 restin /cds=(132,4415) /gb=X648; 35259\_s\_at Cluster Incl. Y11251:H.sapiens mRNA for novel  
 member of serine-argini; 35788\_at Cluster Incl. W28994:54h7 Homo sapiens cDNA /gb=W28994  
 /gi=1308960 /ug=; 36684\_at Cluster Incl. M21154:Human S-adenosylmethionine decarboxylase  
 mRNA, com; 37738\_g\_at Cluster Incl. D25547:Homo sapiens mRNA for PIMT isozyme I, complete
- 20 c; 37747\_at Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U0;  
 38736\_at Cluster Incl. AL050108:Homo sapiens mRNA; cDNA DKFZp586I2219 (from clon;  
 38756\_at Cluster Incl. M22995:Human ras-related protein (Krev-1) mRNA, complete ; 41313\_at  
 Cluster Incl. M86917:Human oxysterol-binding protein (OSBP) mRNA, compl; 32548\_at Cluster  
 Incl. L24804:Human (p23) mRNA, complete cds /cds=(232,714) /gb=; 2085\_s\_at D14705
- 25 /FEATURE= /DEFINITION=HUMALPHAC Human mRNA for alpha-catenin, c; 2069\_s\_at L23805  
 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, ; 2033\_s\_at  
 U10564 /FEATURE= /DEFINITION=HSU10564 Human CDK tyrosine 15-kinase WEE; 2010\_at  
 U33760 /FEATURE= /DEFINITION=HSU33760 Human cyclin A/CDK2-associated p19; 1959\_at  
 D88674 /FEATURE= /DEFINITION=D88674 Homo sapiens mRNA for antizyme inhib; 1423\_at
- 30 D78514 /FEATURE=cds /DEFINITION=D78514 Homo sapiens mRNA for ubiquitin-c; 772\_at  
 D10656 /FEATURE= /DEFINITION=HUMCRK Human mRNA for CRK-II, complete cds ;  
 748\_s\_at D63940 /FEATURE= /DEFINITION=HUMHMXI1HL Human mRNA for Mxi1 protein,  
 co; 621\_at M28211 /FEATURE= /DEFINITION=HUMRAB4A Homo sapiens GTP-binding protein  
 (R; 312\_s\_at Focal Adhesion Kinase ; 227\_g\_at M33336 /FEATURE=
- 35 /DEFINITION=HUMCAMPPK Human cAMP-dependent protein kin; 158\_at U40992 /FEATURE=  
 /DEFINITION=HSU40992 Homo sapiens heat shock protein hsp.  
**Metagene** 363; 37523\_at Cluster Incl. M74096:Human long chain acyl-CoA dehydrogenase  
 (ACADL) mR; 40647\_at Cluster Incl. Z32684:Homo sapiens mRNA for membrane transport protein  
 (; 32709\_at Cluster Incl. L39833:Homo sapiens (clone hKvBeta3) K+ channel beta subu; 32711\_g\_at

- Cluster Incl. X83127:H.sapiens mRNA for voltage gated potassium chann; 33799\_at Cluster Incl.  
 U76248:Human hSIAH2 mRNA, complete cds /cds=(526,1500) /g; 34257\_at Cluster Incl.  
 AB014605:Homo sapiens mRNA for KIAA0705 protein, complete; 34262\_at Cluster Incl.  
 Y15909:Homo sapiens mRNA for dia-156 protein /cds=(350,36; 35730\_at Cluster Incl.
- 5 X03350:Human mRNA for alcohol dehydrogenase beta-1-subuni; 38316\_at Cluster Incl.  
 AF052732:Homo sapiens 10-formyltetrahydrofolate dehydroge; 38717\_at Cluster Incl.  
 AL050159:Homo sapiens mRNA; cDNA DKFZp586A0522 (from clon; 39366\_at Cluster Incl.  
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 AB014595:Homo sapiens mRNA for KIAA0695 protein, complete; 40409\_at Cluster Incl.
- 10 U46689:Human microsomal aldehyde dehydrogenase (ALD10) mR; 40461\_at Cluster Incl.  
 AB007855:Homo sapiens KIAA0395 mRNA, partial cds /cds=(0; 41770\_at Cluster Incl.  
 AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-745750; 41771\_g\_at Cluster Incl.  
 AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-7457; 41772\_at Cluster Incl.  
 M68840:Human monoamine oxidase A (MAOA) mRNA, complete cd; 32251\_at Cluster Incl.
- 15 AA149307:zl25h05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36119\_at Cluster Incl.  
 AF070648:Homo sapiens clone 24651 mRNA sequence /cds=UNKN; 38046\_at Cluster Incl.  
 AJ005579:Homo sapiens mRNA for Prer protein /cds=(0,1673); 38394\_at Cluster Incl.  
 D42047:Human mRNA for KIAA0089 gene, partial cds /cds=(0; 39809\_at Cluster Incl.  
 AF019214:Homo sapiens HMG box containing protein 1 mRNA, ; 41244\_f\_at Cluster Incl.
- 20 X80910:H.sapiens PPP1CB mRNA /cds=(258,1241) /gb=X80910; 1686\_g\_at X82554  
 /FEATURE=mRNA /DEFINITION=HSSPHAR H.sapiens SPHAR gene for cycl; 1182\_at D42108  
 /FEATURE= /DEFINITION=HUMPLCE Human mRNA for phospholipase C, com.  
**Metagene** 364; 36239\_at Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,12;  
 37420\_i\_at Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, ; 33304\_at
- 25 Cluster Incl. U88964:Human HEM45 mRNA, complete cds /cds=(37,582) /gb=U; 41166\_at Cluster  
 Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy ; 34332\_at Cluster Incl.  
 D31766:Human mRNA for KIAA0060 gene, complete cds /cds=(4; 36599\_at Cluster Incl.  
 M55905:Human mitochondrial NAD(P)+ dependent malic enzyme; 40615\_at Cluster Incl.  
 AA780049:zj24f06.s1 Homo sapiens cDNA, 3 end /clone=4512; 41522\_at Cluster Incl.
- 30 Z93096:Human DNA sequence from BAC 390B3 on chromosome 22; 2059\_s\_at M36881  
 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific pr; 1630\_s\_at  
 Tyrosine Kinase Syk.  
**Metagene** 365; 34046\_at Cluster Incl. Z83844:Human DNA sequence from clone 37E16 on  
 chromosome ; 34481\_at Cluster Incl. AF030227:untitled /cds=(97,2634) /gb=AF030227
- 35 /gi=3282618; 36243\_at Cluster Incl. AL050262:Homo sapiens mRNA; cDNA DKFZp547I0610  
 (from clon; 36709\_at Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein;  
 36753\_at Cluster Incl. AF072099:Homo sapiens immunoglobulin-like transcript 3 pr; 36795\_at  
 Cluster Incl. J03077:Human co-beta glucosidase (proactivator) mRNA, com; 37105\_at Cluster Incl.  
 M16117:Human cathepsin G mRNA, complete cds /cds=(8,775) ; 37470\_at Cluster Incl.



- AF013249: Homo sapiens leukocyte-associated Ig-like recept; 40390\_at Cluster Incl. J05037: Human serine dehydratase mRNA, complete cds /cds=(; 40745\_at Cluster Incl. L13939: Homo sapiens beta adaptin (BAM22) mRNA, complete c; 41059\_at Cluster Incl. AF020314: Homo sapiens CMRF-35-H9 mRNA, complete cds /cds=; 31816\_at Cluster Incl. X55079: Human lysosomal alpha-glucosidase gene exon 1 /cds; 31826\_at Cluster Incl. AB014574: Homo sapiens mRNA for KIAA0674 protein, partial ; 31901\_at Cluster Incl. AF044253: Homo sapiens potassium channel beta 2 subunit (H; 32116\_at Cluster Incl. AB002405: Homo sapiens mRNA for LAK-4p, complete cds /cds=; 32128\_at Cluster Incl. Y13710: Homo sapiens mRNA for alternative activated macrop; 32704\_at Cluster Incl. D86964: Human mRNA for KIAA0209 gene, partial cds /cds=(0,; 32715\_at Cluster Incl.
- 10 N90862:zb11b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 33283\_at Cluster Incl. AF106941: Homo sapiens beta-arrestin 2 mRNA, complete cds ; 33813\_at Cluster Incl. AI813532:wj83a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36062\_at Cluster Incl. AF062075: Homo sapiens leupaxin mRNA, complete cds /cds=(9; 36493\_at Cluster Incl. M33552: Human lymphocyte-specific protein 1 (LSP1) mRNA, c; 36495\_at Cluster Incl.
- 15 U21931: Human fructose-1,6-biphosphatase (FBP1) gene /cds=; 36861\_at Cluster Incl. AL049946: Homo sapiens mRNA; cDNA DKFZp564I1922 (from clon; 37591\_at Cluster Incl. U94592: Human uncoupling protein homolog (UCPH) mRNA, comp; 38363\_at Cluster Incl. W60864:zd27g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 38671\_at Cluster Incl. AB014520: Homo sapiens mRNA for KIAA0620 protein, partial ; 39728\_at Cluster Incl.
- 20 J03909: Human gamma-interferon-inducible protein (IP-30) m; 40420\_at Cluster Incl. AB015718: Homo sapiens lok mRNA for protein kinase, comple; 41200\_at Cluster Incl. Z22555: H.sapiens encoding CLA-1 mRNA /cds=(69,1598) /gb=Z; 32207\_at Cluster Incl. M64925: Human palmitoylated erythrocyte membrane protein (; 32773\_at Cluster Incl. AA868382:ak41e04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32794\_g\_at Cluster Incl.
- 25 X00437: Human mRNA for T-cell specific protein /cds=(37,; 33374\_at Cluster Incl. L09708: Human complement component 2 (C2) gene allele b /c; 35820\_at Cluster Incl. X62078: H.sapiens mRNA for GM2 activator protein /cds=UNKN; 36167\_at Cluster Incl. D89052: Homo sapiens mRNA for proton-ATPase-like protein, ; 36197\_at Cluster Incl. Y08374: H.sapiens gene encoding cartilage GP-39 protein, e; 36207\_at Cluster Incl. D67029: Human SEC14L mRNA, complete cds /cds=(303,2450) /g; 36651\_at Cluster Incl. X15525: H.sapiens lysosomal acid phosphatase gene (EC 3.1.; 37039\_at Cluster Incl. J00194: human hla-dr antigen alpha-chain mrna & ivs fragme; 37344\_at Cluster Incl. X62744: Human RING6 mRNA for HLA class II alpha chain-like; 37391\_at Cluster Incl. X12451: Human mRNA for pro-cathepsin L (major excreted pro; 37395\_at Cluster Incl. D49400: Homo sapiens mRNA for vacuolar ATPase, complete cd; 37742\_at Cluster Incl.
- 35 M34423: Human beta-galactosidase (GLB1) mRNA, complete cds; 37759\_at Cluster Incl. U51240: Human lysosomal-associated multitransmembrane prot; 38091\_at Cluster Incl. Z49107: H.sapiens mRNA for galectin /cds=(87,1058) /gb=Z49; 38095\_i\_at Cluster Incl. M83664: Human MHC class II lymphocyte antigen (HLA-DP) b; 38391\_at Cluster Incl. M94345: Homo sapiens macrophage capping protein mRNA, comp; 38482\_at Cluster Incl.

- AJ011497: Homo sapiens mRNA for Claudin-7 /cds=(334,969) /; 38798\_s\_at Cluster Incl.
- AI741833: wg29e04.x1 Homo sapiens cDNA, 3 end /clone=IM; 38833\_at Cluster Incl.
- X00457: Human mRNA for SB classII histocompatibility antigen; 40267\_s\_at Cluster Incl.
- AI880840: at11d06.x1 Homo sapiens cDNA, 3 end /clone=IM; 1583\_at M32315 /FEATURE=
- 5 /DEFINITION=HUMNFR Human tumor necrosis factor receptor; 1445\_at AF014958 /FEATURE=
- /DEFINITION=AF014958 Homo sapiens chemokine receptor ; 1105\_s\_at M12886 /FEATURE=
- /DEFINITION=HUMTCBYY Human T-cell receptor active bet; 1106\_s\_at M12959 /FEATURE=
- /DEFINITION=HUMTCAXB Human T-cell receptor active alp; 1061\_at U00672 /FEATURE=
- /DEFINITION=U00672 Human interleukin-10 receptor mRNA, ; 925\_at J03909 /FEATURE=
- 10 /DEFINITION=HUMIIP Human gamma-interferon-inducible prot; 879\_at M30818
- /FEATURE=mRNA /DEFINITION=HUMMXB Human interferon-induced cellular; 766\_at
- AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens mRNA for galectin-9 ; 677\_s\_at
- J04430 /FEATURE=mRNA /DEFINITION=HUMACP5 Human tartrate-resistant acid ; 512\_at
- U22662 /FEATURE= /DEFINITION=HSU22662 Human nuclear orphan receptor LXR-a; 425\_at
- 15 X67325 /FEATURE=cds /DEFINITION=HSP27 H.sapiens p27 mRNA ; 239\_at M63138
- /FEATURE=mRNA /DEFINITION=HUMCATD5 Human cathepsin D (catD) gene, ; 189\_s\_at
- U09937 /FEATURE=mRNA /DEFINITION=HSUROKR7 Human urokinase-type plasmino.
- Metagene** 366; 31438\_s\_at Cluster Incl. Z22971: H.sapiens mRNA for M130 antigen extracellular
- va; 36255\_at Cluster Incl. L77730: Homo sapiens A3 adenosine receptor (ADORA3) gene /;
- 20 36708\_at Cluster Incl. J04970: Human carboxypeptidase M, 3 end /cds=(0,1319) /gb; 37099\_at
- Cluster Incl. AI806222: wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 31820\_at Cluster
- Incl. X16663: Human HS1 gene for hematopoietic lineage cell spe; 36884\_at Cluster Incl.
- Z22970: H.sapiens mRNA for M130 antigen cytoplasmic variant; 36908\_at Cluster Incl.
- M93221: Human macrophage mannose receptor (MRC1) gene /cds; 37976\_at Cluster Incl.
- 25 AL034397: Human DNA sequence from clone 159A1 on chromosome; 40082\_at Cluster Incl.
- D10040: Homo sapiens mRNA for long-chain acyl-CoA synthetase; 36589\_at Cluster Incl.
- X15414: Human mRNA for aldose reductase (EC 1.1.1.2) /cds=; 36609\_at Cluster Incl.
- D26443: Human mRNA for glutamate transporter, complete cds; 41271\_at Cluster Incl.
- Y18483: Homo sapiens mRNA for SLC7A8 protein /cds=(730,233; 32578\_at Cluster Incl.
- 30 AW005997: wz91c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1795\_g\_at M92287
- /FEATURE= /DEFINITION=HUMCYCD3A Homo sapiens cyclin D3 (CCND3) ; 581\_at M61916
- /FEATURE= /DEFINITION=HUMLAM101 Human laminin B1 chain mRNA, compl.
- Metagene** 367; 32455\_s\_at Cluster Incl. U88153: Homo sapiens p160 mRNA, partial cds
- /cds=(0,3755; 32360\_s\_at Cluster Incl. AF017146: Homo sapiens DNA topoisomerase III beta
- 35 (TOP3b; 35466\_at Cluster Incl. W73046: zd54h09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-;
- 38523\_f\_at Cluster Incl. D49677: Human U2AF1-RS2 mRNA, complete cds /cds=(24,1472;
- 40705\_at Cluster Incl. AF103905: Homo sapiens Rap1 guanine-nucleotide exchange fa; 41426\_at
- Cluster Incl. U38864: Human zinc-finger protein C2H2-150 mRNA, complete ; 31873\_at Cluster
- Incl. U52112: ARD1 N-acetyl transferase related protein /cds=(97; 34758\_at Cluster Incl.

- U23028:Human eukaryotic initiation factor 2B-epsilon mRNA; 35225\_at Cluster Incl.  
M91592:Human zinc-finger protein (ZNF76) gene, partial cd; 37955\_at Cluster Incl.  
AB015631:Homo sapiens mRNA for type II membrane protein, ; 38682\_at Cluster Incl.  
AF045581:Homo sapiens BRCA1 associated protein 1 (BAP1) m; 39067\_at Cluster Incl.
- 5 M27937:Human male-enhanced antigen mRNA (Mea), complete c; 39729\_at Cluster Incl.  
L19185:Human natural killer cell enhancing factor (NKEFB); 40068\_at Cluster Incl. U26648:Homo sapiens syntaxin 5 mRNA, complete cds /cds=(2; 40133\_s\_at Cluster Incl. W28944:54h12 Homo sapiens cDNA /gb=W28944 /gi=1308955 /; 41734\_at Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete; 33838\_at Cluster Incl. M33519:Human HLA-B-associated
- 10 transcript 3 (BAT3) mRNA, c; 34880\_at Cluster Incl. AC002115:Human DNA from overlapping chromosome 19 cosmids; 37319\_at Cluster Incl. M35878:Human insulin-like growth factor-binding protein-3; 37667\_at Cluster Incl. AF104421:Homo sapiens isolate normal patient 1 uroporphyr; 38376\_at Cluster Incl. L46590:Homo sapiens very long chain acyl-CoA dehydrogenas; 38424\_at Cluster Incl. AB018290:Homo sapiens mRNA for KIAA0747 protein, partial ; 41596\_s\_at Cluster
- 15 Incl. U43572:Human alpha-N-acetylglucosaminidase (NAGLU) gene; 1496\_at M34668 /FEATURE= /DEFINITION=HUMPTPAAA Human protein tyrosine phosphatas; 1470\_at U21090 /FEATURE= /DEFINITION=HSU21090 Human DNA polymerase delta small s; 958\_s\_at Rna Polymerase II, 14.5 Kda Subunit .  
**Metagene** 368; 34708\_at Cluster Incl. D88587:Homo sapiens mRNA for Hakata antigen, complete
- 20 cds; 32224\_at Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete; 33200\_at Cluster Incl. D50550:Human LLGL mRNA, complete cds /cds=(45,3143) /gb=D; 1947\_g\_at M60614 /FEATURE= /DEFINITION=HUMWITA Human Wilms tumor (WIT-1) associ; 260\_at M16447 /FEATURE= /DEFINITION=HUMDHPRA Human dihydropteridine reductase (h.  
**Metagene** 369; 33702\_f\_at Cluster Incl. L05144:Homo sapiens (clone lamda-hPEC-3)
- 25 phosphoenolpyr; 39408\_at Cluster Incl. Z80345:H.sapiens SCAD gene, 5 UTR exon 1 and 2 (and joine; 39805\_at Cluster Incl. AF070598:Homo sapiens clone 24410 ABC transporter mRNA, p.  
**Metagene** 370; 36448\_at Cluster Incl. X95677:H.sapiens mRNA for ArgBPIB protein /cds=(134,1033); 36215\_at Cluster Incl. M34181:Human testis-specific cAMP-dependent protein
- 30 kinas; 37162\_at Cluster Incl. S72869:H4(D10S170)=putative cytoskeletal protein [human, ; 37487\_at Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial ; 38208\_at Cluster Incl. AB021981:Homo sapiens mRNA for UDP-N-acetylglucosamine tr; 39927\_at Cluster Incl. U17032:Human p190-B (p190-B) mRNA, complete cds /cds=(302; 40689\_at Cluster Incl. U11037:Human Sel-1 like mRNA, complete cds /cds=(11,298) ; 32638\_s\_at Cluster Incl. AI610467:tp42a10.x1 Homo sapiens cDNA, 3 end /clone=IM; 34195\_at Cluster Incl.
- 35 AL121073:DKFZp762B235\_r1 Homo sapiens cDNA, 5 end /clone; 34684\_at Cluster Incl. L36140:Homo sapiens (clone 1311) DNA helicase (RECQL) mRN; 34716\_at Cluster Incl. AF067730:Homo sapiens TLS-associated protein TASR-2 mRNA,; 34717\_s\_at Cluster Incl. AF047448:Homo sapiens TLS-associated protein TASR mRNA,; 35705\_at Cluster Incl. D16815:Homo sapiens mRNA for EAR-1r, complete cds /cds=(3; 33864\_at Cluster Incl.

- X86098:H.sapiens mRNA for BS69 protein /cds=(244,1932) /g; 34886\_at Cluster Incl.
- L02320:Human radixin mRNA, complete cds /cds=(30,1781) /g; 35258\_f\_at Cluster Incl.
- AF030234:Homo sapiens splicing factor Sip1 mRNA, comple; 36632\_at Cluster Incl.
- U00957:Human clone KDB1.2 (CAC)n/(GTG)n repeat-containing; 37712\_g\_at Cluster Incl.
- 5 S57212:hMEF2C=myocyte enhancer-binding factor 2 [human; 38100\_at Cluster Incl.
- D87127:Homo sapiens mRNA for translocation protein-1, com; 40555\_at Cluster Incl.
- AL043108:DKFZp434C0823\_r1 Homo sapiens cDNA, 5 end /clon; 40928\_at Cluster Incl.
- W26496:30d2 Homo sapiens cDNA /gb=W26496 /gi=1307195 /ug=; 41549\_s\_at Cluster Incl.
- AF091077:Homo sapiens clone 558 unknown mRNA, complete ; 33103\_s\_at Cluster Incl.
- 10 U37122:Human adducin gamma subunit mRNA, complete cds /; 1660\_at D83004 /FEATURE=  
/DEFINITION=D83004 Human epidermoid carcinoma mRNA for ; 930\_at L07590 /FEATURE=  
/DEFINITION=HUMPP2A130 Human protein phosphatase 2A 130 ; 783\_at U96113 /FEATURE=  
/DEFINITION=HSU96113 Homo sapiens Nedd-4-like ubiquitin-; 784\_g\_at U96113 /FEATURE=  
/DEFINITION=HSU96113 Homo sapiens Nedd-4-like ubiquiti; 422\_s\_at X66867
- 15 /FEATURE=cds#2 /DEFINITION=HSMAXG H.sapiens max gene .
- Metagene** 371; 33678\_i\_at Cluster Incl. X02344:Homo sapiens beta 2 gene /cds=(0,1337)  
/gb=X0234; 32347\_at Cluster Incl. AI831572:wj39c02.x1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 37425\_g\_at Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod  
homo; 37817\_at Cluster Incl. AF052087:Homo sapiens clone 23604 mRNA sequence /cds=UNKN;  
20 39973\_at Cluster Incl. U47926:Human unknown protein B mRNA, complete cds /cds=(8; 41047\_at  
Cluster Incl. AI885170:w190e10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41610\_at Cluster  
Incl. AB011105:Homo sapiens mRNA for KIAA0533 protein, partial ; 41659\_at Cluster Incl.  
U46691:Human putative chromatin structure regulator (SUPT; 41720\_r\_at Cluster Incl.  
AF009767:AF009767 Homo sapiens cDNA /clone=C97A-12 /gb=; 34185\_at Cluster Incl.
- 25 W22541:69B4 Homo sapiens cDNA /clone=(not-directional) /g; 34229\_s\_at Cluster Incl.
- D84454:Human mRNA for UDP-galactose translocator, compl; 34726\_at Cluster Incl.
- U07139:Human voltage-gated calcium channel beta subunit m; 35627\_at Cluster Incl.
- U40571:Human alpha1-syntrophin (SNT A1) mRNA, complete cd; 37271\_at Cluster Incl.
- L25444:Homo sapiens (TAFII70-alpha) mRNA, complete cds /c; 37904\_s\_at Cluster Incl.
- 30 X66436:H.sapiens hsr1 mRNA (partial) /cds=UNKNOWN /gb=X; 38971\_r\_at Cluster Incl.
- AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated fa; 39076\_s\_at Cluster Incl.
- AI991040:wu36b05.x1 Homo sapiens cDNA, 3 end /clone=IM; 40151\_s\_at Cluster Incl.
- Z48054:H.sapiens mRNA for peroxisomal targeting signal ; 40470\_at Cluster Incl. D10523:Human  
mRNA for 2-oxoglutarate dehydrogenase, compl; 40867\_at Cluster Incl. J02902:Human protein  
35 phosphatase 2A regulatory subunit al; 41160\_at Cluster Incl. AC005943:Homo sapiens chromosome  
19, cosmid R30538 /cds=(; 32166\_at Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027  
protein, partial ; 32190\_at Cluster Incl. AL050118:Homo sapiens mRNA; cDNA DKFZp586C201  
(from clone; 33396\_at Cluster Incl. U12472:Human glutathione S-transferase (GST phi) gene, co;  
33833\_at Cluster Incl. J05243:Human nonerythroid alpha-spectrin (SPTAN1) mRNA, c; 33888\_at

- Cluster Incl. X82207:H.sapiens mRNA for beta-actin (PC3) /cds=(56,; 34318\_at Cluster Incl.  
 AJ005896:Homo sapiens mRNA for JM4 protein, complete CDS ; 34861\_at Cluster Incl.  
 D63997:Homo sapiens mRNA for GCP170, complete cds /cds=(2; 35265\_at Cluster Incl.  
 U31501:Human fragile X mental retardation syndrome relate; 35740\_at Cluster Incl.
- 5 AL050138:Homo sapiens mRNA; cDNA DKFZp586M121 (from clone; 36116\_at Cluster Incl.  
 AJ000414:Homo sapiens mRNA for Cdc42-interacting protein ; 36125\_s\_at Cluster Incl.  
 L38696:Homo sapiens autoantigen p542 mRNA, complete cds; 36138\_at Cluster Incl.  
 X04106:Human mRNA for calcium dependent protease (small s; 36644\_at Cluster Incl.  
 D29963:Homo sapiens mRNA for CD151, complete cds /cds=(84; 37329\_at Cluster Incl.
- 10 AF053070:Homo sapiens NADH-ubiquinone dehydrogenase 51 kD; 37410\_at Cluster Incl.  
 AJ224358:Homo sapiens surf5a mRNA, clone 1de /cds=(218,64; 37656\_at Cluster Incl.  
 D83782:Human mRNA for KIAA0199 gene, partial cds /cds=(0; 38119\_at Cluster Incl.  
 X12496:Human mRNA for erythrocyte membrane sialoglycoprot; 38750\_at Cluster Incl.  
 U97669:Homo sapiens Notch3 (NOTCH3) mRNA, complete cds /c; 38809\_s\_at Cluster Incl.
- 15 AB011091:Homo sapiens mRNA for KIAA0519 protein, comple; 40597\_g\_at Cluster Incl.  
 U76366:Human Treacher Collins syndrome (TCOF1) mRNA, co; 40955\_at Cluster Incl.  
 U79287:Human clone 23867 mRNA sequence /cds=UNKNOWN /gb=U; 41267\_at Cluster Incl.  
 AB028972:Homo sapiens mRNA for KIAA1049 protein, partial ; 41526\_at Cluster Incl.  
 AF072836:Homo sapiens Sox-like transcriptional factor mRNA; 41831\_at Cluster Incl.
- 20 AF077820:Homo sapiens LDL receptor member LR3 mRNA, compl; 32566\_at Cluster Incl.  
 AA165701:zo75g08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32608\_at Cluster Incl.  
 AF000560:Homo sapiens TTF-I interacting peptide 20 mRNA, ; 33206\_at Cluster Incl.  
 C18655:C18655 Homo sapiens cDNA, 5 end /clone=GEN-565G08; 1590\_s\_at J00277  
 /FEATURE=cds /DEFINITION=HUMRASH Human (genomic clones lambda-; 905\_at L76200
- 25 /FEATURE= /DEFINITION=HUMGUK1R Human guanylate kinase (GUK1) mRNA; 692\_s\_at  
 J02947 /FEATURE=mRNA /DEFINITION=HUMSODEC Human extracellular-superoxid; 564\_at  
 M69013 /FEATURE= /DEFINITION=HUMGTPBRPA Human guanine nucleotide-binding ;  
 330\_s\_at Tubulin, Alpha 1, Isoform 44 .  
**Metagene** 372; 36313\_at Cluster Incl. M55267:Human EV12 protein gene /cds=(0,698)  
 /gb=M55267 /g; 37148\_at Cluster Incl. AF025533:Homo sapiens leucocyte immunoglobulin-like  
 recep; 39248\_at Cluster Incl. N74607:za55a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-;  
 40648\_at Cluster Incl. U08023:Human cellular proto-oncogene (c-mer) mRNA, comple; 41710\_at  
 Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone ; 34215\_at Cluster Incl.  
 L03426:Human XE7 mRNA, complete alternate coding regions ; 35718\_at Cluster Incl.
- 35 L22342:Human nuclear phosphoprotein mRNA, complete cds /c; 36885\_at Cluster Incl.  
 L28824:Homo sapiens protein tyrosine kinase (Syk) mRNA, c; 32227\_at Cluster Incl.  
 X17042:Human mRNA for hematopoietic proteoglycan core prot; 34304\_s\_at Cluster Incl.  
 AL050290:Homo sapiens mRNA; cDNA DKFZp586G1923 (from cl; 35299\_at Cluster Incl.  
 AB000409:Homo sapiens mRNA for MNK1, complete cds /cds=(1; 38403\_at Cluster Incl.

- X77196:H.sapiens mRNA for lysosome-associated membrane pr; 40568\_at Cluster Incl.  
 L35249:Homo sapiens vacuolar H<sup>+</sup>-ATPase Mr 56,000 subunit ; 41253\_s\_at Cluster Incl.  
 AI983043:wz30b11.x1 Homo sapiens cDNA, 3 end /clone=IM; 1173\_g\_at Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2 ; 931\_at L08177 /FEATURE= /DEFINITION=HUMGPCRB Human  
 5 EBV induced G-protein coupled; 855\_at S78085 /FEATURE= /DEFINITION=S78085  
 PDCD2=programmed cell death-2/Rp8 hom; 138\_at U66464 /FEATURE=  
 /DEFINITION=HSU66464 Human hematopoietic progenitor kina.  
**Metagene 373;** 32914\_f\_at Cluster Incl. AC005175:Homo sapiens chromosome 19, cosmid R31449  
 /cds; 35005\_at Cluster Incl. AF051941:Homo sapiens type 6 nucleoside diphosphate kinas; 34207\_at  
 10 Cluster Incl. AB028946:Homo sapiens mRNA for KIAA1023 protein, partial ; 35165\_at Cluster Incl.  
 AF070582:Homo sapiens clone 24766 mRNA sequence /cds=UNKN; 32825\_at Cluster Incl.  
 Y10805:H.sapiens mRNA for arginine methyltransferase, spl; 34853\_at Cluster Incl.  
 AB007865:Homo sapiens KIAA0405 mRNA, complete cds /cds=(1; 35741\_at Cluster Incl.  
 U85245:Human phosphatidylinositol-4-phosphate 5-kinase ty.  
 15 **Metagene 374;** 33487\_at Cluster Incl. D31628:Human gene for 4-hydroxyphenylpyruvic acid  
 dioxyge; 36719\_r\_at Cluster Incl. L42452:Homo sapiens pyruvate dehydrogenase kinase isoen;  
 38950\_r\_at Cluster Incl. AJ005256:Homo sapiens mRNA for MMP-23 /cds=(38,1210) /g; 31855\_at  
 Cluster Incl. U61374:Human novel protein with short consensus repeats o; 37599\_at Cluster Incl.  
 AF017060:untitled /cds=(298,4314) /gb=AF017060 /gi=234315; 39045\_at Cluster Incl.  
 20 W26655:34c9 Homo sapiens cDNA /gb=W26655 /gi=1307498 /ug=; 35366\_at Cluster Incl.  
 M30269:Human nidogen mRNA, complete cds /cds=(90,3833) /g; 38459\_g\_at Cluster Incl.  
 L39945:Human cytochrome b5 (CYB5) gene /cds=(120,548) /; 39154\_at Cluster Incl.  
 AI952982:wp98b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41489\_at Cluster Incl.  
 M99435:Human transducin-like enhancer protein (TLE1) mRNA; 1749\_at AD000092  
 25 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro; 1667\_s\_at J02871  
 /FEATURE= /DEFINITION=HUMCP45IV Human lung cytochrome P450 (IV ; 374\_f\_at Z84718  
 /FEATURE=cds#5 /DEFINITION=HS322B1 Human DNA sequence from clone.  
**Metagene 375;** 35868\_at Cluster Incl. M91211:Human receptor for advanced glycosylation end  
 prod; 41356\_at Cluster Incl. W27619:35c7 Homo sapiens cDNA /gb=W27619 /gi=1307567 /ug=;  
 30 33196\_at Cluster Incl. U08191:Human R kappa B mRNA, complete cds /cds=(2220,5216; 1907\_at  
 L14812 /FEATURE= /DEFINITION=HUMP107B Human retinoblastoma related prote.  
**Metagene 376;** 31993\_f\_at Cluster Incl. U80764:Human EST clone 122887 mariner transposon  
 Hsmar1; 32401\_at Cluster Incl. U78110:Human prepro-neurturin mRNA, complete cds /cds=(0,;  
 33493\_at Cluster Incl. AF048849:Homo sapiens erythroid differentiation and denuc; 33521\_at  
 35 Cluster Incl. M63962:Human gastric H,K-ATPase catalytic subunit gene, c; 34453\_at Cluster Incl.  
 H19081:yn51e03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39684\_at Cluster Incl.  
 U37707:Human dl3 mRNA, complete cds /cds=(336,2093) /gb=; 40643\_at Cluster Incl.  
 M34480:Human platelet glycoprotein IIb (GPIIb) mRNA, comp; 40729\_s\_at Cluster Incl.  
 Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /c; 31819\_at Cluster Incl.

- AI796281:wh49a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35630\_at Cluster Incl.  
 X87342:H.sapiens mRNA for human giant larvae homolog /cds; 36451\_at Cluster Incl.  
 AI743299:wg91b04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39335\_at Cluster Incl.  
 AI074025:oy66g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32228\_at Cluster Incl.
- 5 AB020706:Homo sapiens mRNA for KIAA0899 protein, partial ; 40534\_at Cluster Incl.  
 AA843737:ak01e07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1296\_at D83542 /FEATURE=  
 /DEFINITION=HUMC15A Homo sapiens mRNA for cadherin-15, ; 385\_at X71874  
 /FEATURE=cds#2 /DEFINITION=HSPROSCHY H.sapiens genes for proteasom.  
**Metagene** 377; 32441\_at Cluster Incl. X52142:Human mRNA for CTP synthetase (EC 6.3.4.2)
- 10 /cds=(7; 32371\_at Cluster Incl. AB011099:Homo sapiens mRNA for KIAA0527 protein, partial ;  
 38577\_at Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region; 39932\_at  
 Cluster Incl. AI655015:wb66a10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40318\_at Cluster  
 Incl. AI810807:tu26a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41031\_at Cluster Incl.  
 AB000114:Homo sapiens mRNA for osteomodulin, complete cds; 41464\_at Cluster Incl.
- 15 AB002337:Human mRNA for KIAA0339 gene, complete cds /cds=; 32076\_at Cluster Incl.  
 D83407:ZAKI-4 mRNA in human skin fibroblast, complete cds; 35223\_at Cluster Incl.  
 AB023234:Homo sapiens mRNA for KIAA1017 protein, complete; 35649\_at Cluster Incl.  
 U80055:untitled /cds=(248,850) /gb=U80055 /gi=2138110 /ug; 36092\_at Cluster Incl.  
 AL080213:Homo sapiens mRNA; cDNA DKFZp586I1823 (from clon; 39425\_at Cluster Incl.
- 20 X91247:H.sapiens mRNA for thioredoxin reductase /cds=(439; 40045\_g\_at Cluster Incl.  
 AF009425:Homo sapiens clone 22 mRNA, alternative splici; 33878\_at Cluster Incl. W27472:31d4  
 Homo sapiens cDNA /gb=W27472 /gi=1307276 /ug=; 33905\_at Cluster Incl. AF072242:Homo  
 sapiens methyl-CpG binding protein MBD2 (MB; 35332\_at Cluster Incl. X04714:Human mRNA for  
 apolipoprotein B-100 (apoB-100) /cd; 38028\_at Cluster Incl. AL050152:Homo sapiens mRNA;
- 25 cDNA DKFZp586K1220 (from clon; 38469\_at Cluster Incl. M35252:Human CO-029  
 /cds=(137,850) /gb=M35252 /gi=180925 ; 38748\_at Cluster Incl. U76421:Human dsRNA adenosine  
 deaminase DRADA2b (DRADA2b) ; 40230\_at Cluster Incl. U91903:Human Fritz mRNA, complete  
 cds /cds=(69,1046) /gb=; 40530\_at Cluster Incl. AL080130:Homo sapiens mRNA; cDNA  
 DKFZp434E033 (from clone; 1736\_at M62402 /FEATURE= /DEFINITION=HUMIGFBP4 Human
- 30 insulin-like growth factor ; 1685\_at X82554 /FEATURE=mRNA /DEFINITION=HSSPHAR  
 H.sapiens SPHAR gene for cyclin; 1467\_at U12535 /FEATURE= /DEFINITION=HSU12535  
 Human epidermal growth factor rece.  
**Metagene** 378; 31530\_at Cluster Incl. U89344:Human acetyl-CoA carboxylase (ACC2) mRNA,  
 complete; 32275\_at Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix;
- 35 34922\_at Cluster Incl. AF047826:Homo sapiens cadherin-7 (CDH7) mRNA, partial cds; 41622\_r\_at  
 Cluster Incl. AA868898:ak55b08.s1 Homo sapiens cDNA, 3 end /clone=IM; 34183\_at Cluster Incl.  
 AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone; 36018\_at Cluster Incl.  
 AJ001183:Homo sapiens mRNA for Sox10 protein /cds=(120,15; 35817\_at Cluster Incl.  
 M13577:Human myelin basic protein (MBP) mRNA, complete cd; 38408\_at Cluster Incl.

- L10373:Human (clone CCG-B7) mRNA sequence /cds=UNKNOWN /g; 38747\_at Cluster Incl.  
 M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=; 1252\_at M73547 /FEATURE=  
 /DEFINITION=HUMPOLLA Human polyposis locus (DPI gene) m.
- Metagene 379;** 39236\_s\_at Cluster Incl. AL050372:Homo sapiens mRNA; cDNA DKFZp434A091  
 5 (from clo; 32073\_at Cluster Incl. AB014577:Homo sapiens mRNA for KIAA0677 protein, complete;  
 33287\_at Cluster Incl. AA533071:nj19e03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36876\_at  
 Cluster Incl. M55150:Human fumarylacetoacetate hydrolase mRNA, complete; 32221\_at Cluster  
 Incl. AL050361:Homo sapiens mRNA; cDNA DKFZp564H0223 (from clon; 34775\_at Cluster Incl.  
 AF065388:Homo sapiens tetraspan NET-1 mRNA, complete cds ; 36664\_at Cluster Incl.
- 10 M60091:Homo sapiens galactose-1-phosphate uridyl transfer; 36985\_at Cluster Incl. X17025:Human  
 homolog of yeast IPP isomerase /cds=(50,736); 37315\_f\_at Cluster Incl. AI057607:oy31e07.x1  
 Homo sapiens cDNA, 3 end /clone=IM; 38794\_at Cluster Incl. X53390:Human mRNA for upstream  
 binding factor (hUBF) /cds; 39516\_at Cluster Incl. AI827793:wf33b11.x1 Homo sapiens cDNA, 3  
 end /clone=IMAG; 41540\_at Cluster Incl. Z50749:H.sapiens sds22-like mRNA /cds=(15,1097)  
 15 /gb=Z5074.
- Metagene 380;** 36260\_at Cluster Incl. AB002448:Homo sapiens mRNA from chromosome 5q21-22,  
 clone; 39941\_at Cluster Incl. Z75311:H.sapiens mRNA for RAD50 /cds=(42,3998) /gb=Z75311;  
 32679\_at Cluster Incl. D13634:Human mRNA for KIAA0009 gene, complete cds /cds=(1; 34259\_at  
 Cluster Incl. AB014564:Homo sapiens mRNA for KIAA0664 protein, partial ; 38361\_g\_at Cluster  
 20 Incl. AI688812:wd41c03.x1 Homo sapiens cDNA, 3 end /clone=IM; 38620\_at Cluster Incl.  
 AA905543:oj86h04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33918\_s\_at Cluster Incl.  
 AJ223349:Homo sapiens mRNA for HIRIP3 protein, clone pH; 40228\_at Cluster Incl.  
 Y11392:Homo sapiens mRNA; candidate gene for APECED /cds=; 41806\_at Cluster Incl.  
 J04513:Human basic fibroblast growth factor (bFGF) 22.5 k.
- 25 **Metagene 381;** 34591\_at Cluster Incl. S79854:type 3 iodothyronine deiodinase=selenoenzyme  
 [huma; 36410\_f\_at Cluster Incl. U12431:Human ELAV-like neuronal protein 1 (hel-N1) mRNA;  
 36038\_r\_at Cluster Incl. J05500:Human beta-spectrin (SPTB) mRNA, complete cds /c; 32152\_at  
 Cluster Incl. X16609:Human mRNA for ankyrin (variant 2.1) /cds=(84,5729; 39454\_f\_at Cluster  
 Incl. AJ002607:Homo sapiens HOX11L1 gene, exon 1 and joined C; 1777\_at L36463 /FEATURE=  
 30 /DEFINITION=HUMA Homo sapiens ras interactor (RIN1) mRNA.
- Metagene 382;** 38488\_s\_at Cluster Incl. AF031167:Homo sapiens interleukin 15 precursor (IL-15) ;  
 39592\_r\_at Cluster Incl. Z36531:H.sapiens mRNA for fibrinogen-like protein (pT49; 41436\_at  
 Cluster Incl. AJ224901:Homo sapiens mRNA for ZNF198 protein /cds=(184,4; 41634\_at Cluster  
 Incl. D87445:Human mRNA for KIAA0256 gene, complete cds /cds=(1; 41683\_i\_at Cluster Incl.  
 35 U50708:Human branched chain alpha-ketoacid dehydrogenase; 41713\_at Cluster Incl.  
 U09848:Human zinc finger protein (ZNF139) mRNA, partial c; 32628\_at Cluster Incl.  
 D28118:Human mRNA for DB1, complete cds /cds=(41,1591) /g; 32664\_at Cluster Incl.  
 D37931:Human mRNA for RNase 4, complete cds /cds=(27,470); 32667\_at Cluster Incl.  
 M58526:Human alpha-5 collagen type IV (COL4A5) mRNA, 3 e; 32668\_at Cluster Incl.



- AL080076:Homo sapiens mRNA; cDNA DKFZp564C0362 (from clone; 32740\_at Cluster Incl.  
 AB023158:Homo sapiens mRNA for KIAA0941 protein, complete; 33700\_at Cluster Incl.  
 AF039843:Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cd; 34739\_at Cluster Incl.  
 W26023:18c3 Homo sapiens cDNA /gb=W26023 /gi=1306308 /ug=; 34760\_at Cluster Incl.
- 5 D14664:Human mRNA for KIAA0022 gene, complete cds /cds=(1; 34767\_at Cluster Incl.  
 AI670788:tz10c02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35195\_at Cluster Incl.  
 Y11651:H.sapiens mRNA for phosphate cyclase /cds=(170,127; 35209\_at Cluster Incl.  
 AB018309:Homo sapiens mRNA for KIAA0766 protein, complete; 36074\_at Cluster Incl.  
 U12897:Homo sapiens IPW mRNA sequence /cds=UNKNOWN /gb=U1; 36509\_at Cluster Incl.
- 10 AL049998:Homo sapiens mRNA; cDNA DKFZp564L222 (from clone; 36896\_s\_at Cluster Incl.  
 AF044288:Homo sapiens basic-helix-loop-helix-PAS orphan; 38256\_s\_at Cluster Incl.  
 W21827:57E11 Homo sapiens cDNA /clone=(not-directional); 38659\_at Cluster Incl.  
 AB020669:Homo sapiens mRNA for KIAA0862 protein, complete; 39021\_at Cluster Incl.  
 AB020684:Homo sapiens mRNA for KIAA0877 protein, partial ; 39780\_at Cluster Incl.
- 15 M29551:Human calcineurin A2 mRNA, complete cds /cds=(116; 39793\_at Cluster Incl.  
 AF029786:Homo sapiens GBAS (GBAS) mRNA, complete cds /cds; 40046\_r\_at Cluster Incl.  
 AF009426:Homo sapiens clone 22 mRNA, alternative splice; 40431\_at Cluster Incl.  
 AB007891:Homo sapiens KIAA0431 mRNA, partial cds /cds=(96; 40786\_at Cluster Incl.  
 U37352:Human protein phosphatase 2A Balpha1 regulatory su; 41780\_at Cluster Incl.
- 20 U22816:Human LAR-interacting protein 1b mRNA, complete cd; 32781\_f\_at Cluster Incl.  
 AA058762:zk65d06.r1 Homo sapiens cDNA, 5 end /clone=IM; 32851\_at Cluster Incl.  
 AF036956:Homo sapiens neuroblastoma apoptosis-related RNA; 33440\_at Cluster Incl.  
 U19969:Human two-handed zinc finger protein ZEB mRNA, par; 33831\_at Cluster Incl.  
 U47741:Human CREB-binding protein (CBP) mRNA, complete cd; 34355\_at Cluster Incl.
- 25 AJ132917:Homo sapiens mRNA for methyl-CpG-binding protein; 34383\_at Cluster Incl.  
 AB014458:Homo sapiens hUBP mRNA for ubiquitin specific pr; 34842\_at Cluster Incl.  
 U41303:Human small nuclear ribonucleoprotein particle N (S; 35767\_at Cluster Incl.  
 AI565760:tn20b01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36571\_at Cluster Incl.  
 X68060:H.sapiens topIIb mRNA for topoisomerase IIb /cds=(; 36580\_at Cluster Incl.
- 30 AL050139:Homo sapiens mRNA; cDNA DKFZp586M141 (from clone; 36948\_at Cluster Incl.  
 AL109701:Homo sapiens mRNA full length insert cDNA clone ; 36953\_at Cluster Incl.  
 U44378:Human homozygous deletion target in pancreatic car; 37038\_at Cluster Incl.  
 X83467:H.sapiens PXMP1 gene, exon 1 (and joined CDS) /cds; 37334\_at Cluster Incl.  
 U23803:Human heterogeneous ribonucleoprotein A0 mRNA, com; 37697\_s\_at Cluster Incl.
- 35 L08666:Homo sapiens porin (por) mRNA, complete cds and ; 37727\_i\_at Cluster Incl.  
 X78669:H.sapiens ERC-55 mRNA /cds=(66,1019) /gb=X78669 ; 39091\_at Cluster Incl.  
 AF070523:Homo sapiens JWA protein mRNA, complete cds /cds; 39140\_at Cluster Incl.  
 AL079292:Homo sapiens mRNA full length insert cDNA clone ; 40601\_at Cluster Incl.  
 AI057115:oz23g10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40631\_at Cluster Incl.

- D38305:Human mRNA for Tob, complete cds /cds=(43,1080) /g; 40893\_at Cluster Incl.  
 AF058953:Homo sapiens ATP-specific succinyl-CoA synthetas; 41808\_at Cluster Incl.  
 AF052102:Homo sapiens clone 23926 mRNA sequence /cds=UNKN; 2086\_s\_at D17517  
 /FEATURE= /DEFINITION=HUMSKY Human sky mRNA for Sky, complete c; 1307\_at D14533  
 5 /FEATURE= /DEFINITION=HUMXPAC Human mRNA for XPAC protein ; 1192\_at AB003103  
 /FEATURE= /DEFINITION=AB003103 Homo sapiens mRNA for 26S protea; 779\_at D21337  
 /FEATURE= /DEFINITION=HUMCO Human mRNA for collagen .  
**Metagene 383;** 31909\_at Cluster Incl. AB018297:Homo sapiens mRNA for KIAA0754 protein,  
 partial ; 31790\_at Cluster Incl. AL049801:Novel human gene mapping to chromosome 13, simila;  
 10 32727\_at Cluster Incl. AF037062:Homo sapiens retinol dehydrogenase gene, complet; 33362\_at  
 Cluster Incl. AF094521:Homo sapiens MSE55-related protein (UB1) mRNA, c.  
**Metagene 384;** 31655\_at Cluster Incl. AL031737:Human DNA sequence from clone 8B22 on  
 chromosome; 31692\_at Cluster Incl. M59830:Human MHC class III HSP70-2 gene (HLA), complete  
 c; 36785\_at Cluster Incl. Z23090:H.sapiens mRNA for 28 kDa heat shock protein /cds=; 37158\_at  
 15 Cluster Incl. AF035306:Homo sapiens clone 23771 mRNA sequence /cds=UNKN; 41378\_at Cluster  
 Incl. AF010236:Homo sapiens mRNA from chromosome 5q31-33 region; 32108\_at Cluster Incl.  
 M76231:Human sepiapterin reductase mRNA, complete cds /cd; 33816\_at Cluster Incl.  
 AF020267:Homo sapiens myosin-IXb splice variant (Myo9b) m; 34246\_at Cluster Incl.  
 AA418437:zv92d11.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 35191\_at Cluster Incl.  
 20 AB002373:Human mRNA for KIAA0375 gene, complete cds /cds=; 37579\_at Cluster Incl.  
 L47738:Homo sapiens inducible protein mRNA, complete cds ; 37637\_at Cluster Incl.  
 U27655:Human RGP3 mRNA, complete cds /cds=(287,1846) /gb=; 38700\_at Cluster Incl.  
 M33146:Human cysteine-rich peptide mRNA, complete cds /cd; 39066\_at Cluster Incl.  
 L38486:Human microfibril-associated glycoprotein 4 (MFAP4; 39709\_at Cluster Incl.  
 25 U67171:Human selenoprotein W (selW) mRNA, complete cds /c; 40120\_at Cluster Incl.  
 X90999:H.sapiens mRNA for Glyoxalase II /cds=(36,818) /gb; 40427\_at Cluster Incl.  
 AA149486:zl27g01.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41753\_at Cluster Incl.  
 U48734:Human non-muscle alpha-actinin mRNA, complete cds ; 32164\_at Cluster Incl.  
 S79639:EXT1=putative tumour suppressor/hereditary multipl; 32226\_at Cluster Incl.  
 30 M64571:Human microtubule-associated protein 4 mRNA, compl; 32260\_at Cluster Incl.  
 X86809:H.sapiens mRNA for major astrocytic phosphoprotein; 32749\_s\_at Cluster Incl.  
 AL050396:Homo sapiens mRNA; cDNA DKFZp586K1720 (from cl; 32750\_r\_at Cluster Incl.  
 X53416:Human mRNA for actin-binding protein (filamin) (; 33850\_at Cluster Incl. W28892:53c11  
 Homo sapiens cDNA /gb=W28892 /gi=1308840 /ug; 33882\_at Cluster Incl. AB020664:Homo  
 35 sapiens mRNA for KIAA0857 protein, partial ; 33903\_at Cluster Incl. AB007144:Homo sapiens  
 mRNA for ZIP-kinase, complete cds /; 35365\_at Cluster Incl. U40282:Homo sapiens integrin-linked  
 kinase (ILK) mRNA, co; 36937\_s\_at Cluster Incl. U90878:Homo sapiens carboxyl terminal LIM  
 domain protei; 39115\_at Cluster Incl. AL050275:Homo sapiens mRNA; cDNA DKFZp566D213  
 (from clone; 40900\_at Cluster Incl. AI382123:te30a09.x1 Homo sapiens cDNA, 3 end

- /clone=IMAG; 41288\_at Cluster Incl. AL036744:DKFZp564I1663\_r1 Homo sapiens cDNA, 5 end  
 /clon; 41528\_at Cluster Incl. W72239:zd62h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-;  
 32522\_f\_at Cluster Incl. M20469:Human brain-type clathrin light-chain b mRNA, co; 1561\_at  
 U27193 /FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine phosphatase; 1176\_at  
 5 Integrin, Beta 3 Subunit ; 1104\_s\_at M11717 /FEATURE=mRNA /DEFINITION=HUMHSP70D  
 Human heat shock protein (h; 897\_at L33243 /FEATURE=mRNA /DEFINITION=HUMPKD1A  
 Homo sapiens polycystic kidney ; 635\_s\_at L42374 /FEATURE=mRNA  
 /DEFINITION=HUMPP2ABA Homo sapiens protein phospho; 243\_g\_at M64571  
 /FEATURE=mRNA /DEFINITION=HUMMAP4 Human microtubule-associated p; 222\_at S79639  
 10 /FEATURE= /DEFINITION=S79639 EXT1=putative tumour suppressor/hered.  
**Metagene** 385; 31417\_at Cluster Incl. AF041240:Homo sapiens prepro-orexin mRNA, complete cds  
 /c; 34600\_s\_at Cluster Incl. U54644:Human tub homolog mRNA, complete cds /cds=(152,1;  
 36407\_at Cluster Incl. AL050220:Homo sapiens mRNA; cDNA DKFZp586J1923 (from clon;  
 36408\_at Cluster Incl. AB011082:Homo sapiens ORCTL4 mRNA for organic-cation tran;  
 15 32913\_i\_at Cluster Incl. AC005175:Homo sapiens chromosome 19, cosmid R31449 /cds; 35960\_at  
 Cluster Incl. AF031416:Homo sapiens Ikb kinase beta subunit mRNA, compl; 39570\_at Cluster Incl.  
 W22289:65G5 Homo sapiens cDNA /clone=(not-directional) /g; 39598\_at Cluster Incl.  
 X04325:Human liver mRNA for gap junction protein /cds=(62; 41657\_at Cluster Incl.  
 AF035625:Homo sapiens serine threonine kinase 11 (STK11) ; 40898\_at Cluster Incl.  
 20 U46751:Human phosphotyrosine independent ligand p62 for t.  
**Metagene** 386; 33030\_at Cluster Incl. M60747:Human histone H1 (H1F3) gene, complete cds  
 /cds=(0; 34541\_at Cluster Incl. L02867:Homo sapiens 62 kDa paraneoplastic antigen mRNA, 3;  
 38486\_at Cluster Incl. J04760:Human slow-twitch skeletal troponin I (TNNI) mRNA,; 1332\_f\_at  
 V00520 /FEATURE=mRNA /DEFINITION=HSGROW2 Human germ line gene for grow;  
 25 1033\_g\_at U11872 /FEATURE= /DEFINITION=HSU11872 Human interleukin-8 receptor typ;  
 643\_at L76571 /FEATURE=cds /DEFINITION=HUMSHP Homo sapiens nuclear hormone recep.  
**Metagene** 387; 34595\_at Cluster Incl. AF105424:Homo sapiens brush border myosin I (BBMI)  
 mRNA, ; 32286\_at Cluster Incl. AF012131:Homo sapiens brachyury variant B (TBX1) mRNA, co;  
 37860\_at Cluster Incl. AL049942:Homo sapiens mRNA; cDNA DKFZp564F1422 (from clon;  
 30 32097\_at Cluster Incl. AB007862:Homo sapiens KIAA0402 mRNA, partial cds /cds=(0; 35240\_at  
 Cluster Incl. W28983:54f11 Homo sapiens cDNA /gb=W28983 /gi=1308931 /ug; 36035\_at Cluster  
 Incl. AB002135:Homo sapiens mRNA for glycosylphosphatidylinosit; 33868\_at Cluster Incl.  
 Z93241:dJ222E13.3.2 (PUTATIVE partial isoform 2) /cds=(0; 40222\_s\_at Cluster Incl.  
 AI677689:wd33c06.x1 Homo sapiens cDNA, 3 end /clone=IM.  
 35 **Metagene** 388; 35769\_at Cluster Incl. AJ011001:Homo sapiens mRNA for TM7XN1 protein  
 /cds=(316,2; 619\_s\_at M27394 /FEATURE=cds /DEFINITION=HUMB1LYM Human B-  
 lymphocyte cell-surfac; 459\_s\_at U68485 /FEATURE= /DEFINITION=HSU68485 Homo sapiens  
 bridging integrator .  
**Metagene** 389; 33041\_at Cluster Incl. U03493:Human connexin45 gene, complete cds /cds=(0,1190)

- ; 41861\_at Cluster Incl. AL050019:Homo sapiens mRNA; cDNA DKFZp564C186 (from clone; 1868\_g\_at AF005775 /FEATURE= /DEFINITION=AF005775 Homo sapiens caspase-like apop; 698\_f\_at Zinc Finger Protein, Kruppel-Like .
- Metagene 390;** 31557\_at Cluster Incl. M17733:Human thymosin beta-4 mRNA, complete cds
- 5 /cds=(77;; 33089\_s\_at Cluster Incl. U92896:Human LERK-6 (EPLG6) gene /cds=(0,641) /gb=U9289; 35523\_at Cluster Incl. AF150241:AF150241 Homo sapiens cDNA /clone=CBFAZB10 /gb=A; 38160\_at Cluster Incl. AF011333:Homo sapiens DEC-205 mRNA, complete cds /cds=(53; 40311\_at Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(27,2.
- Metagene 391;** 35039\_at Cluster Incl. D87466:Human mRNA for KIAA0276 gene, partial cds
- 10 /cds=(0;; 38204\_at Cluster Incl. AB007866:Homo sapiens KIAA0406 mRNA, complete cds /cds=(1; 38892\_at Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0;; 39646\_at Cluster Incl. S60415:myasthenic syndrome antigen B [human, fetal brain;; 39989\_at Cluster Incl. X90530:H.sapiens mRNA for ragB protein /cds=(442,1566) /g; 40732\_at Cluster Incl. D83243:Human NPAT mRNA, complete cds /cds=(66,4349) /gb=D; 33760\_at Cluster Incl.
- 15 AB017546:Homo sapiens Pex14 mRNA for peroxisomal membrane; 34198\_at Cluster Incl. U12128:Human protein tyrosine phosphatase 1E (PTP1E) mRNA; 34675\_at Cluster Incl. AL080210:Homo sapiens mRNA; cDNA DKFZp586G0623 (from clon; 35167\_at Cluster Incl. AB007893:Homo sapiens KIAA0433 mRNA, partial cds /cds=(50; 35232\_f\_at Cluster Incl. AI056696:oz26h05.x1 Homo sapiens cDNA, 3 end /clone=IM; 35645\_at Cluster Incl.
- 20 AL050148:Homo sapiens mRNA; cDNA DKFZp586G1520 (from clon; 39036\_g\_at Cluster Incl. AF006010:Human progesterin induced protein (DD5) mRNA, co; 39047\_at Cluster Incl. AB020880:Homo sapiens mRNA for squamous cell carcinoma an; 39346\_at Cluster Incl. M88108:Human p62 mRNA, complete cds /cds=(106,1437) /gb=M; 39390\_at Cluster Incl. AF052123:Homo sapiens clone 23770 mRNA sequence /cds=UNKN; 39443\_s\_at Cluster Incl.
- 25 M19961:Human cytochrome c oxidase subunit Vb (coxVb) mR; 39731\_at Cluster Incl. Z23064:H.sapiens mRNA gene for hnRNP G protein /cds=(11,1; 39782\_at Cluster Incl. X95592:H.sapiens mRNA for C1D protein /cds=(117,542) /gb=; 40763\_at Cluster Incl. U85707:Human leukemogenic homolog protein (MEIS1) mRNA, c; 40781\_at Cluster Incl. U79271:Human clones 23920 and 23921 mRNA sequence /cds=UN; 40826\_at Cluster Incl.
- 30 M80359:Human protein p78 mRNA, complete cds /cds=(171,231; 41219\_at Cluster Incl. AL050376:Homo sapiens mRNA; cDNA DKFZp586J101 (from clone; 32171\_at Cluster Incl. AL080102:Homo sapiens mRNA; cDNA DKFZp564N1916 (from clon; 32172\_at Cluster Incl. AL096858:Novel human gene mapping to chromosome 1 /cds=(33; 32792\_at Cluster Incl. AL031432:Human DNA sequence from clone 465N24 on chromoso; 33847\_s\_at Cluster Incl.
- 35 AI304854:qo19f03.x1 Homo sapiens cDNA, 3 end /clone=IM; 34385\_at Cluster Incl. U57877:Human integral membrane protein CII-3 mRNA, nuclea; 35755\_at Cluster Incl. U51336:Human inositol 1,3,4-trisphosphate 5/6-kinase mRNA; 36153\_at Cluster Incl. L13848:Human RNA helicase A mRNA, complete cds /cds=(80,3; 36164\_at Cluster Incl. U82328:Homo sapiens pyruvate dehydrogenase complex protei; 36974\_at Cluster Incl.

- D88378:Homo sapiens mRNA for proteasome inhibitor hPI31 s; 37034\_at Cluster Incl.  
 U73477:Human acidic nuclear phosphoprotein pp32 mRNA, com; 38481\_at Cluster Incl.  
 M63488:Human replication protein A 70kDa subunit mRNA com; 39864\_at Cluster Incl.  
 D78134:Homo sapiens mRNA for CIRP, complete cds /cds=(80; 40211\_at Cluster Incl.
- 5 X12671:Human gene for heterogeneous nuclear ribonucleopro; 40576\_f\_at Cluster Incl.  
 D89678:Homo sapiens mRNA for A+U-rich element RNA bindi; 41490\_at Cluster Incl.  
 Y00971:Human mRNA for phosphoribosyl pyrophosphate synth; 41544\_at Cluster Incl.  
 AF059617:Homo sapiens serum-inducible kinase mRNA, comple; 32609\_at Cluster Incl.  
 AI885852:wl62d08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1488\_at L77886 /FEATURE=
- 10 /DEFINITION=HUMPTPC Human protein tyrosine phosphatase .  
**Metagene** 392; 31460\_f\_at Cluster Incl. AF043586:Homo sapiens clone CPRF1-T2 immunoglobulin  
 lam; 33627\_at Cluster Incl. U57843:Human phosphatidylinositol 3-kinase delta catalyti; 35601\_at  
 Cluster Incl. L00022:Human Ig active epsilon1 5 UT, V-D-J region subgro; 41054\_at Cluster Incl.  
 AB006628:Homo sapiens mRNA for KIAA0290 gene, partial cds.
- 15 **Metagene** 393; 41676\_at Cluster Incl. U79248:Human clone 23826 mRNA sequence  
 /cds=UNKNOWN /gb=U; 32045\_at Cluster Incl. AB002331:Human mRNA for KIAA0333 gene,  
 partial cds /cds=(; 40138\_at Cluster Incl. U70735:Homo sapiens 34 kDa Mov34 homolog mRNA,  
 complete c; 32241\_at Cluster Incl. AL050265:Homo sapiens mRNA; cDNA DKFZp564O1716 (from  
 clon; 33854\_at Cluster Incl. AA877795:nr10g08.s1 Homo sapiens cDNA, 3 end /clone=IMAG;
- 20 39196\_i\_at Cluster Incl. W25875:14f10 Homo sapiens cDNA /gb=W25875 /gi=1306016 /.  
**Metagene** 394; 36734\_at Cluster Incl. M21302:Human small proline rich protein (sprII) mRNA, clo;  
 37424\_at Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homolo; 40711\_at  
 Cluster Incl. AL049340:Homo sapiens mRNA; cDNA DKFZp564P056 (from clone; 33321\_r\_at  
 Cluster Incl. M33494:Homo sapiens tryptase-I gene, complete cds /cds=; 35650\_at Cluster Incl.
- 25 AB002354:Human mRNA for KIAA0356 gene, complete cds /cds=; 38995\_at Cluster Incl.  
 AF000959:Homo sapiens transmembrane protein mRNA, complet; 33895\_at Cluster Incl.  
 AL050373:Homo sapiens mRNA; cDNA DKFZp586F1318 (from clon; 38104\_at Cluster Incl.  
 U78302:Human 2,4-dienoyl-CoA reductase gene /cds=(73,1080; 1128\_s\_at L09230 /FEATURE=
- 30 /DEFINITION=HUMCCCKR1A Human C-C chemokine receptor t; 802\_at X84002  
 /FEATURE=cds /DEFINITION=HSTAFII20 H.sapiens TAFII20 mRNA for tran.  
**Metagene** 395; 34976\_at Cluster Incl. M60052:Human histidine-rich calcium binding protein  
 (HRC); 41110\_at Cluster Incl. X81882:H.sapiens mRNA for for vasopressin activated calci;  
 35203\_at Cluster Incl. AB002381:Human mRNA for KIAA0383 gene, partial cds /cds=(; 37995\_s\_at  
 Cluster Incl. M67468:Human Fragile X mental retardation 1 FMR-1 gene; 32552\_at Cluster Incl.
- 35 X00129:Human mRNA for retinol binding protein (RBP) /cds=; 1453\_at U68018 /FEATURE=
- /DEFINITION=HSU68018 Human mad protein homolog (hMAD-2).  
**Metagene** 396; 39574\_at Cluster Incl. AB021292:Homo sapiens mRNA for semaphorin W, splicing  
 var; 40309\_at Cluster Incl. X66839:H.sapiens MaTu MN mRNA for p54/58N protein /cds=(4;  
 40782\_at Cluster Incl. AF061741:Homo sapiens retinal short-chain dehydrogenase/r; 32177\_s\_at

- Cluster Incl. AC004084:Homo sapiens BAC clone RG158O17 from 7q22-q31.; 34407\_at Cluster Incl. U77594:Human tazarotene-induced gene 2 (TIG2) mRNA, compl; 2051\_at M31767 /FEATURE=mRNA /DEFINITION=HUMDNAMET Human O6-methylguanine-DNA me; 1057\_at M97815 /FEATURE=expanded\_cds /DEFINITION=HUMCRABP02 Human retinoic acid-.
- 5 **Metagene** 397; 37122\_at Cluster Incl. AB005293:Homo sapiens mRNA for perilipin, complete cds /c; 37513\_at Cluster Incl. Y13647:Homo sapiens mRNA for stearyl-CoA desaturase /cds; 40657\_r\_at Cluster Incl. H15814:yl28b07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40658\_r\_at Cluster Incl. D45371:Human apM1 mRNA for GS3109 (novel adipose specif; 33703\_f\_at Cluster Incl. L12760:Human phosphoenolpyruvate carboxykinase (PCK1) g; 38320\_s\_at Cluster Incl.
- 10 L11706:Human hormone-sensitive lipase (LIPE) gene, comp; 33902\_at Cluster Incl. L34041:Homo sapiens L-glycerol-3-phosphate-NAD oxidoreduc; 38429\_at Cluster Incl. U29344:Human breast carcinoma fatty acid synthase mRNA, c; 40282\_s\_at Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete.
- Metagene** 398; 31584\_at Cluster Incl. X16064:Human mRNA for translationally controlled tumor pr; 34030\_at Cluster Incl. U82468:Human tubby related protein 1 (TULP1) mRNA, comple; 36306\_at Cluster Incl. AF033347:Homo sapiens potassium channel homolog (KCNQ3) m; 33457\_at Cluster Incl. AB029028:Homo sapiens mRNA for KIAA1105 protein, partial ; 37009\_at Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079; 1815\_g\_at D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIIIR .
- 20 **Metagene** 399; 36736\_f\_at Cluster Incl. Y10275:H.sapiens mRNA for L-3-phosphoserine phosphatase; 37208\_at Cluster Incl. AJ001612:Homo sapiens mRNA for L-3-phosphoserine-phosphat; 37209\_g\_at Cluster Incl. AJ001612:Homo sapiens mRNA for L-3-phosphoserine-phosph; 40272\_at Cluster Incl. D78012:Homo sapiens mRNA for dihydropyrimidinase related ; 1572\_s\_at M10051 /FEATURE= /DEFINITION=HUMINSR Human insulin receptor mRNA, comp; 1130\_at
- 25 L11284 /FEATURE= /DEFINITION=HUMMEK1NF Homosapiens ERK activator kinase .
- Metagene** 400; 39296\_at Cluster Incl. W28319:45c1 Homo sapiens cDNA /gb=W28319 /gi=1308267 /ug=; 41057\_at Cluster Incl. AI760162:wg58e09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41371\_at Cluster Incl. Y07595:H.sapiens mRNA for 52 kD subunit of transcription ; 35149\_at Cluster Incl. AI865431:wk11h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36867\_at
- 30 Cluster Incl. W03846:za60a02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 37986\_at Cluster Incl. M60459:Human erythropoietin receptor mRNA, complete cds /; 41230\_at Cluster Incl. U71087:Human MAP kinase kinase MEK5b mRNA, complete cds /; 35360\_at Cluster Incl. Y17711:Homo sapiens mRNA for atopy related autoantigen CA; 32532\_at Cluster Incl. L14837:Human tight junction (zonula occludens) protein ZO; 533\_g\_at U17418 /FEATURE=
- 35 /DEFINITION=HSU17418 Human parathyroid hormone/parathy.
- Metagene** 401; 34438\_at Cluster Incl. U71364:Human serine proteinase inhibitor (P19) mRNA, comp; 37152\_at Cluster Incl. L07592:Human peroxisome proliferator activated receptor m; 38564\_at Cluster Incl. U40152:Human origin recognition complex 1 (HsORC1) mRNA, ; 41698\_at Cluster Incl. AL031685:dJ963K23.4 (KIAA0939 (novel Sodium/hydrogen exch; 35182\_f\_at Cluster Incl.

- W25874:14e9 Homo sapiens cDNA /gb=W25874 /gi=1306015 /u; 37609\_at Cluster Incl.  
 U01833:Human nucleotide-binding protein mRNA, complete cd; 33921\_at Cluster Incl.  
 Y15409:Homo sapiens mRNA for putative glucose 6-phosphate; 1680\_at D43772 /FEATURE=  
 /DEFINITION=HUMGRB7 Human squamous cell carcinoma of es; 1498\_at L05148 /FEATURE=  
 5 /DEFINITION=HUMTYRKIN Human protein tyrosine kinase rel; 489\_at U63329 /FEATURE=cds  
 /DEFINITION=HSU63329 Human mutY homolog (hMYH) gene, .  
**Metagene 402;** 35094\_f\_at Cluster Incl. AF025527:Homo sapiens leucocyte immunoglobulin-like  
 rec; 39221\_at Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related rece;  
 39992\_at Cluster Incl. AF030302:Homo sapiens p45-BWR1A (BWR1-A) mRNA, complete c;  
 10 40439\_at Cluster Incl. AF047469:Homo sapiens arsenite translocating ATPase (ASNA).  
**Metagene 403;** 36269\_at Cluster Incl. AB002364:Human mRNA for KIAA0366 gene, partial cds  
 /cds=(; 32051\_at Cluster Incl. AJ224875:Homo sapiens mRNA for putative glucosyltransfera;  
 33334\_at Cluster Incl. X84194:H.sapiens mRNA for acylphosphatase, erythrocyte (C; 35214\_at  
 Cluster Incl. AF061016:Homo sapiens UDP-glucose dehydrogenase (UGDH) mR; 37640\_at Cluster  
 15 Incl. M31642:Human hypoxanthine phosphoribosyltransferase (HPRT; 38985\_at Cluster Incl.  
 AF063605:Homo sapiens brain my047 protein mRNA, complete ; 40108\_at Cluster Incl.  
 D13630:Human mRNA for KIAA0005 gene, complete cds /cds=(8; 40113\_at Cluster Incl.  
 D87119:Homo sapiens mRNA for GS3955, complete cds /cds=(1; 41177\_at Cluster Incl.  
 AW024285:wt69d06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38739\_at Cluster Incl.  
 20 AF017257:Homo sapiens chromosome 21 derived BAC containin; 39127\_f\_at Cluster Incl.  
 X73478:H.sapiens hPTPA mRNA /cds=(189,1160) /gb=X73478 ; 41354\_at Cluster Incl.  
 U25997:Homo sapiens stanniocalcin precursor (STC) mRNA, c; 32607\_at Cluster Incl.  
 AF039656:Homo sapiens neuronal tissue-enriched acidic pro; 1368\_at M27492 /FEATURE=  
 /DEFINITION=HUMIL1RA Human interleukin 1 receptor mRNA,; 717\_at D87119 /FEATURE=  
 25 /DEFINITION=D87119 Homo sapiens mRNA for GS3955, complet.  
**Metagene 404;** 38960\_at Cluster Incl. U45975:Human phosphatidylinositol (4,5)bisphosphate 5-  
 pho; 41103\_at Cluster Incl. M91585:Human Br140 mRNA, complete cds /cds=(28,3672) /gb=;  
 38706\_at Cluster Incl. AA552140:ng48e07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36932\_at  
 Cluster Incl. D13636:Human mRNA for KIAA0011 gene, complete cds /cds=(3; 40602\_at Cluster  
 30 Incl. AF052178:Homo sapiens clone 24523 mRNA sequence /cds=UNKN; 33193\_at Cluster Incl.  
 AW052084:wy86f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG.  
**Metagene 405;** 36447\_at Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1;  
 34010\_at Cluster Incl. U90908:Human clones 23549 and 23762 mRNA, complete cds /c; 36802\_at  
 Cluster Incl. M23197:Human differentiation antigen (CD33) mRNA, complet; 37834\_at Cluster Incl.  
 35 Y17999:Homo sapiens mRNA for protein kinase Dyrk1B /cds=(; 38235\_at Cluster Incl.  
 AB020722:Homo sapiens mRNA for KIAA0915 protein, complete; 38516\_at Cluster Incl.  
 L10338:Human sodium channel beta-1 subunit (SCN1B) mRNA, ; 40768\_s\_at Cluster Incl.  
 X64228:H.sapiens can mRNA /cds=(94,6366) /gb=X64228 /gi; 33919\_at Cluster Incl.  
 AF022813:Homo sapiens tetraspan (NAG-2) mRNA, complete cd; 35350\_at Cluster Incl.

- AB011170: Homo sapiens mRNA for KIAA0598 protein, complete; 41347\_at Cluster Incl.  
 A1814659:wj75g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33141\_at Cluster Incl.  
 M84472: Human 17-beta-hydroxysteroid dehydrogenase (EDH17B; 2019\_s\_at M68892 /FEATURE=  
 /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mR; 1673\_at M14764
- 5 /FEATURE=mRNA /DEFINITION=HUMNGFR Human nerve growth factor recep.  
**Metagene** 406; 33252\_at Cluster Incl. D38073: Human mRNA for hRlf beta subunit (p102 protein),  
 c; 37927\_at Cluster Incl. X12654: Human mRNA for cell cycle gene RCC1 /cds=(182,1447;  
 32180\_s\_at Cluster Incl. AB000461: Homo sapiens mRNA, complete cds, clone-RES4-22; 646\_s\_at  
 L29218 /FEATURE=mRNA /DEFINITION=HUMCLK2B Homo sapiens clk2 mRNA, compl.
- 10 **Metagene** 407; 35858\_at Cluster Incl. AA996066:os33d01.s1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 39668\_at Cluster Incl. X95694: H.sapiens mRNA for AP-2 beta transcription factor ;  
 40645\_at Cluster Incl. L33801: Human protein kinase mRNA, complete cds /cds=(39,1; 36524\_at  
 Cluster Incl. AB029035: Homo sapiens mRNA for KIAA1112 protein, partial ; 36538\_at Cluster Incl.  
 AB018314: Homo sapiens mRNA for KIAA0771 protein, partial ; 32192\_g\_at Cluster Incl.
- 15 D13969: Human mRNA for Mel-18 protein, complete cds /cds.  
**Metagene** 408; 34907\_at Cluster Incl. AB014541: Homo sapiens mRNA for KIAA0641 protein,  
 complete; 35008\_at Cluster Incl. AB002345: Human mRNA for KIAA0347 gene, complete cds  
 /cds=; 35379\_at Cluster Incl. X54412: Human mRNA for alpha1(IX) collagen (long form) /cd;  
 38209\_at Cluster Incl. L22647: Human prostaglandin receptor ep1 subtype mRNA, com; 38944\_at
- 20 Cluster Incl. U68019: Homo sapiens mad protein homolog (hMAD-3) mRNA, co; 33293\_at Cluster  
 Incl. AB023167: Homo sapiens mRNA for KIAA0950 protein, partial ; 34682\_at Cluster Incl.  
 AL050271: Homo sapiens mRNA; cDNA DKFZp566H0824 (from clon; 37639\_at Cluster Incl.  
 X07732: Human hepatoma mRNA for serine protease hepsin /cd; 36581\_at Cluster Incl.  
 U09510: Human glycyl-tRNA synthetase mRNA, complete cds /c; 38093\_at Cluster Incl.
- 25 U90909: Human clone 23722 mRNA sequence /cds=UNKNOWN /gb=U; 39547\_at Cluster Incl.  
 AB008515: Homo sapiens mRNA for RanBPM, complete cds /cds=; 713\_at Helix-Loop-Helix  
 Protein Delta Max, Alt. Splice 1 ; 416\_s\_at X61755 /FEATURE=mRNA /DEFINITION=HSHOX3D  
 Human HOX3D gene for homeoprot.  
**Metagene** 409; 106\_at Z35278 /FEATURE=mRNA /DEFINITION=HSAML1RN H.sapiens
- 30 PEBP2aC1 acute myeloi.  
**Metagene** 410; 31952\_at Cluster Incl. X69391: H.sapiens mRNA for ribosomal protein L6  
 /cds=(26,8; 32433\_at Cluster Incl. Z97353: Human DNA sequence from clone 90L6 on chromosome  
 2; 32436\_at Cluster Incl. U14968: Human ribosomal protein L27a mRNA, complete cds /c; 34570\_at  
 Cluster Incl. S79522: ubiquitin carboxyl extension protein [human, mRNA,; 34646\_at Cluster Incl.
- 35 Z25749: H.sapiens gene for ribosomal protein S7 /cds=(81,6; 35508\_at Cluster Incl.  
 X79781: H.sapiens ray mRNA /cds=(81,686) /gb=X79781 /gi=76; 32883\_at Cluster Incl.  
 X77744: H.sapiens F11 mRNA /cds=UNKNOWN /gb=X77744 /gi=456; 39298\_at Cluster Incl.  
 AB022918: Homo sapiens mRNA for alpha2,3-sialyltransferase; 31899\_at Cluster Incl.  
 D14659: Human mRNA for KIAA0103 gene, complete cds /cds=(6; 34773\_at Cluster Incl.



- AF038952:Homo sapiens cofactor A protein mRNA, complete c; 35642\_at Cluster Incl.
- AF053551:Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene; 36517\_at Cluster Incl.
- M96982:Homo sapiens U2 snRNP auxiliary factor small subun; 37242\_at Cluster Incl.
- U79260:Human clone 23745 mRNA, complete cds /cds=(609,102; 38318\_at Cluster Incl.
- 5 AL050128:Homo sapiens mRNA; cDNA DKFZp586G051 (from clone; 39757\_at Cluster Incl.
- J04621:Human heparan sulfate proteoglycan (HSPG) core pro; 40411\_at Cluster Incl.
- D80003:Human mRNA for KIAA0181 gene, partial cds /cds=(0;; 40467\_at Cluster Incl.
- AB006202:Homo sapiens mRNA for cytochrome b small subunit; 40811\_at Cluster Incl.
- AB011148:Homo sapiens mRNA for KIAA0576 protein, partial ; 41156\_g\_at Cluster Incl.
- 10 U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=; 41746\_at Cluster Incl.
- Z83840:Human DNA sequence from clone 216E10 on chromosome; 41768\_at Cluster Incl.
- M33336:Human cAMP-dependent protein kinase type I-alpha s; 41785\_at Cluster Incl.
- U73824:Human p97 mRNA, complete cds /cds=(306,3029) /gb=U; 32789\_at Cluster Incl.
- AA149428:z126a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32833\_at Cluster Incl.
- 15 M59287:Human protein kinase mRNA /cds=UNKNOWN /gb=M59287 ; 33351\_at Cluster Incl.
- AF064607:Homo sapiens GC20 protein mRNA, complete cds /cd; 33817\_at Cluster Incl.
- S63912:D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt] ; 33891\_at Cluster Incl.
- AL080061:Homo sapiens mRNA; cDNA DKFZp564H182 (from clone; 34307\_at Cluster Incl.
- U81006:Human p76 mRNA, complete cds /cds=(133,2124) /gb=U; 35738\_at Cluster Incl.
- 20 AI347088:qp60d09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35821\_at Cluster Incl.
- U75697:Human transcription regulator RPD3-2B mRNA, comple; 35842\_at Cluster Incl.
- AL049265:Homo sapiens mRNA; cDNA DKFZp564F053 (from clone; 36098\_at Cluster Incl.
- M72709:Human alternative splicing factor mRNA, complete c; 36601\_at Cluster Incl.
- M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /; 37308\_at Cluster Incl.
- 25 AI888084:wm29g09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37373\_at Cluster Incl.
- U27460:Human uridine diphosphoglucose pyrophosphorylase m; 37677\_at Cluster Incl.
- V00572:Human mRNA encoding phosphoglycerate kinase /cds=(; 37707\_i\_at Cluster Incl.
- M81118:Human alcohol dehydrogenase chi polypeptide (ADH; 37717\_at Cluster Incl.
- L03532:Human M4 protein mRNA, complete cds /cds=(11,2200); 38837\_at Cluster Incl.
- 30 W26226:22e3 Homo sapiens cDNA /gb=W26226 /gi=1306637 /ug=; 39839\_at Cluster Incl.
- M24069:Human DNA-binding protein A (dbpA) gene, 3 end /c; 40916\_at Cluster Incl.
- AL035494:Human DNA sequence from clone 635G19 on chromoso; 40961\_at Cluster Incl.
- X72889:H.sapiens hbrm mRNA /cds=(222,4982) /gb=X72889 /gi; 41292\_at Cluster Incl.
- L22009:Human hnRNP H mRNA, complete cds /cds=(72,1421) /g; 1450\_g\_at D00763 /FEATURE=
- 35 /DEFINITION=HUMPSC9 Human mRNA for proteasome subunit; 1295\_at L19067 /FEATURE=
- /DEFINITION=HUMNFKB65A Human NF-kappa-B transcription f; 1250\_at U47077 /FEATURE=
- /DEFINITION=HSU47077 Homo sapiens DNA-dependent protein; 950\_at D87127 /FEATURE=
- /DEFINITION=D87127 Homo sapiens mRNA for translocation p; 853\_at S74017 /FEATURE=
- /DEFINITION=S74017 Nrf2=NF-E2-like basic leucine zipper ; 292\_s\_at Protein Kinase ; 140\_s\_at

- U68063 /FEATURE= /DEFINITION=HSU68063 Human transformer-2 beta (htra-2 .  
**Metagene** 411; 32402\_s\_at Cluster Incl. Y10931:H.sapiens mRNA for symplekin /cds=(459,3887)  
 /gb; 35190\_at Cluster Incl. AL031447:dJ126A5.2.1 (novel protein) (isoform 1) /cds=(0; 36828\_at  
 Cluster Incl. AB002324:Human mRNA for KIAA0326 gene, partial cds /cds=(; 37903\_at Cluster  
 5 Incl. L25665:Human GTP-binding protein (HSR1) mRNA, complete cd; 39004\_at Cluster Incl.  
 AI432190:tg77f11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39372\_at Cluster Incl.  
 W26480:30b8 Homo sapiens cDNA /gb=W26480 /gi=1307179 /ug=; 34310\_at Cluster Incl.  
 Y00486:Human APRT gene for adenine phosphoribosyltransfer; 34845\_at Cluster Incl.  
 AL035398:Human DNA sequence from clone 796I17 on chromoso; 36658\_at Cluster Incl.  
 10 D13643:Human mRNA for KIAA0018 gene, complete cds /cds=(3; 36984\_f\_at Cluster Incl.  
 X89214:H.sapiens mRNA for haptoglobin related protein /; 37739\_at Cluster Incl. M86737:Human  
 high mobility group box (SSRP1) mRNA, comple.  
**Metagene** 412; 40367\_at Cluster Incl. M22489:Human bone morphogenetic protein 2A (BMP-2A)  
 mRNA ; 41051\_at Cluster Incl. X95073:H.sapiens mRNA for translin associated protein X /;  
 15 32099\_at Cluster Incl. D50928:Human mRNA for KIAA0138 gene, complete cds /cds=(3; 32659\_at  
 Cluster Incl. AL050109:Homo sapiens mRNA; cDNA DKFZp586J0119 (from clon; 32695\_at  
 Cluster Incl. Z97632:dJ196E23.2 (HIV-1 transcriptional elongation facto; 34685\_at Cluster Incl.  
 AI685944:tu38g02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36083\_at Cluster Incl.  
 U01160:Human transmembrane 4 superfamily protein (SAS) mR; 37199\_at Cluster Incl.  
 20 AI760932:wi70d01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38669\_at Cluster Incl.  
 D86959:Human mRNA for KIAA0204 gene, complete cds /cds=(5; 38685\_at Cluster Incl.  
 AL035306:H.sapiens gene from PAC 42616, similar to syntax; 38983\_at Cluster Incl.  
 AI223047:qg70a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39784\_at Cluster Incl.  
 U26032:Human translation initiation factor eIF-2alpha mRN; 40418\_at Cluster Incl.  
 25 X74262:H.sapiens RbAp48 mRNA encoding retinoblastoma bind; 40437\_at Cluster Incl.  
 AL049944:Homo sapiens mRNA; cDNA DKFZp564G2022 (from clon; 41737\_at Cluster Incl.  
 AF048977:Homo sapiens Ser/Arg-related nuclear matrix prot; 41754\_at Cluster Incl.  
 M92439:Human leucine-rich protein mRNA, complete cds /cds; 32205\_at Cluster Incl.  
 AF072860:Homo sapiens protein activator of the interferon; 32234\_at Cluster Incl. AF007871:Homo  
 30 sapiens torsinA (DYT1) mRNA, complete cds /; 33420\_g\_at Cluster Incl. U83857:Human Aac11  
 (aac11) mRNA, complete cds /cds=(77; 36111\_s\_at Cluster Incl. X75755:H.sapiens PR264 gene  
 /cds=(98,763) /gb=X75755 /g; 36968\_s\_at Cluster Incl. AL050353:Homo sapiens mRNA; cDNA  
 DKFZp547C0410 (from cl; 38380\_at Cluster Incl. Y18863:Homo sapiens mRNA for ribonuclease P  
 protein subun; 38410\_at Cluster Incl. X72964:H.sapiens mRNA for caltractin /cds=(47,565) /gb=X7;  
 35 38817\_at Cluster Incl. AF047437:Homo sapiens sperm acrosomal protein mRNA, compl; 41830\_at  
 Cluster Incl. AB007963:Homo sapiens mRNA for KIAA0494 protein, complete; 33175\_at Cluster  
 Incl. AA156237:z150c09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 2060\_at M13995  
 /FEATURE=mRNA /DEFINITION=HUMBCL2B Human B-cell leukemia/lymphoma; 1211\_s\_at  
 U84388 /FEATURE= /DEFINITION=HSU84388 Human death domain containing pr; 1017\_at

- U73737 /FEATURE=mRNA /DEFINITION=HUMMSH06 Human hMSH6 gene, exons 6-10 a;  
 585\_at M30938 /FEATURE=mRNA#2 /DEFINITION=HUMKUP Human Ku (p70/p80) subunit  
 mRNA; 507\_s\_at U43189 /FEATURE= /DEFINITION=HSU43189 Human Ets transcription factors  
 N; 174\_s\_at U61167 /FEATURE= /DEFINITION=HSU61167 Human SH3 domain-containing prote.
- 5 **Metagene** 413; 35524\_at Cluster Incl. U08198:Human complement C8 gamma subunit precursor  
 (C8G) ; 32975\_g\_at Cluster Incl. U07563:Human ABL gene, exon 1b and intron 1b, and putat;  
 37451\_at Cluster Incl. AL109695:Homo sapiens mRNA full length insert cDNA clone ; 38171\_at  
 Cluster Incl. U94747:Human WD repeat protein HAN11 mRNA, complete cds /; 39223\_at Cluster  
 Incl. AL096749:Homo sapiens mRNA; cDNA DKFZp434G153 (from clone; 39934\_at Cluster Incl.
- 10 AB023061:Homo sapiens mRNA for small GTP-binding protein ; 36121\_at Cluster Incl.  
 AB028988:Homo sapiens mRNA for KIAA1065 protein, complete; 40207\_g\_at Cluster Incl.  
 AI767675:wh38d11.x1 Homo sapiens cDNA, 3 end /clone=IM; 40641\_at Cluster Incl.  
 AF038362:Homo sapiens TBP-associated factor 172 (TAF-172).  
**Metagene** 414; 34651\_at Cluster Incl. M58525:Homo sapiens catechol-O-methyltransferase  
 (COMT) m; 35176\_at Cluster Incl. Z82022:H.sapiens mRNA for GlcNac-1-P transferase /cds=(10;  
 33863\_at Cluster Incl. U65785:Human 150 kDa oxygen-regulated protein ORP150 mRNA; 39113\_at  
 Cluster Incl. AI262789:qk35e02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40932\_at Cluster  
 Incl. H18080:ym38h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 32543\_at Cluster Incl.  
 M84739:Human autoantigen calreticulin mRNA, complete cds ; 2075\_s\_at L36719
- 20 /FEATURE=mRNA /DEFINITION=HUMMKK3A Homo sapiens MAP kinase kina; 1752\_at  
 AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chro;  
 1438\_at X75208 /FEATURE=cds /DEFINITION=HSPTKR H.sapiens HEK2 mRNA for protein t;  
 442\_at X15187 /FEATURE=cds /DEFINITION=HSTRA1 Human tra1 mRNA for human homologu.  
**Metagene** 415; 37978\_at Cluster Incl. D78177:Homo sapiens mRNA for quinolinate phosphoribosyl  
 t; 32249\_at Cluster Incl. M65292:Human factor H homologue mRNA, complete cds /cds=(;  
 33867\_s\_at Cluster Incl. X77494:H.sapiens MSSP-2 mRNA /cds=(231,1400) /gb=X77494; 35848\_at  
 Cluster Incl. AL049432:Homo sapiens mRNA; cDNA DKFZp586J231 (from clone; 40626\_at  
 Cluster Incl. AI693193:wd68f02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1846\_at L78132  
 /FEATURE= /DEFINITION=HUMPCTA1A Human prostate carcinoma tumor an; 332\_at Zinc
- 30 Finger Protein Kup ; 166\_at U48405 /FEATURE=cds /DEFINITION=HSU48405 Human G protein  
 coupled receptor.  
**Metagene** 416; 32487\_s\_at Cluster Incl. AB002533:Homo sapiens mRNA for Qip1, complete cds  
 /cds=; 34445\_at Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete;  
 36695\_at Cluster Incl. AI290480:ql98b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36730\_at  
 Cluster Incl. U66684:HSU66684 Homo sapiens cDNA /gb=U66684 /gi=1906569 ; 37422\_at Cluster  
 Incl. S71018:cyclophilin C [human, kidney, mRNA, 883 nt] /cds=(; 38220\_at Cluster Incl.  
 U20938:Human lymphocyte dihydropyrimidine dehydrogenase m; 39211\_at Cluster Incl.  
 AF091080:Homo sapiens clone 614 unknown mRNA, complete se; 40349\_at Cluster Incl.  
 AL049442:Homo sapiens mRNA; cDNA DKFZp586N1720 (from clon; 40399\_r\_at Cluster Incl.

- AI743406:wg92g12.x1 Homo sapiens cDNA, 3 end /clone=IM; 31892\_at Cluster Incl.
- X58288:H.sapiens hR-PTPu gene for protein tyrosine phosph; 32696\_at Cluster Incl.
- X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 ; 33267\_at Cluster Incl.
- AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence; 34759\_at Cluster Incl.
- 5 U68494:Human hbc647 mRNA sequence /cds=UNKNOWN /gb=U68494; 35193\_at Cluster Incl.
- AF060219:Homo sapiens RCC1-like G exchanging factor RLG m; 35677\_at Cluster Incl.
- AL035369:H.sapiens novel gene from PAC 117P20, chromosome; 35682\_at Cluster Incl.
- AI133727:Habcs0217 Homo sapiens cDNA /gb=AI133727 /gi=360; 36061\_at Cluster Incl.
- AF009314:Homo sapiens clone TUA8 Cri-du-chat region mRNA ; 36069\_at Cluster Incl.
- 10 AB007925:Homo sapiens mRNA for KIAA0456 protein, partial ; 36821\_at Cluster Incl.
- AL050367:Homo sapiens mRNA; cDNA DKFZp564A026 (from clone; 37229\_at Cluster Incl.
- U49844:Human FRAP-related protein (FRP1) mRNA, complete c; 37280\_at Cluster Incl.
- U59912:Human chromosome 4 Mad homolog Smad1 mRNA, complet; 37571\_at Cluster Incl.
- AB028981:Homo sapiens mRNA for KIAA1058 protein, partial ; 38306\_at Cluster Incl.
- 15 AA477576:zu44b03.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 38364\_at Cluster Incl.
- AF068197:Homo sapiens BCE-1 mRNA, complete cds /cds=(516; 39741\_at Cluster Incl.
- D16481:Homo sapiens mRNA for mitochondrial 3-ketoacyl-CoA; 39771\_at Cluster Incl.
- AB018283:Homo sapiens mRNA for KIAA0740 protein, complete; 40516\_at Cluster Incl.
- L19872:Human AH-receptor mRNA, complete cds /cds=(375,292; 40805\_at Cluster Incl.
- 20 AB007900:Homo sapiens KIAA0440 mRNA, partial cds /cds=(0; 40818\_at Cluster Incl.
- D14041:Homo sapiens mRNA for H-2K binding factor-2, compl; 41763\_g\_at Cluster Incl.
- D64015:Homo sapiens mRNA for T-cluster binding protein,; 32218\_at Cluster Incl.
- AF034176:AF034176 Homo sapiens cDNA /clone=ntcon5-contig ; 36689\_at Cluster Incl.
- AL040446:DKFZp434D1414\_r1 Homo sapiens cDNA, 5 end /clon; 37733\_at Cluster Incl.
- 25 L35263:Human CSaids binding protein (CSBP1) mRNA, complet; 38062\_at Cluster Incl.
- D87467:Human mRNA for KIAA0277 gene, complete cds /cds=(5; 38411\_at Cluster Incl.
- U90916:Human clone 23815 mRNA sequence /cds=UNKNOWN /gb=U; 41335\_at Cluster Incl.
- AL050084:Homo sapiens mRNA; cDNA DKFZp566O1646 (from clon; 32510\_at Cluster Incl.
- AF026947:Homo sapiens aflatoxin aldehyde reductase AFAR m; 32576\_at Cluster Incl.
- 30 U94855:Homo sapiens translation initiation factor 3 47 kD; 33102\_at Cluster Incl. D67031:Homo sapiens ADDL mRNA for adducin-like protein, c; 1596\_g\_at L06139 /FEATURE= /DEFINITION=HUMTEKRPTK Homo sapiens receptor protein-; 995\_g\_at X58288 /FEATURE=mRNA /DEFINITION=HSHRPTPU H.sapiens hR-PTPu gene for pr.
- Metagene** 417; 31463\_s\_at Cluster Incl. AL022097:Homo sapiens DNA sequence from PAC
- 35 256G22 on c; 36443\_at Cluster Incl. X99947:Homo sapiens mRNA dynein-related protein /cds=(529; 33485\_at Cluster Incl. D23660:Human mRNA for ribosomal protein, complete cds /cd; 39995\_s\_at Cluster Incl. U13395:Human oxidoreductase (HHCMA56) mRNA, complete cd; 40395\_at Cluster Incl. AB007932:Homo sapiens mRNA for KIAA0463 protein, partial ; 41408\_at Cluster Incl. AF042169:Homo sapiens putative ATP-dependent mitochondria; 41719\_i\_at Cluster

- Incl. AF009767:AF009767 Homo sapiens cDNA /clone=C97A-12 /gb=; 32724\_at Cluster Incl.  
 AF023462:Homo sapiens peroxisomal phytanoyl-CoA alpha-hyd; 33223\_at Cluster Incl.  
 AB011133:Homo sapiens mRNA for KIAA0561 protein, partial ; 36073\_at Cluster Incl.  
 U35139:Human NECDIN related protein mRNA, complete cds /c; 37980\_at Cluster Incl.
- 5 U03644:Human receptin mRNA, complete cds /cds=(32,1387) /g; 38689\_at Cluster Incl.  
 AL021937:dJ149A16.6 (novel protein, human ortholog of wor; 39367\_at Cluster Incl.  
 AA522537:ni38e08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40139\_at Cluster Incl.  
 U88966:Human protein rapamycin associated protein (FRAP2); 40486\_g\_at Cluster Incl.  
 AA176780:zp32a10.s1 Homo sapiens cDNA, 3 end /clone=IM; 41765\_at Cluster Incl.
- 10 AI541285:pec1.2-4.D10.r Homo sapiens cDNA, 5 end /clone\_; 32173\_at Cluster Incl. X95384:Homo sapiens mRNA for translational inhibitor prot; 32745\_at Cluster Incl. AF034091:Homo sapiens nuclear localization signal contain; 33359\_at Cluster Incl. AB018311:Homo sapiens mRNA for KIAA0768 protein, partial ; 34299\_at Cluster Incl. AL096880:Novel human mRNA containing Zinc finger C2H2 typ; 34391\_at Cluster Incl. Y08915:H.sapiens mRNA for alpha 4 protein /cds=(8,1027) /; 34826\_at Cluster Incl. L21936:Human succinate dehydrogenase flavoprotein subunit; 34828\_at Cluster Incl. AL037557:DKFZp564H2472\_r1 Homo sapiens cDNA, 5 end /clon; 35358\_at Cluster Incl. AB028998:Homo sapiens mRNA for KIAA1075 protein, partial ; 35760\_at Cluster Incl. AF087135:Homo sapiens FIFO-type ATPase subunit d mRNA, nu; 35836\_at Cluster Incl. AB019408:Homo sapiens mRNA, expressed in fibroblasts of p; 36137\_at Cluster Incl.
- 20 X86691:H.sapiens mRNA for 218kD Mi-2 protein /cds=(89,582; 37002\_at Cluster Incl. D32143:Human mRNA for biliverdin-IXbeta reductase I /cds=; 37704\_at Cluster Incl. Z14093:H.sapiens mRNA for branched chain decarboxylase al; 37766\_s\_at Cluster Incl. AF035309:Homo sapiens clone 23598 mRNA, complete cds /c; 38762\_at Cluster Incl. AF083255:Homo sapiens RNA helicase-related protein mRNA, ; 39184\_at Cluster Incl.
- 25 AI857469:wl57f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41302\_at Cluster Incl. R59606:yh02e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 326\_i\_at Ribosomal Protein S20 . **Metagene** 418; 34969\_s\_at Cluster Incl. AL096750:Homo sapiens mRNA; cDNA DKFZp434H244 (from clo; 38219\_at Cluster Incl. D10656:Human mRNA for CRK-II, complete cds /cds=(105,1019; 34656\_at Cluster Incl. X82895:H.sapiens mRNA for DLG2 /cds=(87,1817) /gb=X82895 ; 35198\_at Cluster Incl. AF070596:Homo sapiens clone 24796 mRNA sequence /cds=UNKN; 40485\_at Cluster Incl. AA176780:zp32a10.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32611\_at Cluster Incl. X75252:H.sapiens phosphatidylethanolamine binding protein; 160033\_s\_at NM\_006297 /FEATURE=mRNA /DEFINITION=Homo sapiens X-ray repair comple. **Metagene** 419; 40425\_at Cluster Incl. M57730:Human B61 mRNA, complete cds /cds=(73,690) /gb=M57.
- 35 **Metagene** 420; 33651\_at Cluster Incl. AB013456:Homo sapiens hAQP8 mRNA for aquaporin 8, complet; 39567\_at Cluster Incl. AB006190:Homo sapiens mRNA for aquaporin adipose, complet; 39051\_at Cluster Incl. U31767:Human neuronatin alpha and neuronatin beta genes, ; 32507\_at Cluster Incl. AW043925:wy82b07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1754\_at

- AF006041 /FEATURE= /DEFINITION=AF006041 Homo sapiens Fas-binding protein; 1641\_s\_at  
 U32986 /FEATURE= /DEFINITION=HSU32986 Human xeroderma pigmentosum grou; 1001\_at  
 X60957 /FEATURE=cds /DEFINITION=HSTIEMR Human tie mRNA for putative rece; 485\_at  
 U59748 /FEATURE= /DEFINITION=HSU59748 Human desert hedgehog (hDHH) mRNA, ;  
 5 145\_s\_at U80987 /FEATURE= /DEFINITION=HSU80987 Human transcription factor TBX5 m;  
 107\_at Z95624 /FEATURE=cds /DEFINITION=HSU237H1 Human DNA sequence from cosmid U.  
**Metagene** 421; 35106\_at Cluster Incl. Z46967:H.sapiens mRNA for calicin (partial) /cds=(0,1757);  
 35390\_at Cluster Incl. AI651024:wa96h06.x1 Homo sapiens cDNA, 3 end /clone=IMAG;  
 35419\_g\_at Cluster Incl. J04178:Human abnormal beta-hexosaminidase alpha chain (; 38551\_at  
 10 Cluster Incl. U52112:neural cell adhesion molecule L1 /cds=(19,3792) /g; 40762\_g\_at Cluster Incl.  
 AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=37; 38005\_at Cluster Incl.  
 AJ005866:Homo sapiens mRNA for putative Sqv-7-like protei; 38691\_s\_at Cluster Incl.  
 J03553:Human pulmonary surfactant protein (SP5) mRNA, c; 32768\_at Cluster Incl.  
 AL048308:DKFZp586A2224\_s1 Homo sapiens cDNA /clone=DKFZp5; 35266\_at Cluster Incl.  
 15 AL049288:Homo sapiens mRNA; cDNA DKFZp564M053 (from clone; 35809\_g\_at Cluster Incl.  
 AL031681:dJ862K6.2.2 (splicing factor, arginine/serine-; 38454\_g\_at Cluster Incl. X15606:Human  
 mRNA for ICAM-2, cell adhesion ligand for ; 1461\_at M69043 /FEATURE=  
 /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA encoding I; 1347\_at S78187  
 /FEATURE= /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human, mRNA].  
 20 **Metagene** 422; 32319\_at Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glyc;  
 34454\_r\_at Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, compl; 37417\_at  
 Cluster Incl. M36542:Human lymphoid-specific transcription factor mRNA,; 39645\_r\_at Cluster  
 Incl. AF033105:Homo sapiens X-arrestin mRNA, complete cds /cd; 41442\_at Cluster Incl.  
 AB010419:Homo sapiens mRNA for MTG8-related protein MTG16; 33737\_f\_at Cluster Incl.  
 25 AI871359:wl81b11.x1 Homo sapiens cDNA, 3 end /clone=IM; 40233\_at Cluster Incl.  
 AI198214:qi55c03.x1 Homo sapiens cDNA, 3 end /clone=IMAG.  
**Metagene** 423; 31906\_at Cluster Incl. AF068754:Homo sapiens heat shock factor binding protein 1;  
 32316\_s\_at Cluster Incl. X15183:Human mRNA for 90-kDa heat-shock protein /cds=(6; 41450\_at  
 Cluster Incl. AI553878:tn30a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34678\_at Cluster  
 30 Incl. AL096713:Homo sapiens mRNA; cDNA DKFZp564E1616 (from clon; 35236\_g\_at Cluster  
 Incl. AA099265:zk84f07.r1 Homo sapiens cDNA, 5 end /clone=IM; 38331\_at Cluster Incl.  
 Y07566:H.sapiens mRNA for RIT protein /cds=(145,804) /gb=; 38684\_at Cluster Incl.  
 AJ010953:Homo sapiens mRNA for putative Ca2+-transporting; 39756\_g\_at Cluster Incl.  
 Z93930:Human DNA sequence from clone 292E10 on chromoso; 36614\_at Cluster Incl.  
 35 X87949:H.sapiens mRNA for BiP protein /cds=(222,2183) /gb; 37720\_at Cluster Incl.  
 M22382:Human mitochondrial matrix protein P1 (nuclear enc; 39118\_at Cluster Incl.  
 L08069:Human heat shock protein, E. coli DnaJ homologue m; 1957\_s\_at AF054598  
 /FEATURE=mRNA /DEFINITION=HSTGFBR1G9 Homo sapiens TGF-beta ty; 1262\_s\_at M19154  
 /FEATURE=mRNA /DEFINITION=HUMTGF2A Human transforming growth f; 1161\_at J04988

- /FEATURE=cds /DEFINITION=HUMHSP90B Human 90 kD heat shock protein; 1102\_s\_at  
M10901 /FEATURE=mRNA /DEFINITION=HUMGCRA Human glucocorticoid receptor; 809\_at  
U57094 /FEATURE= /DEFINITION=HSU57094 Human small GTP-binding protein mRNA; 714\_at  
Adenylyl Cyclase-Associated Protein 2 ; 276\_at L08069 /FEATURE=
- 5 /DEFINITION=HUMDNAJHOM Human heat shock protein, E. coli.  
**Metagene** 424; 31736\_at Cluster Incl. AA975427: oq28g02.s1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 31944\_at Cluster Incl. AI028290: ov84f11.x1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 33690\_at Cluster Incl. AL080190: Homo sapiens mRNA; cDNA DKFZp434A202  
(from clone; 32872\_at Cluster Incl. AL049279: Homo sapiens mRNA; cDNA DKFZp564I083 (from  
10 clone; 36707\_s\_at Cluster Incl. X89059: H.sapiens mRNA for unknown protein expressed in ;  
40725\_at Cluster Incl. AF047438: Homo sapiens GOS28/P28 protein mRNA, complete cd; 41388\_at  
Cluster Incl. AF017418: Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA; 41438\_at Cluster  
Incl. AL049923: Homo sapiens mRNA; cDNA DKFZp547E2210 (from clone; 32064\_at Cluster Incl.  
Y13467: Homo sapiens mRNA for RB18A protein /cds=(235,4935; 32127\_at Cluster Incl.
- 15 U90030: Homo sapiens bicaudal-D (BICD) mRNA, alternatively; 32643\_at Cluster Incl.  
L07956: Homo sapiens 1,4-alpha-glucan branching enzyme (HG; 32662\_at Cluster Incl.  
AL041663: DKFZp434M0217\_s1 Homo sapiens cDNA, 3 end /clone; 34697\_at Cluster Incl.  
AF074264: Homo sapiens LDL receptor-related protein 6 (LRP; 37984\_s\_at Cluster Incl.  
M57763: Human ADP-ribosylation factor (hARF6) mRNA, comp; 32802\_at Cluster Incl.
- 20 AB011169: Homo sapiens mRNA for KIAA0597 protein, partial ; 33418\_at Cluster Incl.  
AL096752: Homo sapiens mRNA; cDNA DKFZp434A012 (from clone; 33845\_at Cluster Incl.  
W28483: 47e11 Homo sapiens cDNA /gb=W28483 /gi=1308431 /ug; 36991\_at Cluster Incl.  
L14076: Human pre-mRNA splicing factor SRp75 mRNA, complet; 37710\_at Cluster Incl.  
L08895: Homo sapiens MADS/MEF2-family transcription factor; 40191\_s\_at Cluster Incl.
- 25 AI761647: wg66h09.x1 Homo sapiens cDNA, 3 end /clone=IM; 33188\_at Cluster Incl.  
U37221: Human cyclophilin-like protein mRNA, partial cds /; 1383\_at M64929 /FEATURE=  
/DEFINITION=HUMPROP2AA Human protein phosphatase 2A alp.  
**Metagene** 425; 31745\_at Cluster Incl. AF007194: Homo sapiens mucin (MUC3) mRNA, partial cds  
/cds; 32007\_at Cluster Incl. W29045: 55e12 Homo sapiens cDNA /gb=W29045 /gi=1309002 /ug;  
30 36355\_at Cluster Incl. M13903: Human involucrin mRNA /cds=(0,1757) /gb=M13903 /gi; 35913\_at  
Cluster Incl. U88047: Homo sapiens DNA binding protein homolog (DRIL1) m; 38205\_at Cluster  
Incl. AB021742: Homo sapiens NDRF gene for neuroD-related factor; 40700\_at Cluster Incl.  
U36500: Human lymphoid-specific SP100 homolog (LYSP100-B) ; 41050\_at Cluster Incl.  
X95525: H.sapiens mRNA for TAFII100 protein /cds=(23,2422); 41647\_at Cluster Incl.
- 35 W28742: 51a7 Homo sapiens cDNA /gb=W28742 /gi=1308690 /ug=; 32710\_at Cluster Incl.  
X83127: H.sapiens mRNA for voltage gated potassium channel; 33744\_at Cluster Incl.  
AL080150: Homo sapiens mRNA; cDNA DKFZp434D174 (from clone; 35687\_at Cluster Incl.  
Z24459: H.sapiens MTCP1 gene, exons 2A to 7 (and joined mR; 35990\_at Cluster Incl.  
AB007947: Homo sapiens mRNA for KIAA0478 protein, complete; 38629\_at Cluster Incl.

- AF047863:untitled /cds=(17,1075) /gb=AF047863 /gi=2909668; 32810\_at Cluster Incl.  
 AF019369:untitled /cds=(89,826) /gb=AF019369 /gi=2623563 ; 39834\_at Cluster Incl.  
 X66403:H.sapiens mRNA for acetylcholine receptor (epsilon; 1684\_s\_at X69950  
 /FEATURE=exon#3 /DEFINITION=HSWT1WIT H.sapiens DNA sequence for; 1689\_at AB000895  
 5 /FEATURE= /DEFINITION=AB000895 Homo sapiens mRNA for cadherin F; 1339\_s\_at X14675  
 /FEATURE=cds /DEFINITION=HSBCR3C Human bcr-abl mRNA 5 fragment; 1116\_at M28170  
 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD.  
**Metagene** 426; 33467\_at Cluster Incl. X66171:H.sapiens CMRF35 mRNA, complete CDS  
 /cds=(239,913); 33503\_at Cluster Incl. W29105:56d8 Homo sapiens cDNA /gb=W29105  
 10 /gi=1309071 /ug=; 35402\_at Cluster Incl. AF068868:Homo sapiens TNFR-related death receptor-6  
 (DR6); 35869\_at Cluster Incl. AB020499:Homo sapiens BCG-regulated mRNA for MD-1 homolog;  
 40331\_at Cluster Incl. AF035819:Homo sapiens macrophage receptor MARCO mRNA, com;  
 41677\_at Cluster Incl. AF035279:Homo sapiens clone 23888 mRNA sequence /cds=(162; 36472\_at  
 Cluster Incl. U32849:Homo sapiens Nmi mRNA, complete cds /cds=(280,1203; 39061\_at Cluster  
 15 Incl. D28137:Human mRNA for BST-2, complete cds /cds=(9,551) /g; 39721\_at Cluster Incl.  
 U09303:Human T cell leukemia LERK-2 (EPLG2) mRNA, complet; 37749\_at Cluster Incl.  
 D78611:Human MEST mRNA, complete cds /cds=(223,1230) /gb=; 1939\_at M22898  
 /FEATURE=mRNA /DEFINITION=HUMP53A11 Human phosphoprotein p53 gene; 1890\_at  
 AB000584 /FEATURE= /DEFINITION=AB000584 Homo sapiens mRNA for TGF-beta s; 626\_s\_at  
 20 L78833 /FEATURE=cds#5 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vatI g.  
**Metagene** 427; 35446\_at Cluster Incl. AA767013:oa42a08.s1 Homo sapiens cDNA /clone=IMAGE-  
 130760; 41222\_at Cluster Incl. AF067575:untitled /cds=(21,2564) /gb=AF067575 /gi=3789867;  
 1326\_at U60519 /FEATURE= /DEFINITION=HSU60519 Human apoptotic cysteine protease ;  
 574\_s\_at M87507 /FEATURE= /DEFINITION=HUMIL1BCE Homo sapien interleukin-1 beta c.  
 25 **Metagene** 428; 38278\_at Cluster Incl. M62324:Human modulator recognition factor I (MRF-1)  
 mRNA,; 39052\_at Cluster Incl. J00124:Homo sapiens 50 kDa type I epidermal keratin gene,;  
 32855\_at Cluster Incl. L00352:Human low density lipoprotein receptor gene /cds=(; 35850\_at  
 Cluster Incl. AI950382:wp10g06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41828\_at Cluster  
 Incl. Y10746:H.sapiens mRNA for protein containing MBD 1 /cds=(; 1842\_at Oncogene Tls/Chop,  
 30 Fusion Activated ; 287\_at L19871 /FEATURE= /DEFINITION=HUMATF3X Human activating  
 transcription fact.  
**Metagene** 429; 33045\_r\_at Cluster Incl. AI830463:wh51e03.x1 Homo sapiens cDNA, 3 end  
 /clone=IM; 32928\_at Cluster Incl. AJ012214:Homo sapiens mRNA for PLA-1 protein /cds=(0,1310;  
 39611\_at Cluster Incl. AI557322:PT2.1\_16\_F11.r Homo sapiens cDNA, 3 end /clone\_ ; 37201\_at  
 35 Cluster Incl. D38535:Human mRNA for PK-120 /cds=(129,2921) /gb=D38535 /; 37653\_at Cluster  
 Incl. AF018081:Homo sapiens type XVIII collagen (COL18A1) mRNA,; 1400\_at M13207  
 /FEATURE=expanded\_cds /DEFINITION=HUMCSFGMA Human granulocyte-mac.  
**Metagene** 430; 37432\_g\_at Cluster Incl. AF077953:Homo sapiens protein inhibitor of activated ST;  
 38192\_at Cluster Incl. AB014543:Homo sapiens mRNA for KIAA0643 protein, partial ; 40026\_g\_at



- Cluster Incl. AF052186:Homo sapiens clone 24431 mRNA sequence /cds=UN; 33720\_at Cluster Incl. L48692:Homo sapiens (clone p5-23-3) mRNA /cds=UNKNOWN /gb; 34667\_at Cluster Incl. U15306:Human cysteine-rich sequence-specific DNA-binding ; 36504\_at Cluster Incl. AF097441:Homo sapiens phenylalanine-tRNA synthetase (FARS; 37178\_at Cluster Incl.
- 5 M74089:Human TB1 gene mRNA, 3 end /cds=(0,1305) /gb=M740; 39012\_g\_at Cluster Incl. X99906:Homo sapiens mRNA for alpha endosulfine /cds=(12; 40132\_g\_at Cluster Incl. D89937:Homo sapiens mRNA for follistatin-related protei; 40823\_s\_at Cluster Incl. U85430:Human transcription factor NFATx4 mRNA, complete; 32812\_at Cluster Incl. AB029025:Homo sapiens mRNA for KIAA1102 protein, partial ; 33932\_at Cluster Incl. X17644:Human GST1-Hs mRNA for
- 10 GTP-binding protein /cds=(6; 38390\_at Cluster Incl. Z34975:H.sapiens LDLC mRNA /cds=(95,2311) /gb=Z34975 /gi=; 33180\_at Cluster Incl. U68111:Human protein phosphatase inhibitor 2 (PPP1R2) gen; 2093\_s\_at J04977 /FEATURE=mRNA /DEFINITION=HUMKUANT Human Ku autoimmune antigen ; 1550\_at U19796 /FEATURE= /DEFINITION=HSU19796 Human melanoma antigen p15 mRNA, c; 1206\_at X66364 /FEATURE=cds /DEFINITION=HSSTHPKE
- 15 H.sapiens mRNA PSSALRE for seri; 913\_at M21535 /FEATURE= /DEFINITION=HUMERG11 Human erg protein (ets-related gene).  
**Metagene** 431; 37785\_at Cluster Incl. U69563:U69563 Homo sapiens cDNA /clone=25050 /gb=U69563 /; 41542\_at Cluster Incl. AF062346:Homo sapiens zinc finger protein 216 splice vari; 376\_at AB000220 /FEATURE= /DEFINITION=AB000220 Homo sapiens mRNA for semaphorin .
- 20 **Metagene** 432; 36233\_at Cluster Incl. AF091242:Homo sapiens ATP sulfurylase/APS kinase 2 mRNA, ; 32075\_at Cluster Incl. D89859:Homo sapiens mRNA for zinc finger 5 protein, compl; 33761\_s\_at Cluster Incl. AB007962:Homo sapiens mRNA, chromosome 1 specific trans; 36042\_at Cluster Incl. X75958:H.sapiens trkB mRNA for protein-tyrosine kinase /c; 41735\_at Cluster Incl. AI808958:wf67a09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1929\_at U83508 /FEATURE=
- 25 /DEFINITION=HSU83508 Human angiopoietin-1 mRNA, complet; 1867\_at AF005775 /FEATURE= /DEFINITION=AF005775 Homo sapiens caspase-like apopto; 1115\_at M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) m.  
**Metagene** 433; 34169\_s\_at Cluster Incl. U57627:Human fetal brain oculocerebrorenal syndrome (OC; 35074\_at Cluster Incl. AF004715:Homo sapiens jerky gene product homolog mRNA, co;
- 30 36792\_at Cluster Incl. Z24727:H.sapiens tropomyosin isoform mRNA, complete CDS /; 37828\_at Cluster Incl. AL050064:Homo sapiens mRNA; cDNA DKFZp566L033 (from clone; 38139\_at Cluster Incl. AF017445:Homo sapiens GDP-L-fucose pyrophosphorylase (GFP; 38568\_at Cluster Incl. U82939:Homo sapiens p53 binding protein mRNA, complete cd; 40338\_at Cluster Incl. U52827:Homo sapiens Cri-du-chat region mRNA, clone NIBB11; 40701\_at Cluster Incl.
- 35 U75362:Homo sapiens isopeptidase T-3 (ISOT-3) mRNA, compl; 41366\_at Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete; 41421\_at Cluster Incl. AB020716:Homo sapiens mRNA for KIAA0909 protein, partial ; 41612\_at Cluster Incl. AB007872:Homo sapiens KIAA0412 mRNA, partial cds /cds=(36; 31851\_at Cluster Incl. AJ224819:Homo sapiens mRNA for candidate tumor suppressor; 31854\_at Cluster Incl.

- AF035582:Homo sapiens CASK mRNA, complete cds /cds=(15,27; 32087\_at Cluster Incl.  
M65217:Human heat shock factor 2 (HSF2) mRNA, complete cd; 32119\_at Cluster Incl.  
AL049423:Homo sapiens mRNA; cDNA DKFZp586B211 (from clone; 32730\_at Cluster Incl.  
AL080059:Homo sapiens mRNA; cDNA DKFZp564H142 (from clone; 33241\_at Cluster Incl.  
5 AB014526:Homo sapiens mRNA for KIAA0626 protein, complete; 33809\_at Cluster Incl.  
AL049933:Homo sapiens mRNA; cDNA DKFZp564K1216 (from clon; 34249\_at Cluster Incl.  
AF084535:Homo sapiens laforin (EPM2A) mRNA, partial cds /; 34745\_at Cluster Incl.  
AF070570:Homo sapiens clone 24473 mRNA sequence /cds=UNKN; 35234\_at Cluster Incl.  
D50406:Homo sapiens ST15 mRNA, complete cds /cds=(109,302; 35720\_at Cluster Incl.  
10 AB020700:Homo sapiens mRNA for KIAA0893 protein, complete; 36002\_at Cluster Incl.  
AB023229:Homo sapiens mRNA for KIAA1012 protein, complete; 36089\_at Cluster Incl.  
AB023183:Homo sapiens mRNA for KIAA0966 protein, complete; 36827\_at Cluster Incl.  
AF020762:Homo sapiens clone 1400 unknown protein mRNA, pa; 36905\_at Cluster Incl.  
AB009356:Homo sapiens mRNA for TGF-beta activated kinase ; 36909\_at Cluster Incl.  
15 X62048:H.sapiens Wee1 hu gene /cds=(170,2110) /gb=X62048 ; 37535\_at Cluster Incl.  
M27691:Human transactivator protein (CREB) mRNA, complete; 37581\_at Cluster Incl.  
X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21; 37891\_at Cluster Incl.  
U79272:Human clone 23720 mRNA sequence /cds=UNKNOWN /gb=U; 38674\_at Cluster Incl.  
AA115140:z110d12.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 38698\_at Cluster Incl.  
20 AL080070:Homo sapiens mRNA; cDNA DKFZp564M112 (from clone; 39376\_at Cluster Incl.  
AB014530:Homo sapiens mRNA for KIAA0630 protein, partial ; 39692\_at Cluster Incl.  
AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clon; 39707\_at Cluster Incl.  
AB014547:Homo sapiens mRNA for KIAA0647 protein, partial ; 40105\_at Cluster Incl.  
M65131:Human methylmalonyl-CoA mutase (MCM) mRNA, complet; 40438\_at Cluster Incl.  
25 D87930:Homo sapiens mRNA for myosin phosphatase target su; 40488\_at Cluster Incl.  
M18533:Homo sapiens dystrophin (DMD) mRNA, complete cds /; 40492\_at Cluster Incl.  
AB020633:Homo sapiens mRNA for KIAA0826 protein, partial ; 40780\_at Cluster Incl.  
AF016507:Homo sapiens C-terminal binding protein 2 mRNA, ; 40853\_at Cluster Incl.  
AI478147:tm34f06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40859\_at Cluster Incl.  
30 AI561196:tq27a01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32160\_at Cluster Incl.  
U76247:Human hSIAH1 mRNA, complete cds /cds=(186,1034) /g; 32854\_at Cluster Incl.  
AB014596:Homo sapiens mRNA for KIAA0696 protein, partial ; 33340\_at Cluster Incl.  
AB007898:Homo sapiens KIAA0438 mRNA, complete cds /cds=(1; 34335\_at Cluster Incl.  
AI765533:wi81c01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34344\_at Cluster Incl.  
35 AF044195:Homo sapiens IkappaB kinase complex associated p; 35319\_at Cluster Incl.  
U25435:Human transcriptional repressor (CTCF) mRNA, compl; 35321\_at Cluster Incl.  
AB004884:Homo sapiens mRNA for PKU-alpha, partial cds /cd; 35843\_at Cluster Incl.  
L40402:Homo sapiens (clone Zap2) mRNA fragment /cds=UNKNO; 36117\_at Cluster Incl.  
L13616:Human focal adhesion kinase (FAK) mRNA, complete c; 36192\_at Cluster Incl.

- D83777:Human mRNA for KIAA0193 gene, complete cds /cds=(3; 36198\_at Cluster Incl.  
D13641:Human mRNA for KIAA0016 gene, complete cds /cds=(1; 36587\_at Cluster Incl.  
Z11692:H.sapiens mRNA for elongation factor 2 /cds=(0,257; 36934\_at Cluster Incl.  
AL035447:Human DNA sequence from clone 1183I21 on chromos; 36944\_f\_at Cluster Incl.
- 5 U72621:Human LOT1 mRNA, complete cds /cds=(657,2048) /g; 36946\_at Cluster Incl.  
D86550:Human mRNA for serine/threonine protein kinase, co; 37662\_at Cluster Incl.  
AI701164:we10g07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37736\_at Cluster Incl.  
D13892:Human mRNA for carboxyl methyltransferase, complet; 38011\_at Cluster Incl.  
AB006572:Homo sapiens RMP mRNA for RPB5 meidating protein; 38075\_at Cluster Incl.
- 10 X68194:H.sapiens h-Sp1 mRNA /cds=(33,812) /gb=X68194 /gi=; 38821\_at Cluster Incl.  
AJ002030:Homo sapiens mRNA for putative progesterone bind; 39132\_at Cluster Incl.  
AB010882:Homo sapiens mRNA for hSNF2H, complete cds /cds=; 39150\_at Cluster Incl.  
U69559:U69559 Homo sapiens cDNA /clone=26077 /gb=U69559 /; 39509\_at Cluster Incl.  
AI692348:wd85g12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40899\_at Cluster Incl.
- 15 Y00503:Human mRNA for keratin 19 /cds=(32,1234) /gb=Y0050; 41343\_at Cluster Incl.  
Y16521:Homo sapiens mRNA for CDS2 protein /cds=(258,1595); 32530\_at Cluster Incl.  
X56468:Human mRNA for 14.3.3 protein, a protein kinase re; 32569\_at Cluster Incl. L13385:Homo sapiens(clone 71) Miller-Dieker lissencephaly; 1940\_at M54968 /FEATURE=  
/DEFINITION=HUMKRASM Human K-ras oncogene protein mRNA,; 1530\_g\_at U50534
- 20 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequenc; 851\_s\_at S62539  
/FEATURE= /DEFINITION=S62539 insulin receptor substrate-1 [human; 755\_at D26070  
/FEATURE=mRNA /DEFINITION=HUMINSP3R1 Human mRNA for type 1 inosito; 160\_at  
U43899 /FEATURE= /DEFINITION=HSU43899 Human signal transducing adaptor mo.  
**Metagene** 434; 31525\_s\_at Cluster Incl. J00153:Human alpha globin gene cluster on chromosome
- 25 16; 31687\_f\_at Cluster Incl. M25079:Human sickle cell beta-globin mRNA, complete cds; 32052\_at  
Cluster Incl. L48215:Homo sapiens beta-globin (HBB) gene, with a to c a; 32799\_at Cluster Incl.  
AF023268:Homo sapiens clk2 kinase (CLK2), propin1, cotel.; 215\_g\_at M97676 /FEATURE=  
/DEFINITION=HUMHOX7 Homo sapiens (region 7) homeobox p.  
**Metagene** 435; 35092\_at Cluster Incl. AF032387:Homo sapiens snRNA activating protein complex
- 30 19; 38935\_at Cluster Incl. X72790:Human endogenous retrovirus mRNA for ORF /cds=(524;  
38337\_at Cluster Incl. U62392:Homo sapiens zinc finger protein mRNA, complete cd; 40221\_at  
Cluster Incl. L39059:Homo sapiens transcription factor SL1 mRNA, comple; 1468\_at U12595  
/FEATURE= /DEFINITION=HSU12595 Human tumor necrosis factor type 1; 576\_at M93718  
/FEATURE= /DEFINITION=HUMNIOXSYN Human nitric oxide synthase mRNA,.
- 35 **Metagene** 436; 35948\_at Cluster Incl. D25303:Human mRNA for integrin alpha subunit, complete  
cd; 39324\_at Cluster Incl. AL050078:Homo sapiens mRNA; cDNA DKFZp566G0746 (from clon;  
40673\_at Cluster Incl. U12778:Human acyl-CoA dehydrogenase mRNA, complete cds /c; 40731\_at  
Cluster Incl. L07515:Human heterochromatin protein homologue (HP1) mRNA; 32142\_at Cluster  
Incl. U26424:Human Ste20-like kinase (MST2) mRNA, complete cds ; 34288\_at Cluster Incl.

- U67784:Human orphan G protein-coupled receptor (RDC1) mRNA; 35246\_at Cluster Incl.  
 U18934:Human receptor tyrosine kinase (DTK) mRNA, complet; 37532\_at Cluster Incl.  
 M91432:Human medium-chain acyl-CoA dehydrogenase (MCAD) g; 39009\_at Cluster Incl.  
 N98670:yy66d08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 39690\_at Cluster Incl.
- 5 AF002282:Homo sapiens alpha-actinin-2 associated LIM prot; 40876\_at Cluster Incl.  
 U31525:Human glycogenin mRNA, complete cds /cds=(127,1128; 41188\_at Cluster Incl.  
 W28186:43c2 Homo sapiens cDNA /gb=W28186 /gi=1308134 /ug=; 33456\_at Cluster Incl.  
 U24166:Homo sapiens EB1 mRNA, complete cds /cds=(64,870) ; 33876\_at Cluster Incl.  
 AL050107:Homo sapiens mRNA; cDNA DKFZp586I1419 (from clon; 34809\_at Cluster Incl.
- 10 H53921:yq87g03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 35837\_at Cluster Incl.  
 AJ224677:Homo sapiens mRNA for scrapie responsive protein; 36149\_at Cluster Incl.  
 D78014:Homo sapiens mRNA for dihydropyrimidinase related ; 36211\_at Cluster Incl.  
 D87461:Human mRNA for KIAA0271 gene, complete cds /cds=(1; 36650\_at Cluster Incl.  
 D13639:Human mRNA for KIAK0002 gene, complete cds /cds=(2; 37035\_at Cluster Incl.
- 15 AI557272:PT2.1\_15\_G02.r Homo sapiens cDNA, 3 end /clone\_ ; 37318\_at Cluster Incl.  
 X81625:H.sapiens mRNA for C11 protein /cds=(135,1448) /gb; 37347\_at Cluster Incl.  
 AA926959:om68h08.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38033\_at Cluster Incl.  
 AL049934:Homo sapiens mRNA; cDNA DKFZp564M1416 (from clon; 38802\_at Cluster Incl.  
 Y12711:H.sapiens mRNA for putative progesterone binding p; 39147\_g\_at Cluster Incl.
- 20 U72936:Human putative DNA dependent ATPase and helicase; 40213\_at Cluster Incl.  
 M88163:Human global transcription activator homologous se; 1845\_at L36870 /FEATURE=mRNA  
 /DEFINITION=HUMMKK4A Homo sapiens MAP kinase kinase; 1448\_at D00762 /FEATURE=  
 /DEFINITION=HUMPSC8 Human mRNA for proteasome subunit H; 949\_s\_at D78275  
 /FEATURE= /DEFINITION=D78275 Homo sapiens mRNA for proteasome su; 539\_at S59184
- 25 /FEATURE= /DEFINITION=S59184 RYK=related to receptor tyrosine kina.  
**Metagene** 437; 36446\_s\_at Cluster Incl. L24521:Human transformation-related protein mRNA, 3 en;  
 36694\_at Cluster Incl. AF043472:Homo sapiens Shab-related delayed-rectifier K+ c; 38170\_at  
 Cluster Incl. AF070595:Homo sapiens clone 24583 mRNA sequence /cds=UNKN; 38856\_at Cluster  
 Incl. AL109724:Homo sapiens mRNA full length insert cDNA clone ; 40000\_f\_at Cluster Incl.
- 30 AB023203:Homo sapiens mRNA for KIAA0986 protein, partia; 41419\_at Cluster Incl.  
 AL080142:Homo sapiens mRNA; cDNA DKFZp434N103 (from clone; 41655\_at Cluster Incl.  
 AL034399:dA191P20.2 (novel Fibronectin type III domain co; 31792\_at Cluster Incl.  
 M20560:Human lipocortin-III mRNA, complete cds /cds=(46,1; 32026\_s\_at Cluster Incl.  
 AB002311:Human mRNA for KIAA0313 gene, complete cds /cd; 33222\_at Cluster Incl.
- 35 AB017365:Homo sapiens mRNA for frizzled-7, complete cds /; 33716\_at Cluster Incl.  
 N95443:zb81c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 33759\_at Cluster Incl.  
 X04327:Human erythrocyte 2,3-bisphosphoglycerate mutase m; 34654\_at Cluster Incl.  
 AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990; 35237\_at Cluster Incl.  
 AL034452:Human DNA sequence from clone 682J15 on chromoso; 36542\_at Cluster Incl.

- AF030409: Homo sapiens sodium-hydrogen exchanger 6 (NHE-6); 37273\_at Cluster Incl.
- AF007153: Homo sapiens clone 23736 mRNA sequence /cds=UNKN; 37619\_at Cluster Incl.
- D42084: Human mRNA for KIAA0094 gene, partial cds /cds=(0,; 38279\_at Cluster Incl.
- D90150: Human Gx-alpha gene /cds=(619,1686) /gb=D90150 /gi; 38980\_at Cluster Incl.
- 5 AB018276: Homo sapiens mRNA for KIAA0733 protein, partial ; 39410\_at Cluster Incl.
- AB007860: Homo sapiens KIAA0400 mRNA, complete cds /cds=(3; 41128\_at Cluster Incl.
- AF070537: Homo sapiens clone 24606 mRNA sequence /cds=UNKN; 41747\_s\_at Cluster Incl.
- U49020: Human myocyte-specific enhancer factor 2A (MEF2A; 32805\_at Cluster Incl.
- U05861: Human hepatic dihydrodiol dehydrogenase gene /cds=; 35310\_at Cluster Incl.
- 10 D45288: HUMHG2121 Homo sapiens cDNA /gb=D45288 /gi=1136684; 35371\_at Cluster Incl.
- M83822: Human beige-like protein (BGL) mRNA, partial cds /; 36636\_at Cluster Incl.
- M12267: Human ornithine aminotransferase mRNA, complete cd; 38385\_at Cluster Incl.
- S65738: actin depolymerizing factor [human, fetal brain, m; 39136\_at Cluster Incl. AB017642: Homo sapiens mRNA for oxidative-stress responsiv; 40220\_at Cluster Incl. AB021179: Homo sapiens
- 15 mRNA for HEXIM1 protein, complete c; 41536\_at Cluster Incl. AL022726: Human DNA sequence from clone 625H18 on chromoso; 1593\_at J04513 /FEATURE=mRNA /DEFINITION=HUMGFB Human basic fibroblast growth fa; 1495\_at M34057 /FEATURE= /DEFINITION=HUMTGFB1B Human transforming growth factor-; 857\_at S87759 /FEATURE= /DEFINITION=S87759 protein phosphatase 2C alpha [human, ; 160043\_at X66087 /FEATURE=cds /DEFINITION=HSAMYB2
- 20 H.sapiens a-myb mRNA /NOTE=rep.
- Metagene** 438; 34949\_at Cluster Incl. AB028971: Homo sapiens mRNA for KIAA1048 protein, complete; 37085\_g\_at Cluster Incl. AF088219: Homo sapiens CC chemokine gene cluster, comple; 38733\_at Cluster Incl. M30938: Human Ku (p70/p80) subunit mRNA, complete cds /cds.
- Metagene** 439; 31936\_s\_at Cluster Incl. AB007890: Homo sapiens KIAA0430 mRNA, complete cds
- 25 /cds=; 33666\_at Cluster Incl. M16342: Human nuclear ribonucleoprotein particle (hnRNP) C; 34987\_s\_at Cluster Incl. X79536: H.sapiens mRNA for hnRNPcore protein A1 /cds=(26; 38908\_s\_at Cluster Incl. AL096744: Homo sapiens mRNA; cDNA DKFZp566H033 (from clo; 41457\_at Cluster Incl. AB007883: Homo sapiens KIAA0423 mRNA, partial cds /cds=(0,; 41669\_at Cluster Incl. D83776: Human mRNA for KIAA0191 gene, partial cds /cds=(0,; 32085\_at Cluster Incl.
- 30 AB023198: Homo sapiens mRNA for KIAA0981 protein, partial ; 32654\_g\_at Cluster Incl. AW020536: df11b12.y1 Homo sapiens cDNA, 5 end /clone=IM; 33264\_at Cluster Incl. X89602: H.sapiens mRNA for rTS beta protein /cds=(17,1267); 33774\_at Cluster Incl. X98172: H.sapiens mRNA for MACH-alpha-1 protein /cds=(291,; 34225\_at Cluster Incl. AF101434: Homo sapiens Wolf-Hirschhorn syndrome candidate ; 34269\_at Cluster Incl.
- 35 AL050102: Homo sapiens mRNA; cDNA DKFZp586F1019 (from clon; 35163\_at Cluster Incl. AB028964: Homo sapiens mRNA for KIAA1041 protein, complete; 35614\_at Cluster Incl. AB012124: Homo sapiens TCFL5 mRNA for transcription factor; 36032\_at Cluster Incl. AL031427: dJ167A19.3 (novel protein) /cds=(123,557) /gb=AL; 36046\_at Cluster Incl. AL050144: Homo sapiens mRNA; cDNA DKFZp586C1620 (from clon; 36514\_at Cluster Incl.

- U66469:Human cell growth regulator CGR19 mRNA, complete c; 36551\_at Cluster Incl.
- AL049382:Homo sapiens mRNA; cDNA DKFZp586K1318 (from clon; 36845\_at Cluster Incl.
- D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,; 36910\_at Cluster Incl.
- L36870:Homo sapiens MAP kinase kinase 4 (MKK4) mRNA, comp; 37197\_s\_at Cluster Incl.
- 5 AL050006:Homo sapiens mRNA; cDNA DKFZp564A033 (from clo; 37212\_at Cluster Incl.
- D28588:Human mRNA for KIAA0048 gene, complete cds /cds=(3; 37895\_at Cluster Incl.
- D87969:Homo sapiens mRNA for CMP-sialic acid transporter,; 38344\_at Cluster Incl.
- R40666:yf79c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 38357\_at Cluster Incl.
- AL049321:Homo sapiens mRNA; cDNA DKFZp564D156 (from clone; 38365\_at Cluster Incl.
- 10 AF026086:Homo sapiens peroxisome biogenesis disorder prot; 39415\_at Cluster Incl.
- X72727:H.sapiens tunc mRNA for transformation upregulated; 40091\_at Cluster Incl.
- U00115:Human zinc-finger protein (bcl-6) mRNA, complete c; 40864\_at Cluster Incl.
- D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D; 41129\_at Cluster Incl.
- D26067:Human mRNA for KIAA0033 gene, partial cds /cds=(0,; 41224\_at Cluster Incl.
- 15 AB018331:Homo sapiens mRNA for KIAA0788 protein, partial ; 41784\_at Cluster Incl.
- AL080186:Homo sapiens mRNA; cDNA DKFZp564B0769 (from clon; 32165\_at Cluster Incl.
- L41887:Homo sapiens splicing factor, arginine/serine-rich; 32183\_at Cluster Incl. M74002:Human arginine-rich nuclear protein mRNA, complete; 32255\_i\_at Cluster Incl. U40705:Homo sapiens telomeric repeat binding factor (TR; 32259\_at Cluster Incl. AB002386:Human mRNA for
- 20 KIAA0388 gene, complete cds /cds=; 32857\_at Cluster Incl. L13858:Human guanine nucleotide exchange factor mRNA, com; 33348\_at Cluster Incl. M80627:Human HEB helix-loop-helix protein (HEB) mRNA, com; 33373\_at Cluster Incl. AL049951:Homo sapiens mRNA; cDNA DKFZp564O0122 (from clon; 33835\_at Cluster Incl. AB018264:Homo sapiens mRNA for KIAA0721 protein, partial ; 34330\_at Cluster Incl. AB007618:Homo sapiens mRNA for COX7RP,
- 25 complete cds /cds=; 34804\_at Cluster Incl. AL049246:Homo sapiens mRNA; cDNA DKFZp564C053 (from clone; 34877\_at Cluster Incl. AL039831:DKFZp434D1112\_s1 Homo sapiens cDNA, 3 end /clon; 34879\_at Cluster Incl. AF007875:Homo sapiens dolichol monophosphate mannose synt; 35283\_at Cluster Incl. H05692:yl76b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35762\_at Cluster Incl. AB007952:Homo sapiens mRNA for KIAA0483 protein,
- 30 partial ; 35829\_at Cluster Incl. AL080181:Homo sapiens mRNA; cDNA DKFZp434O111 (from clone; 36633\_at Cluster Incl. AA114830:zk88e06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36635\_at Cluster Incl. AB023173:Homo sapiens mRNA for KIAA0956 protein, partial ; 36648\_at Cluster Incl. AF031383:Homo sapiens hMed7 (MED7) mRNA, complete cds /cd; 36660\_at Cluster Incl. AF000231:Homo sapiens rab11a GTPase mRNA, complete cds /c; 36690\_at Cluster Incl.
- 35 M10901:Human glucocorticoid receptor alpha mRNA, complete; 37694\_at Cluster Incl.
- D87685:Human mRNA for KIAA0244 gene, partial cds /cds=(0,; 37703\_at Cluster Incl.
- Y08201:Homo sapiens mRNA for rab geranylgeranyl transferase; 37732\_at Cluster Incl.
- AL049940:Homo sapiens mRNA; cDNA DKFZp564E1922 (from clon; 38050\_at Cluster Incl.
- D79986:Human mRNA for KIAA0164 gene, complete cds /cds=(2; 38818\_at Cluster Incl.

- Y08685:H.sapiens mRNA for serine palmitoyltransferase, su; 40605\_at Cluster Incl.  
 AA524345:ng43a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40885\_s\_at Cluster Incl.  
 N30151:yx81f01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40988\_at Cluster Incl.  
 AJ132637:Homo sapiens mRNA for ATP-dependent metalloprote; 41283\_at Cluster Incl.
- 5 AF052131:Homo sapiens clone 23930 mRNA sequence /cds=UNKN; 41547\_at Cluster Incl.  
 AF047472:Homo sapiens spleen mitotic checkpoint BUB3 (BUB; 41573\_at Cluster Incl.  
 X68560:H.sapiens SPR-2 mRNA for GT box binding protein /c; 1527\_s\_at U50527 /FEATURE=  
 /DEFINITION=HSU50527 Human BRCA2 region, mRNA sequenc; 1512\_at D86550 /FEATURE=  
 /DEFINITION=D86550 Human mRNA for serine/threonine prot; 1030\_s\_at U07806 /FEATURE=
- 10 /DEFINITION=HSU07806 Human camptothecin resistant clo; 582\_g\_at M29960  
 /FEATURE=mRNA /DEFINITION=HUMTR211 Human steroid receptor (TR2-1; 192\_at U18062  
 /FEATURE= /DEFINITION=HSU18062 Human TFIID subunit TAFII55 (TAFII5.  
**Metagene** 440; 33948\_at Cluster Incl. U34587:Human corticotropin-releasing factor receptor 2 mR;  
 35909\_at Cluster Incl. Z50194:H.sapiens mRNA for PQ-rich protein /cds=(159,1361); 41447\_at
- 15 Cluster Incl. AB023207:Homo sapiens mRNA for KIAA0990 protein, complete; 32066\_g\_at Cluster  
 Incl. S68134:CREM=cyclic AMP-responsive element modulator bet; 32067\_at Cluster Incl.  
 S68271:CREM=cyclic AMP-responsive element modulator [huma; 33305\_at Cluster Incl.  
 M93056:Human monocyte/neutrophil elastase inhibitor mRNA; 33705\_at Cluster Incl.  
 L20971:Human phosphodiesterase mRNA, complete cds /cds=(7; 33803\_at Cluster Incl.
- 20 J02973:Human thrombomodulin gene, complete cds /cds=(541; 37985\_at Cluster Incl.  
 L37747:Homo sapiens lamin B1 gene /cds=(340,2100) /gb=L37; 38326\_at Cluster Incl.  
 M69199:Human G0S2 protein gene, complete cds /cds=(160,47; 40790\_at Cluster Incl.  
 AB004066:Homo sapiens mRNA for DEC1, complete cds /cds=(1; 32186\_at Cluster Incl.  
 M80244:Human E16 mRNA, complete cds /cds=(310,1035) /gb=M; 33428\_s\_at Cluster Incl.
- 25 AF034957:Homo sapiens secreted T cell activation protei; 33849\_at Cluster Incl. U02020:Human  
 pre-B cell enhancing factor (PBEF) mRNA, com; 34375\_at Cluster Incl. M28225:Human JE gene  
 encoding a monocyte secretory protei; 34777\_at Cluster Incl. D14874:Homo sapiens mRNA for  
 adrenomedullin precursor, co; 36100\_at Cluster Incl. AF022375:Homo sapiens vascular endothelial  
 growth factor ; 38740\_at Cluster Incl. X79067:H.sapiens ERF-1 mRNA 3 end /cds=UNKNOWN
- 30 /gb=X7906; 40968\_at Cluster Incl. AB004904:Homo sapiens mRNA for STAT induced STAT  
 inhibito; 1953\_at AF024710 /FEATURE= /DEFINITION=AF024710 Homo sapiens vascular  
 endothelia; 1936\_s\_at Proto-Oncogene C-Myc, Alt. Splice 3, Orf 114 ; 1519\_at J04102 /FEATURE=  
 /DEFINITION=HUMETS2A Human erythroblastosis virus oncog; 1372\_at M31165  
 /FEATURE=mRNA /DEFINITION=HUMTSG6A Human tumor necrosis factor-in; 1237\_at S81914
- 35 /FEATURE= /DEFINITION=S81914 IEX-1=radiation-inducible immediate-; 1069\_at U04636  
 /FEATURE=mRNA /DEFINITION=HSU04636 Human cyclooxygenase-2 (hCox-2; 874\_at M26683  
 /FEATURE= /DEFINITION=HUMIFNIND Human interferon gamma treatment i; 875\_g\_at  
 M26683 /FEATURE= /DEFINITION=HUMIFNIND Human interferon gamma treatment; 669\_s\_at  
 L05072 /FEATURE=expanded\_cds /DEFINITION=HUMIFNRF1A Homo sapiens interfe.

- Metagene 441**; 31931\_f\_at Cluster Incl. AI632247:tt20f10.x1 Homo sapiens cDNA, 3 end /clone=IM; 32474\_at Cluster Incl. X96744:H.sapiens PAX7 gene, exon 1 (and joined CDS) /cds=; 33037\_at Cluster Incl. AL022165:dJ71L16.4 (putative Chondroitin 6-Sulfotransfera; 34901\_at Cluster Incl. AF079564:Homo sapiens ubiquitin-specific protease UBP41 (; 34903\_at Cluster Incl.
- 5 AI017382:ou92e06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40033\_at Cluster Incl. AL022328:Human DNA sequence from clone 402G11 on chromoso; 40360\_at Cluster Incl. X12458:Human P3 gene /cds=(494,1927) /gb=X12458 /gi=35187; 32101\_at Cluster Incl. AA112483:zn69a06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36522\_at Cluster Incl. AB014516:Homo sapiens mRNA for KIAA0616 protein, partial ; 38282\_at Cluster Incl.
- 10 U41767:Human metargidin precursor mRNA, complete cds /cds; 37368\_at Cluster Incl. AA292277:zt51a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33204\_at Cluster Incl. AI080288:oz51f04.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1592\_at J04088 /FEATURE= /DEFINITION=HUMTOPII Human DNA topoisomerase II (top2) ; 1263\_at M20137 /FEATURE=mRNA /DEFINITION=HUMIL3A Human interleukin 3 (IL-3) mRNA.
- 15 **Metagene 442**; 31508\_at Cluster Incl. S73591:brain-expressed HHCPA78 homolog [human, HL-60 acut; 34110\_g\_at Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial; 41638\_at Cluster Incl. D38552:Human mRNA for KIAA0073 gene, partial cds /cds=(0; 33325\_at Cluster Incl. W26667:11a1 Homo sapiens cDNA /gb=W26667 /gi=1305733 /ug=; 34695\_at Cluster Incl. AI816724:wj43c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34740\_at Cluster Incl.
- 20 AF032886:Homo sapiens forkhead protein (FKHRL1) mRNA, com; 36906\_at Cluster Incl. U73304:Human CB1 cannabinoid receptor (CNR1) gene, comple; 37909\_at Cluster Incl. L34155:Homo sapiens laminin-related protein (LamA3) mRNA,; 38653\_at Cluster Incl. D11428:Homo sapiens mRNA for PMP-22(PAS-II/SR13/Gas-3), c; 39053\_at Cluster Incl. AF016370:Homo sapiens U4/U6 small nuclear ribonucleoprote; 39725\_at Cluster Incl.
- 25 L10910:Homo sapiens splicing factor (CC1.3) mRNA, complet; 40103\_at Cluster Incl. X51521:Human mRNA for ezrin /cds=(117,1877) /gb=X51521 /g; 40841\_at Cluster Incl. AF049910:Homo sapiens TACC1 (TACC1) mRNA, complete cds /c; 32804\_at Cluster Incl. AF091263:Homo sapiens RNA binding motif protein 5 (RBM5) ; 35785\_at Cluster Incl. W28281:47e7 Homo sapiens cDNA /gb=W28281 /gi=1308436 /ug=; 36629\_at Cluster Incl.
- 30 AI635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36961\_at Cluster Incl. AL050286:Homo sapiens mRNA; cDNA DKFZp586A011 (from clone; 39533\_at Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(2; 39545\_at Cluster Incl. U22398:Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete ; 39827\_at Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40570\_at Cluster Incl.
- 35 AF032885:Homo sapiens forkhead protein (FKHR) mRNA, compl; 1629\_s\_at Tyrosine Phosphatase 1, Non-Receptor, Alt. Splice 3 .
- Metagene 443**; 38858\_at Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) m; 39078\_at Cluster Incl. U43286:Human selenophosphate synthetase 2 (SPS2) mRNA, co; 40559\_at Cluster Incl. AL096727:Homo sapiens mRNA; cDNA DKFZp434B104 (from clone.



- Metagene 444;** 35756\_at Cluster Incl. AF089816:Homo sapiens RGS-GAIP interacting protein GIPC m; 39124\_r\_at Cluster Incl. X89066:H.sapiens mRNA for TRPC1 protein /cds=(137,2416); 33207\_at Cluster Incl. AI095508:qb29a06.x1 Homo sapiens cDNA, 3 end /clone=IMAG.
- Metagene 445;** 34621\_at Cluster Incl. AF019084:Homo sapiens keratin 2e (KRT2E) gene, complete
- 5 c; 36411\_s\_at Cluster Incl. U29943:Human ELAV-like neuronal protein-2 Hel-N2 mRNA, ; 32971\_at Cluster Incl. L27479:Human X123 mRNA, 3 end /cds=(2,739) /gb=L27479 /g; 33516\_at Cluster Incl. V00505:Human gene for delta-globin /cds=(50,493) /gb=V005; 37140\_s\_at Cluster Incl. AF061193:Homo sapiens ectodysplasin-A isoform EDA-E (ED; 39245\_at Cluster Incl. U72507:Human 40871 mRNA partial sequence /cds=UNKNOWN /gb; 35999\_r\_at Cluster Incl.
- 10 AB018324:Homo sapiens mRNA for KIAA0781 protein, partia; 37593\_at Cluster Incl. X14608:Human mRNA for propionyl-CoA carboxylase alpha-cha; 33142\_at Cluster Incl. AF034633:Homo sapiens orphan G protein-coupled receptor (; 1683\_at X69950 /FEATURE=exon#2 /DEFINITION=HSWT1WIT H.sapiens DNA sequence for W; 1289\_at L02321 /FEATURE= /DEFINITION=HUMGSTM5 Human glutathione S-transferase (G.
- 15 **Metagene 446;** 39808\_at Cluster Incl. Y12692:Homo sapiens mRNA for WNT11 gene /cds=(123,1187) /; 40532\_at Cluster Incl. U75285:Homo sapiens apoptosis inhibitor survivin gene, co; 33109\_f\_at Cluster Incl. L07335:Homo sapiens (clone 6AR33) HMG box mRNA, 3 end ; 33120\_at Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10; 2082\_s\_at L08599 /FEATURE= /DEFINITION=HUMUVOECAD Human uvomorulin (E-cadherin) ; 907\_at
- 20 M13792 /FEATURE=cds /DEFINITION=HUMADAG Human adenosine deaminase (ADA) g; 405\_at X52773 /FEATURE=cds /DEFINITION=HSRARLP Human mRNA for retinoic acid rece.
- Metagene 447;** 35521\_at Cluster Incl. AJ130941:Homo sapiens claudin-9 (CLDN9) gene /cds=(0,653); 36406\_at Cluster Incl. AA401397:zu68b01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33558\_at Cluster Incl. Y09445:H.sapiens mRNA for transcription factor TBX5 /cds=;
- 25 35375\_at Cluster Incl. AJ011311:Homo sapiens mRNA for AP endonuclease XTH2, puta; 36742\_at Cluster Incl. U34249:Human putative zinc finger protein (ZNFB7) mRNA, c; 41078\_at Cluster Incl. D63484:Human mRNA for KIAA0150 gene, partial cds /cds=(0,; 40494\_at Cluster Incl. AF043733:Homo sapiens death effector domain-containing te; 34858\_at Cluster Incl. D79998:Human mRNA for KIAA0176 gene, partial cds /cds=(0,; 1552\_i\_at U22028
- 30 /FEATURE=expanded\_cds /DEFINITION=HSU22028 Human cytochrome P45; 1091\_at M65066 /FEATURE= /DEFINITION=HUMRIB Human cAMP-dependent protein kinase .
- Metagene 448;** 34647\_at Cluster Incl. X52104:Human mRNA for p68 protein /cds=(175,2019) /gb=X52; 33570\_at Cluster Incl. U34962:Human transcription factor HCSX (hCsx) mRNA, compl; 34008\_at Cluster Incl. AF084465:Homo sapiens Ras-like GTP-binding protein REM mR; 41462\_at
- 35 Cluster Incl. AF065482:Homo sapiens sorting nexin 2 (SNX2) mRNA, comple; 32639\_at Cluster Incl. U97198:Homo sapiens CG1 mRNA, complete cds /cds=(219,1490; 36565\_at Cluster Incl. X98253:H.sapiens ZNF183 gene /cds=(210,1241) /gb=X98253 /; 39403\_at Cluster Incl. AB014578:Homo sapiens mRNA for KIAA0678 protein, partial ; 32589\_at Cluster Incl. U20979:Human chromatin assembly factor-I p150 subunit mRN; 33149\_at Cluster Incl.

- U73524:Human putative ATP/GTP-binding protein (HEAB) mRNA.
- Metagene 449;** 36334\_at Cluster Incl. L42621:Homo sapiens Ly-9 mRNA, complete cds /cds=(0,1832); 33506\_at Cluster Incl. U96919:Homo sapiens inositol polyphosphate 4-phosphatase ; 33971\_f\_at Cluster Incl. U66078:Human DAZLA mRNA, complete cds /cds=(226,1113) /; 34493\_at
- 5 Cluster Incl. AF014794:Homo sapiens TNF related TRAIL receptor (TRAIL-R; 36754\_at Cluster Incl. X60435:H.sapiens gene PACAP for pituitary adenylate cyclase; 37831\_at Cluster Incl. AB011117:Homo sapiens mRNA for KIAA0545 protein, partial ; 38521\_at Cluster Incl. X59350:H.sapiens mRNA for B cell membrane protein CD22 /c; 36874\_at Cluster Incl. M26004:Human CR2/CD21/C3d/Epstein-Barr virus receptor mRN; 1201\_at D14889 /FEATURE=
- 10 /DEFINITION=HUMSGBP Human mRNA for small GTP-binding pr.
- Metagene 450;** 41429\_at Cluster Incl. M65254:Protein phosphatase 2A 65 kDa regulatory subunit-b; 36848\_r\_at Cluster Incl. AC005258:Homo sapiens chromosome 19, cosmid R30783 /cds; 37205\_at Cluster Incl. AB020647:Homo sapiens mRNA for KIAA0840 protein, partial ; 37890\_at Cluster Incl. X69398:H.sapiens mRNA for OA3 antigenic surface determina; 39375\_g\_at Cluster Incl.
- 15 AL022325:Homo sapiens DNA sequence from Fosmid 27C3 on ; 37664\_at Cluster Incl. X80754:Homo sapiens mRNA for GTP-binding protein /cds=(47; 37764\_at Cluster Incl. D87328:Homo sapiens mRNA for HCS, complete cds /cds=(1231; 41545\_at Cluster Incl. X66365:H.sapiens mRNA PLSTIRE for serine/threonine protei; 1191\_s\_at AB003102 /FEATURE=
- /DEFINITION=AB003102 Homo sapiens mRNA for 26S prot.
- 20 **Metagene 451;** 34117\_at Cluster Incl. AL080232:Homo sapiens mRNA; cDNA DKFZp586A061 (from clone; 35041\_at Cluster Incl. X53655:H.sapiens mRNA for NGF-2 /cds=(43,816) /gb=X53655 ; 41690\_at Cluster Incl. AL049471:Homo sapiens mRNA; cDNA DKFZp586N012 (from clone; 32102\_at Cluster Incl. AB018273:Homo sapiens mRNA for KIAA0730 protein, partial ; 35186\_at Cluster Incl. AJ009770:Homo sapiens mRNA for putative transcription fac; 37218\_at Cluster Incl.
- 25 D64110:Homo sapiens mRNA for ANA, complete cds /cds=(94,8; 37574\_at Cluster Incl. L43821:Homo sapiens enhancer of filamentation (HEF1) mRNA; 37934\_at Cluster Incl. AL080078:Homo sapiens mRNA; cDNA DKFZp564D1462 (from clon; 38632\_at Cluster Incl. AF088982:Homo sapiens heat shock protein hsp40-3 mRNA, co; 40079\_at Cluster Incl. AA156240:zl50c12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40099\_at Cluster Incl.
- 30 AB014551:Homo sapiens mRNA for KIAA0651 protein, complete; 33924\_at Cluster Incl. AB029014:Homo sapiens mRNA for KIAA1091 protein, partial ; 34822\_at Cluster Incl. U58334:Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53B; 35291\_at Cluster Incl. AL050287:Homo sapiens mRNA; cDNA DKFZp586C021 (from clone; 35335\_at Cluster Incl. AB014519:Homo sapiens mRNA for KIAA0619 protein, complete; 37026\_at Cluster Incl.
- 35 AF001461:Homo sapiens Kruppel-like zinc finger protein Zf; 37678\_at Cluster Incl. U23070:Human putative transmembrane protein (nma) mRNA, c; 41346\_at Cluster Incl. AJ007583:Homo sapiens mRNA for acetylglucosaminyltransfer; 1895\_at J04111 /FEATURE=exon#1
- /DEFINITION=HUMJUNA Human c-jun proto oncogene (J; 1860\_at U58334 /FEATURE=
- /DEFINITION=HSU58334 Human Bcl2, p53 binding protein Bb; 1801\_at U76638 /FEATURE=

- /DEFINITION=HSU76638 Human BRCA1-associated RING domain; 1562\_g\_at U27193  
 /FEATURE= /DEFINITION=HSU27193 Human protein-tyrosine phosphata.
- Metagene** 452; 32983\_at Cluster Incl. U03865:Human adrenergic alpha-1b receptor protein mRNA,  
 c; 33629\_at Cluster Incl. AJ001982:Homo sapiens WWp2-like mRNA complete cds/cds=UN;  
 5 32312\_at Cluster Incl. X06825:Human mRNA for skeletal beta-tropomyosin /cds=(106; 32932\_at  
 Cluster Incl. AL050040:Homo sapiens mRNA; cDNA DKFZp566K0524 (from clon; 34016\_s\_at  
 Cluster Incl. X78338:Synthetic adenovirus transformed human retina ce; 34904\_at Cluster Incl.  
 S40369:glutamate receptor subunit=kainate receptor subuni; 36248\_at Cluster Incl. AF070572:Homo  
 sapiens clone 24778 unknown mRNA /cds=(0,17; 37133\_at Cluster Incl. AF027406:Homo sapiens  
 10 muscle-specific serine kinase 1 (MS; 38954\_at Cluster Incl. Y18423:Homo sapiens VIP2R gene,  
 exons 1-2 (and joined CDS; 32105\_f\_at Cluster Incl. U66063:Homo sapiens calcium/calmodulin-  
 dependent protei; 37250\_at Cluster Incl. AB007191:Homo sapiens mRNA for AMY-1, complete cds  
 /cds=(; 37996\_s\_at Cluster Incl. L08835:Homo sapiens DMR-N9, partial cds; and myotonic d;  
 39018\_at Cluster Incl. AF026977:Homo sapiens microsomal glutathione S-transferas; 39030\_at  
 15 Cluster Incl. AJ133534:Homo sapiens mRNA for prenylated Rab acceptor 1 ; 41139\_at Cluster Incl.  
 W26633:34b1 Homo sapiens cDNA /gb=W26633 /gi=1307476 /ug=; 41760\_at Cluster Incl.  
 AA978033:0q55e04.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 33412\_at Cluster Incl.  
 AI535946:vicpro2.D07.r Homo sapiens cDNA, 5 end /clone\_e; 34413\_at Cluster Incl.  
 AF038203:Homo sapiens clone 23596 mRNA sequence /cds=UNKN; 35361\_at Cluster Incl.  
 20 W28299:44h4 Homo sapiens cDNA /gb=W28299 /gi=1308247 /ug=; 37309\_at Cluster Incl.  
 L09159:Homo sapiens RHOA proto-oncogene multi-drug-resist; 38810\_at Cluster Incl.  
 AF039241:AF039241 Homo sapiens cDNA /clone=11-67js /gb=AF; 41534\_at Cluster Incl.  
 AB006755:Homo sapiens mRNA for PCDH7 (BH-Pcdh)a, complete; 41807\_at Cluster Incl.  
 AL040137:DKFZp434D1813\_s1 Homo sapiens cDNA, 3 end /clon; 835\_at U41745 /FEATURE=  
 25 /DEFINITION=HSU41745 Human PDGF associated protein mRNA,; 650\_s\_at L07044  
 /FEATURE= /DEFINITION=HUMCCDPKB Homo sapiens calcium/calmodulin-; 616\_s\_at M24748  
 /FEATURE=cds#2 /DEFINITION=HUMTHRA1A Human thyroid hormone recep.
- Metagene** 453; 36390\_at Cluster Incl. U79526:Human orphan G-protein coupled receptor Dez  
 isofor; 33535\_at Cluster Incl. U45448:Human P2x1 receptor mRNA, complete cds /cds=(196,1;  
 30 37788\_at Cluster Incl. AF052115:Homo sapiens clone 23688 mRNA sequence /cds=UNKN;  
 37855\_at Cluster Incl. M95767:Homo sapiens di-N-acetylchitobiase mRNA, complete ; 35692\_at  
 Cluster Incl. AL080235:Homo sapiens mRNA; cDNA DKFZp586E1621 (from clon; 37562\_at  
 Cluster Incl. L11370:Human protocadherin 42 mRNA, complete cds for abbr; 37959\_at Cluster Incl.  
 D63876:Human mRNA for KIAA0154 gene, partial cds /cds=(0,; 33366\_at Cluster Incl.  
 35 AL022238:dJ1042K10.2.1 (novel protein with probable rabGA; 34379\_at Cluster Incl.  
 AF082657:Homo sapiens Era GTPase A protein (HERA-A) mRNA,; 41789\_r\_at Cluster Incl.  
 AB014569:Homo sapiens mRNA for KIAA0669 protein, comple; 1852\_at X02910  
 /FEATURE=expanded\_cds /DEFINITION=HSTNFA Human gene for tumor nec.  
**Metagene** 454; 32988\_at Cluster Incl. Z30643:H.sapiens mRNA for chloride channel (putative) 213;

- 32877\_i\_at Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-9542;  
 38498\_at Cluster Incl. Z99916:Human DNA sequence from clone 221G9 on chromosome ; 38661\_at  
 Cluster Incl. X75315:H.sapiens seb4B mRNA /cds=(0,693) /gb=X75315 /gi=4; 38089\_at Cluster  
 Incl. D63478:Human mRNA for KIAA0144 gene, complete cds /cds=(1.
- 5 **Metagene** 455; 39672\_at Cluster Incl. M64322:Human protein tyrosine phosphatase (LTPase)  
 mRNA.; 34290\_f\_at Cluster Incl. W29091:56c5 Homo sapiens cDNA /gb=W29091 /gi=1309057 /u.  
**Metagene** 456; 33010\_at Cluster Incl. AL008723:dJ90G24.4 (SAAT1 (low affinity sodium glucose  
 co; 34912\_at Cluster Incl. AF052941:Homo sapiens DAP-kinase related protein 1 mRNA, ;  
 32092\_at Cluster Incl. AB007937:Homo sapiens mRNA for KIAA0468 protein, complete; 34250\_at
- 10 Cluster Incl. AB029033:Homo sapiens mRNA for KIAA1110 protein, partial ; 37556\_at Cluster Incl.  
 M81637:Human grancalcin mRNA, complete cds /cds=(119,772); 37563\_at Cluster Incl.  
 AB007871:Homo sapiens KIAA0411 mRNA, complete cds /cds=(0; 34810\_at Cluster Incl.  
 AC004382:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-.
- Metagene** 457; 31317\_r\_at Cluster Incl. M21388:Human unproductively rearranged Ig mu-chain  
 mRNA; 31391\_at Cluster Incl. AF040723:Homo sapiens neuroan1 mRNA, complete cds /cds=(1;  
 31393\_r\_at Cluster Incl. AB011076:Homo sapiens mRNA for UTF1, complete cds /cds=;  
 31419\_r\_at Cluster Incl. AF023203:Homo sapiens homeobox protein Ogl2 (OGL12) mRN;  
 31426\_at Cluster Incl. U34806:Human G protein-coupled receptor (GPR15) gene, com; 31559\_at  
 Cluster Incl. U26209:Human renal sodium/dicarboxylate cotransporter (NA; 34166\_at Cluster Incl.
- 20 S80071:hPROT=brain-specific L-proline transporter [human; 36352\_at Cluster Incl.  
 AI275093:ql65c10.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 36359\_at Cluster Incl.  
 M34182:Human testis-specific protein kinase gamma-subunit; 32897\_at Cluster Incl.  
 AJ237672:Homo sapiens mRNA for methylenetetrahydrofolate ; 33470\_at Cluster Incl.  
 AF052177:Homo sapiens clone 24510 mRNA sequence /cds=UNKN; 33510\_s\_at Cluster Incl.
- 25 U31216:Human metabotropic glutamate receptor 1 beta (mG; 34970\_r\_at Cluster Incl.  
 AI655458:tt13a03.x1 Homo sapiens cDNA, 3 end /clone=IM; 35853\_at Cluster Incl.  
 AL049654:Novel human mRNA similar to mouse gene PICK1 (TR; 36765\_at Cluster Incl.  
 AL080154:Homo sapiens mRNA; cDNA DKFZp434I114 (from clone; 36784\_at Cluster Incl.  
 J03071:Human growth hormone (GH-1 and GH-2) and chorionic; 37153\_at Cluster Incl.
- 30 AB014573:Homo sapiens mRNA for KIAA0673 protein, partial ; 38897\_at Cluster Incl.  
 AJ000730:Homo sapiens mRNA for cationic amino acid transp; 39274\_at Cluster Incl.  
 X58521:Human mRNA for p62 nucleoporin /cds=(151,1719) /gb; 39667\_at Cluster Incl.  
 AF083898:Homo sapiens RNA-binding protein Nova-2 mRNA, co; 40295\_at Cluster Incl.  
 AB009288:Homo sapiens mRNA for N-copine, complete cds /cd; 41705\_at Cluster Incl.
- 35 U69198:U69198 Homo sapiens cDNA /clone=c-32h10 /gb=U69198; 34206\_at Cluster Incl.  
 AB018325:Homo sapiens mRNA for KIAA0782 protein, partial ; 37238\_s\_at Cluster Incl.  
 AF014118:Homo sapiens membrane-associated kinase (Myt1); 37968\_at Cluster Incl.  
 AF031137:Homo sapiens 1C7 precursor, mRNA, alternatively ; 38644\_at Cluster Incl.  
 U14588:Human paxillin mRNA, complete cds /cds=(74,1747) /; 41181\_r\_at Cluster Incl.

- U49785:Human D-dopachrome tautomerase mRNA, complete cd; 41324\_g\_at Cluster Incl.  
 U90917:Human clone 23641 mRNA sequence /cds=UNKNOWN /gb; 41553\_at Cluster Incl.  
 AI738702:wi22b11.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41566\_at Cluster Incl.  
 AI218364:qh21h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 2078\_s\_at M13228
- 5 /FEATURE=cds /DEFINITION=HUMNMCY1A Human N-myc oncogene protein; 2032\_s\_at  
 U07375 /FEATURE=cds /DEFINITION=HSU07375 Human integrin alpha v gene, ; 1944\_f\_at  
 AF001359 /FEATURE= /DEFINITION=AF001359 Homo sapiens DNA mismatch repa; 1442\_at  
 X99101 /FEATURE=cds /DEFINITION=HSRNAERB H.sapiens mRNA for estrogen rec; 1134\_at  
 L13738 /FEATURE=mRNA /DEFINITION=HUMNRTYKIN Human activated p21cdc42Hs k;
- 10 939\_at P97 Antigen, Melanoma-Specific ; 888\_s\_at M62302 /FEATURE=cds#1  
 /DEFINITION=HUMGDF1 Human growth/differentiation ; 715\_s\_at D87002 /FEATURE=cds#4  
 /DEFINITION=D87002 Homo sapiens immunoglobulin la; 632\_at L40027 /FEATURE=mRNA  
 /DEFINITION=HUMGLYSYN Homo sapiens glycogen synthase; 344\_s\_at D13146  
 /FEATURE=mRNA#1 /DEFINITION=HUM3CNP3 Homo sapiens gene for 2,3 ; 188\_at U09303
- 15 /FEATURE= /DEFINITION=HSU09303 Human T cell leukemia LERK-2 (EPLG2.  
**Metagene** 458; 34637\_f\_at Cluster Incl. M12963:Human class I alcohol dehydrogenase (ADH1)  
 alpha; 36247\_f\_at Cluster Incl. M12272:Homo sapiens alcohol dehydrogenase class I gamma;  
 36533\_at Cluster Incl. D83402:Homo sapiens gene for prostacyclin synthase /cds=(; 38342\_at  
 Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0; 32545\_r\_at Cluster  
 20 Incl. L12535:Human RSU-1/RSP-1 mRNA, complete cds /cds=(827,1; 32551\_at Cluster Incl.  
 U03877:Human extracellular protein (S1-5) mRNA, complete ; 32600\_at Cluster Incl.  
 AC004382:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-.
- Metagene** 459; 34151\_at Cluster Incl. AL050284:Homo sapiens mRNA; cDNA DKFZp586M1019  
 (from clon; 32317\_s\_at Cluster Incl. U34804:Human thermostable phenol sulfotransferase (STP2;  
 25 35388\_at Cluster Incl. U14755:Human LIM domain transcription factor LIM-1 (hLIM-; 41709\_at  
 Cluster Incl. AF034803:Homo sapiens liprin-beta2 mRNA, partial cds /cds; 32138\_at Cluster Incl.  
 L07807:Human dynamin mRNA, alternative exons and complete; 37539\_at Cluster Incl.  
 AB023176:Homo sapiens mRNA for KIAA0959 protein, partial ; 40071\_at Cluster Incl.  
 U03688:Human dioxin-inducible cytochrome P450 (CYP1B1) mR; 40436\_g\_at Cluster Incl.
- 30 J03592:Human ADP/ATP translocase mRNA, 3 end, clone pH; 32754\_at Cluster Incl.  
 X04201:Human skeletal muscle 1.3 kb mRNA for tropomyosin ; 34851\_at Cluster Incl.  
 AF011468:Homo sapiens serine/threonine kinase (BTAK) mRNA; 38738\_at Cluster Incl.  
 X99584:H.sapiens mRNA for SMT3A protein /cds=(94,405) /gb; 40527\_at Cluster Incl.  
 AF000571:Homo sapiens kidney and cardiac voltage dependen; 40923\_at Cluster Incl.
- 35 AA290994:zs45d07.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 41798\_at Cluster Incl.  
 AJ222801:Homo sapiens mRNA for neutral sphingomyelinase /.  
**Metagene** 460; 32139\_at Cluster Incl. Y09538:H.sapiens mRNA for ZNF185 gene /cds=(40,1398)  
 /gb=; 33247\_at Cluster Incl. U86782:Human 26S proteasome-associated pad1 homolog (POH1;  
 36561\_at Cluster Incl. X73424:Homo sapiens gene for propionyl-CoA carboxylase a ; 38713\_at

- Cluster Incl. Z99716:bK250D10.1 (sterol regulatory element binding tran; 40784\_at Cluster Incl.  
Z69030:H.sapiens mRNA for gamma 1 isoform of 61kDa regula; 41757\_at Cluster Incl.  
W25933:15b2 Homo sapiens cDNA /gb=W25933 /gi=1306056 /ug=; 32770\_at Cluster Incl.  
AB018298:Homo sapiens mRNA for KIAA0755 protein, complete; 32829\_at Cluster Incl.
- 5 X97544:H.sapiens mRNA for TIM17 preprotein translocase /c; 36199\_at Cluster Incl.  
X76105:H.sapiens DAP-1 mRNA /cds=(159,467) /gb=X76105 /gi; 40567\_at Cluster Incl.  
X01703:Human gene for alpha-tubulin (b alpha 1) /cds=(213; 41516\_at Cluster Incl. U95735:Human  
SNARE protein Ykt6 (YKT6) mRNA, complete cds; 41517\_g\_at Cluster Incl. U95735:Human  
SNARE protein Ykt6 (YKT6) mRNA, complete c; 1449\_at D00763 /FEATURE=
- 10 /DEFINITION=HUMPSC9 Human mRNA for proteasome subunit H.  
**Metagene 461**; 31849\_at Cluster Incl. AB011136:Homo sapiens mRNA for KIAA0564 protein,  
partial ; 32058\_at Cluster Incl. AF070594:Homo sapiens clone 24570 HNK-1 sulfotransferase ;  
38771\_at Cluster Incl. D50405:Human mRNA for RPD3 protein, complete cds /cds=(63; 2065\_s\_at  
L22473 /FEATURE= /DEFINITION=HUMBAXA Human Bax alpha mRNA, complete cd; 131\_at
- 15 X83928 /FEATURE=cds /DEFINITION=HISTAFII28 H.sapiens mRNA for transcriptio.  
**Metagene 462**; 40325\_at Cluster Incl. AB014460:Homo sapiens TSC2, NTHL1/NTH1 and  
SLC9A3R2/E3KAR; 33232\_at Cluster Incl. AI017574:ou23f10.x1 Homo sapiens cDNA, 3 end  
/clone=IMAG; 33788\_at Cluster Incl. AB002390:Human mRNA for KIAA0392 gene, partial cds  
/cds=(; 36843\_at Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein;;
- 20 37543\_at Cluster Incl. D25304:Human mRNA for KIAA0006 gene, partial cds /cds=(0; 37943\_at  
Cluster Incl. AB002319:Human mRNA for KIAA0321 gene, partial cds /cds=(; 38259\_at Cluster  
Incl. AB002559:Homo sapiens mRNA for hunc18b2, complete cds /cd; 38635\_at Cluster Incl.  
Z69043:H.sapiens mRNA translocon-associated protein delta; 32195\_at Cluster Incl.  
AL049450:Homo sapiens mRNA; cDNA DKFZp586B1922 (from clon; 32806\_at Cluster Incl.
- 25 M36035:Human peripheral benzodiazepine receptor (hpbs) mR; 35282\_r\_at Cluster Incl.  
M33680:Human 26-kDa cell surface protein TAPA-1 mRNA, c; 36131\_at Cluster Incl.  
AJ012008:Homo sapiens genes encoding RNCC protein, DDAH p; 36666\_at Cluster Incl.  
M22806:Human prolyl 4-hydroxylase beta-subunit and disulf; 38066\_at Cluster Incl.  
M81600:Human NAD(P)H-quinone oxidoreductase gene /cds=(111; 38418\_at Cluster Incl.
- 30 X59798:Human PRAD1 mRNA for cyclin /cds=(147,1034) /gb=X5; 38477\_at Cluster Incl.  
S81752:DPH2L=candidate tumor suppressor gene {ovarian can; 1797\_at U40343 /FEATURE=  
/DEFINITION=HSU40343 Human CDK inhibitor p19INK4d mRNA.; 149\_at U90426 /FEATURE=  
/DEFINITION=HSU90426 Human nuclear RNA helicase, complet.
- Metagene 463**; 36751\_at Cluster Incl. AF035154:Homo sapiens regulator of G-protein signalling 1;  
35 38157\_at Cluster Incl. AF059252:Homo sapiens clone 1 HLA class III protein Dom3z; 31823\_at  
Cluster Incl. M74099:Human displacement protein (CCAAT) mRNA /cds=UNKNO; 34700\_at  
Cluster Incl. AF045239:Homo sapiens brain expressed ring finger protein; 34713\_at Cluster Incl.  
AB002357:Human mRNA for KIAA0359 gene, complete cds /cds=; 35644\_at Cluster Incl.  
AB014598:Homo sapiens mRNA for KIAA0698 protein, complete; 38334\_g\_at Cluster Incl.

- Y11731:H.sapiens mRNA for DNA glycosylase /cds=(338,137; 39068\_at Cluster Incl.  
 L76702:Homo sapiens protein phosphatase 2A B56-delta (PP2; 34869\_at Cluster Incl.  
 AJ133766:Homo sapiens mRNA for ZASP protein, partial /cds; 36118\_at Cluster Incl.  
 AJ000882:Homo sapiens mRNA for steroid receptor coactivat; 36598\_s\_at Cluster Incl.
- 5 L36818:Human (clone 51C-3) 51C protein mRNA, complete c; 1113\_at M22489 /FEATURE=  
 /DEFINITION=HUMBMP2A Human bone morphogenetic protein 2; 840\_at U47742 /FEATURE=  
 /DEFINITION=HSU47742 Human monocytic leukaemia zinc fing; 278\_at L13436  
 /FEATURE=mRNA /DEFINITION=HUMGUANCYC Homo sapiens guanylate cyclas.  
**Metagene 464;** 32410\_at Cluster Incl. X17651:Human Myf-4 mRNA for myogenic determination
- 10 factor; 32898\_at Cluster Incl. U20582:Human actin-like peptide mRNA, partial cds /cds=(2;  
 33568\_at Cluster Incl. U48861:Human beta 4 nicotinic acetylcholine receptor subu; 35412\_at Cluster  
 Incl. D13705:Human mRNA for fatty acids omega-hydroxylase (cyto; 36298\_at Cluster Incl.  
 L14565:Human peripherin (PRPH) gene exons 1-9, complete c; 38221\_at Cluster Incl.  
 AF100153:Homo sapiens connector enhancer of KSR-like prot; 40317\_at Cluster Incl.
- 15 U57352:Human sodium channel 1 (hBNaC1) mRNA, complete cds; 41002\_at Cluster Incl.  
 U59299:Homo sapiens putative monocarboxylate transporter ; 33699\_at Cluster Incl.  
 M18667:Human pepsinogen C gene /cds=(73,1230) /gb=M18667 ; 35997\_g\_at Cluster Incl.  
 X98261:H.sapiens mRNA for M-phase phosphoprotein, mpp5 ; 38309\_r\_at Cluster Incl.  
 AA805659:nz41b04.s1 Homo sapiens cDNA /clone=IMAGE-1290; 39016\_r\_at Cluster Incl.
- 20 L42611:Homo sapiens keratin 6 isoform K6e (KRT6E) mRNA,; 39720\_g\_at Cluster Incl.  
 X56777:H.sapiens mRNA for ZP3 gene /cds=(30,1148) /gb=X; 34301\_r\_at Cluster Incl.  
 Z19574:H.sapiens gene for cytokeratin 17 /cds=(64,1362); 40266\_at Cluster Incl. AB028959:Homo  
 sapiens mRNA for KIAA1036 protein, complete; 40270\_at Cluster Incl. AA969267:on57d12.s1  
 Homo sapiens cDNA, 3 end /clone=IMAG.
- 25 **Metagene 465;** 40379\_at Cluster Incl. J02625:Human cytochrome P-450j mRNA, complete cds  
 /cds=(1; 37240\_at Cluster Incl. U18937:Human histidyl-tRNA synthetase homolog (HO3) mRNA,;  
 36109\_at Cluster Incl. J04605:Human prolidase (imidodipeptidase) mRNA, complete .  
**Metagene 466;** 31342\_at Cluster Incl. X85019:H.sapiens mRNA for UDP-GalNAc-polypeptide N-  
 acetyl; 31699\_at Cluster Incl. S67334:phosphatidylinositol 3-kinase p110 beta isoform=11; 33581\_at
- 30 Cluster Incl. AF023259:Homo sapiens RNA-binding protein (RBMS3) mRNA, c; 37450\_r\_at  
 Cluster Incl. X04409:Human mRNA for coupling protein G(s) alpha-subun; 37814\_g\_at Cluster Incl.  
 AL079273:Homo sapiens mRNA full length insert cDNA clon; 33718\_at Cluster Incl.  
 AC006128:Homo sapiens chromosome 19, cosmid F20900 /cds=(; 34694\_at Cluster Incl.  
 U66618:Human SWI/SNF complex 60 KDa subunit (BAF60b) mRNA; 34742\_at Cluster Incl.
- 35 Z23115:H.sapiens bcl-xL mRNA /cds=(134,835) /gb=Z23115 /g; 39011\_at Cluster Incl.  
 X99906:Homo sapiens mRNA for alpha endosulfine /cds=(125,; 39694\_at Cluster Incl.  
 W27517:31h6 Homo sapiens cDNA /gb=W27517 /gi=1307321 /ug=; 40847\_at Cluster Incl.  
 AB018293:Homo sapiens mRNA for KIAA0750 protein, complete; 33843\_g\_at Cluster Incl.  
 AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds; 35339\_at Cluster Incl.

- AI743606:wg51f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38022\_s\_at Cluster Incl.  
 Z54367:H.sapiens gene for plectin /cds=(0,14054) /gb=Z5; 39537\_at Cluster Incl. X98248:H.sapiens  
 mRNA for sortilin /cds=(21,2522) /gb=X98; 39879\_s\_at Cluster Incl. H16917:ym39e02.r1 Homo  
 sapiens cDNA, 5 end /clone=IMAG; 41291\_at Cluster Incl. AC004528:Homo sapiens chromosome  
 5 19, cosmid R32184 /cds=(; 41594\_at Cluster Incl. M64174:Human protein-tyrosine kinase (JAK1)  
 mRNA, complet; 2041\_i\_at M14752 /FEATURE= /DEFINITION=HUMABLA Human c-abl gene,  
 complete cds ; 2043\_s\_at M15025 /FEATURE=cds /DEFINITION=HUMBCRABL Human  
 BCR/ABL mRNA (product ; 1974\_s\_at X02469 /FEATURE=cds /DEFINITION=HSP53 Human  
 mRNA for p53 cellular tumo; 1906\_at Ras Inhibitor Inf ; 1917\_at X03484 /FEATURE=cds  
 10 /DEFINITION=HSRAFR Human mRNA for raf oncogene ; 1781\_at M25269 /FEATURE=  
 /DEFINITION=HUMELK1A Homo sapiens tyrosine kinase (ELK1; 1764\_s\_at D85131  
 /FEATURE= /DEFINITION=D85131 Homo sapiens mRNA for Myc-associat; 1703\_g\_at S75174  
 /FEATURE= /DEFINITION=S75174 E2F-4=transcription factor [human,; 1615\_at Z23115  
 /FEATURE=cds /DEFINITION=HSBCLXL H.sapiens bcl-xL mRNA ; 1439\_s\_at X75346  
 15 /FEATURE=cds /DEFINITION=HSMAPKAP H.sapiens mRNA for MAP kinase; 1362\_s\_at  
 M84820 /FEATURE= /DEFINITION=HUMRXRB Human retinoid X receptor beta (R; 919\_at  
 Guanine Nucleotide-Binding Protein, Alpha 12 ; 826\_at U50553 /FEATURE=  
 /DEFINITION=HSU50553 Homo sapiens helicase like protein ; 716\_at D87002 /FEATURE=cds#5  
 /DEFINITION=D87002 Homo sapiens immunoglobulin lamb; 727\_at Ornithine Aminotransferase-  
 20 Like 3 ; 463\_g\_at U70862 /FEATURE= /DEFINITION=HSU70862 Human nuclear factor I B3  
 mRNA, c; 446\_at U89896 /FEATURE= /DEFINITION=HSU89896 Homo sapiens casein kinase I  
 gamma ; 424\_s\_at X66945 /FEATURE=cds /DEFINITION=HSNSAMTK H.sapiens N-sam mRNA  
 for fibro; 368\_at Z29083 /FEATURE=cds /DEFINITION=HS5T4OA H.sapiens 5T4 gene for 5T4  
 Oncofe; 352\_at D30036 /FEATURE= /DEFINITION=HUMPITPA Human mRNA for  
 25 phosphatidylinositol; 111\_at Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens  
 mRNA for rab geranyl.
- Metagene** 467; 39309\_at Cluster Incl. M88714:Human bradykinin receptor (BK-2) mRNA, complete  
 cd; 40684\_at Cluster Incl. U78190:Human GTP cyclohydrolase I feedback regulatory pro;  
 41718\_g\_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 ;  
 30 34738\_at Cluster Incl. L11931:Human cytosolic serine hydroxymethyltransferase (S; 33931\_at  
 Cluster Incl. X71973:H.sapiens GPx-4 mRNA for phospholipid hydroperoxid; 36945\_at Cluster Incl.  
 X94910:Homo sapiens mRNA for ERp28 protein /cds=(11,796) ; 38426\_at Cluster Incl.  
 X83928:H.sapiens mRNA for transcription factor TFIID subu.
- Metagene** 468; 31633\_g\_at Cluster Incl. Z95118:Human DNA sequence from clone 354J5 on  
 35 chromosom; 33024\_at Cluster Incl. M69136:Human heart chymase mRNA, complete cds  
 /cds=(15,75; 36431\_at Cluster Incl. AL109709:Homo sapiens mRNA full length insert cDNA clone ;  
 37870\_at Cluster Incl. AF073771:Homo sapiens RNA polymerase II termination facto; 38570\_at  
 Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chai; 32061\_at Cluster  
 Incl. U96629:Human chromosome 8 BAC clone CIT987SK-2A8 complete; 32651\_at Cluster Incl.



- W28770:51d8 Homo sapiens cDNA /gb=W28770 /gi=1308718 /ug=; 35671\_at Cluster Incl.  
 U02619:Human TFIIC Box B-binding subunit mRNA, complete ; 1331\_s\_at U83598 /FEATURE=  
 /DEFINITION=HSU83598 Human death domain receptor 3 so.
- Metagene** 469; 40448\_at Cluster Incl. M92843:H.sapiens zinc finger transcriptional regulator mR;  
 5 32583\_at Cluster Incl. J04111:Human c-jun proto oncogene (JUN), complete cds, cl; 2094\_s\_at  
 K00650 /FEATURE=cds /DEFINITION=HUMFOS Human fos proto-oncogene (c-fos; 1915\_s\_at  
 V01512 /FEATURE=mRNA#1 /DEFINITION=HSCFOS Human cellular oncogene c-fo; 1916\_s\_at  
 V01512 /FEATURE=mRNA#2 /DEFINITION=HSCFOS Human cellular oncogene c-fo; 1005\_at  
 X68277 /FEATURE=cds /DEFINITION=HSCL100 H.sapiens CL 100 mRNA for protei.
- 10 **Metagene** 470; 31443\_at Cluster Incl. S76346:AML1=AML1 {alternatively spliced, exons 5 and b}  
 [; 31497\_at Cluster Incl. U19142:Human GAGE-1 protein mRNA, complete cds /cds=(48,4;  
 37077\_at Cluster Incl. D13243:Homo sapiens gene for pyruvate kinase L /cds=(39,1; 37498\_at  
 Cluster Incl. AL050404:Human DNA sequence from clone 955M13 on chromoso; 38181\_at Cluster  
 Incl. X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766 ; 35219\_at Cluster Incl.
- 15 AL050202:Homo sapiens mRNA; cDNA DKFZp586E2023 (from clon; 37270\_at Cluster Incl.  
 AF007876:Homo sapiens Na,K-ATPase beta 2 subunit gene, co; 39862\_at Cluster Incl.  
 AA528252:nh92c11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 40277\_at Cluster Incl.  
 AI799984:wc46f12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1072\_g\_at M77810 /FEATURE=  
 /DEFINITION=HUMGATA2A Human transcription factor GATA.
- 20 **Metagene** 471; 35467\_g\_at Cluster Incl. W73046:zd54h09.r1 Homo sapiens cDNA, 5 end  
 /clone=IMAG; 32808\_at Cluster Incl. X07979:Human mRNA for integrin beta 1 subunit  
 /cds=(103,2.  
**Metagene** 472; 32372\_at Cluster Incl. L22569:Homo sapiens cathepsin B mRNA, 3 UTR with a  
 stem-l; 38849\_at Cluster Incl. AF038966:Homo sapiens secretory carrier-associated membra;  
 25 32125\_at Cluster Incl. AA928996:oo27f06.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32144\_at  
 Cluster Incl. AL050135:Homo sapiens mRNA; cDNA DKFZp586K091 (from clone; 33297\_at  
 Cluster Incl. AL031778:dJ34B21.3 (PUTATIVE novel protein) /cds=(297,557; 38665\_at Cluster  
 Incl. D85939:Homo sapiens mRNA for p97 homologous protein, comp; 32777\_at Cluster Incl.  
 Y12478:H.sapiens mRNA for CHD5 protein /cds=(42,566) /gb=; 33451\_s\_at Cluster Incl.
- 30 AI526079:DU3.2-7.G09 Homo sapiens cDNA, 3 end /clone\_e; 35292\_at Cluster Incl.  
 Z37166:H.sapiens BAT1 mRNA for nuclear RNA helicase (DEAD; 36639\_at Cluster Incl.  
 AF067853:Homo sapiens adenylosuccinate lyase (ADSL) mRNA,; 37010\_at Cluster Incl.  
 AI203737:qf76b12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37672\_at Cluster Incl.  
 Z72499:H.sapiens mRNA for herpesvirus associated ubiquiti; 38097\_at Cluster Incl.
- 35 AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds; 38368\_at Cluster Incl.  
 U31930:Human deoxyuridine nucleotidohydrolase mRNA, compl; 38413\_at Cluster Incl.  
 D15057:Human mRNA for DAD-1, complete cds /cds=(66,407) /; 38455\_at Cluster Incl.  
 AL049650:dJ734P14.2.1 (snRNP (small nuclear ribonucleopro; 39131\_at Cluster Incl.  
 N36842:yy35g03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 39924\_at Cluster Incl.

- AB020660:Homo sapiens mRNA for KIAA0853 protein, partial ; 40953\_at Cluster Incl.  
 S80562:acidic calponin [human, kidney, mRNA, 1607 nt] /cd; 41308\_at Cluster Incl. U37408:Homo sapiens phosphoprotein CtBP mRNA, complete cd; 41328\_s\_at Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from cl; 32585\_at Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /c; 33117\_r\_at Cluster Incl. AA977163:oaq25a04.s1 Homo sapiens cDNA, 3 end /clone=IM; 1151\_at Epstein-Barr Virus Small Rna-Associated Protein ; 989\_at X17576 /FEATURE=cds /DEFINITION=HSNCK Human melanoma mRNA for nck protein; 735\_s\_at Protein Kinase Ht31, Camp-Dependent .
- 5 **Metagene** 473; 39230\_at Cluster Incl. AL022318:bK150C2.2 (Phorbolin 3) /cds=(29,1177) /gb=AL022; 36503\_at Cluster Incl. AB002409:Homo sapiens mRNA for SLC, complete cds /cds=(58.
- 10 **Metagene** 474; 36377\_at Cluster Incl. U43672:Human putative transmembrane receptor IL-1Rrp mRNA; 39229\_at Cluster Incl. W27883:39b10 Homo sapiens cDNA /gb=W27883 /gi=1307831 /ug; 32653\_at Cluster Incl. AW020536:df11b12.y1 Homo sapiens cDNA, 5 end /clone=IMAG; 34677\_f\_at Cluster Incl. AJ012755:Homo sapiens mRNA for TL132 /cds=(1241,2305) /; 39863\_at
- 15 Cluster Incl. AB002294:Human mRNA for KIAA0296 gene, complete cds /cds=; 1927\_s\_at U77713 /FEATURE=mRNA /DEFINITION=HSALK07 Human activin receptor like k; 1351\_at U07695 /FEATURE= /DEFINITION=HSU07695 Human tyrosine kinase (HTK) mRNA, ; 288\_s\_at L25931 /FEATURE= /DEFINITION=HUMLBK Human lamin B receptor (LBR) mRNA, .
- 20 **Metagene** 475; 35384\_at Cluster Incl. Z34897:H.sapiens mRNA for H1 histamine receptor /cds=(0,1; 35230\_at Cluster Incl. AF070530:Homo sapiens clone 24751 unknown mRNA /cds=(0,12; 39353\_at Cluster Incl. AI912041:wd84b06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 40788\_at Cluster Incl. U84371:Human adenylate kinase 2A (AK2A) mRNA, complete cd; 35759\_at Cluster Incl. AF026166:Homo sapiens chaperonin-containing TCP-1 beta su;
- 25 36941\_at Cluster Incl. U16954:Human (AF1q) mRNA, complete cds /cds=(355,627) /gb; 38421\_at Cluster Incl. AF070546:Homo sapiens clone 24607 mRNA sequence /cds=UNKN; 39199\_at Cluster Incl. W28661:49h1 Homo sapiens cDNA /gb=W28661 /gi=1308609 /ug=; 40979\_at Cluster Incl. AJ243310:Homo sapiens mRNA for C14orf3 protein /cds=(131,; 32529\_at Cluster Incl. X69910:H.sapiens p63 mRNA for transmembrane protein /cds=; 1636\_g\_at U07563
- 30 /FEATURE=Poly\_A\_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogen.
- Metagene** 476; 41658\_at Cluster Incl. AF001436:Human clone zeta unknown protein mRNA, complete ; 37194\_at Cluster Incl. M68891:Human GATA-binding protein (GATA2) mRNA, complete ; 40468\_at Cluster Incl. AB011126:Homo sapiens mRNA for KIAA0554 protein, partial ; 41493\_at Cluster Incl. AI094610:oy64f07.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41834\_g\_at
- 35 Cluster Incl. AB016492:Homo sapiens hJTB gene, complete cds /cds=(464; 431\_at X02530 /FEATURE=cds /DEFINITION=HSINFGF Human mRNA for gamma-interferon .
- Metagene** 477; 32010\_at Cluster Incl. Z82180:Human DNA sequence from clone E81G9 on chromosome ; 32423\_at Cluster Incl. U48408:Human kidney water channel (hKID) mRNA, complete c; 33096\_r\_at Cluster Incl. U48224:Human beaded filament protein CP49 (LIFL-L)

- mRNA; 33950\_g\_at Cluster Incl. AF011406:Homo sapiens corticotropin releasing hormone r;  
34047\_at Cluster Incl. AF016045:Homo sapiens OVO-like 1 binding protein (OVOL1) ; 35445\_at  
Cluster Incl. AC002398:Human DNA from chromosome 19-specific cosmid F25; 33712\_at Cluster  
Incl. N63574:yy63f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 35194\_at Cluster Incl.
- 5 X53463:Human mRNA for glutathione peroxidase-like protein; 36557\_at Cluster Incl.  
M92303:Human voltage-dependent calcium channel beta-1 sub; 37926\_at Cluster Incl.  
D14520:Human mRNA for GC-Box binding protein BTEB2, compl; 39915\_at Cluster Incl.  
AB001535:Homo sapiens mRNA, complete cds /cds=(445,4956) ; 1223\_at X66362 /FEATURE=cds  
/DEFINITION=HSSTHPKG H.sapiens mRNA PCTAIRE-3 for se.
- 10 **Metagene 478**; 35042\_at Cluster Incl. L12398:Homo sapiens dopamine D4 receptor (DRD4) mRNA  
(D4.; 37166\_at Cluster Incl. Z29481:H.sapiens mRNA for 3-hydroxyanthranilic acid dioxy;  
40294\_at Cluster Incl. U66676:HSU66676 Homo sapiens cDNA /gb=U66676 /gi=1906561 ;  
41079\_at Cluster Incl. AB010575:Homo sapiens mRNA for sodium channel, complete c; 36546\_r\_at  
Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, comple; 36815\_at Cluster
- 15 Incl. AF038185:Homo sapiens clone 23700 mRNA sequence /cds=UNKN; 37993\_at Cluster Incl.  
X63422:H.sapiens mRNA for delta-subunit of mitochondrial ; 40415\_at Cluster Incl.  
X14813:Human liver mRNA for 3-oxoacyl-CoA thiolase /cds=(; 32757\_at Cluster Incl.  
U84720:Homo sapiens mRNA export protein (RAE1) mRNA, comp; 32852\_at Cluster Incl.  
U78678:Human thioredoxin mRNA, nuclear gene encoding mito; 38449\_at Cluster Incl.
- 20 W28931:56f3 Homo sapiens cDNA /gb=W28931 /gi=1309086 /ug=; 33215\_g\_at Cluster Incl.  
Y11681:Homo sapiens mRNA for mitochondrial ribosomal pr; 870\_f\_at M93311 /FEATURE=cds  
/DEFINITION=HUMMETIII Human metallothionein-III gen.
- Metagene 479**; 35526\_at Cluster Incl. K02766:Human complement component C9 mRNA, complete  
cds /; 33261\_at Cluster Incl. M16941:Human MHC class II HLA-DR7-associated glycoprotein;  
25 36623\_at Cluster Incl. AB011406:Homo sapiens mRNA for alkalin phosphatase, compl; 38784\_g\_at  
Cluster Incl. J05581:Human polymorphic epithelial mucin (PEM) mRNA, c; 33197\_at Cluster Incl.  
U39226:Human myosin VIIA (USH1B) mRNA, complete cds /cds=.
- Metagene 480**; 32884\_at Cluster Incl. L09749:Homo sapiens (clone F4) transmembrane protein  
mRNA; 36491\_at Cluster Incl. D82345:Homo sapiens mRNA for NB thymosin beta, complete c;  
30 35341\_at Cluster Incl. U90547:Human Ro/SSA ribonucleoprotein homolog (RoRet) mRN; 41822\_at  
Cluster Incl. AF060503:Homo sapiens zinc finger protein (ZF5128) mRNA, ; 1924\_at U11791  
/FEATURE= /DEFINITION=HSU11791 Human cyclin H mRNA, complete cds ; 966\_at X97795  
/FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. c.
- Metagene 481**; 35038\_at Cluster Incl. Y10129:H.sapiens mybpc3 gene /cds=(33,3857) /gb=Y10129  
35 /g; 39674\_r\_at Cluster Incl. AB011792:Homo sapiens mRNA for extracellular matrix pro; 35141\_at  
Cluster Incl. Z97029:Homo sapiens mRNA for ribonuclease H I large subun; 33345\_at Cluster Incl.  
AF035621:Homo sapiens kinesin-related protein (KIF3C) mRN; 41269\_r\_at Cluster Incl.  
Y15906:Homo sapiens mRNA for XAGL protein /cds=(132,164.
- Metagene 482**; 34650\_at Cluster Incl. U36798:Homo sapiens platelet cGI-PDE mRNA, complete

- cds /; 32974\_at Cluster Incl. U07563:Human ABL gene, exon 1b and intron 1b, and putativ;  
 37818\_at Cluster Incl. Y10936:H.sapiens mRNA for hypothetical protein downstream; 35732\_at  
 Cluster Incl. AL031427:dJ167A19.4 (novel protein) /cds=(0,1286) /gb=AL0; 36031\_at Cluster Incl.  
 AB024401:Homo sapiens mRNA for p33, complete cds /cds=(45; 36460\_at Cluster Incl.
- 5 AF008442:Homo sapiens RNA polymerase I subunit hRPA39 mRN; 39773\_at Cluster Incl.  
 W28235:43h8 Homo sapiens cDNA /gb=W28235 /gi=1308183 /ug=; 40077\_at Cluster Incl.  
 Z11559:H.sapiens mRNA for iron regulatory factor /cds=(10.  
**Metagene** 483; 40333\_at Cluster Incl. U43842:Homo sapiens bone morphogenetic protein-4 (hBMP-  
 4); 836\_at U43148 /FEATURE= /DEFINITION=HSU43148 Human patched homolog (PTC)  
 mRNA, c.
- 10 **Metagene** 484; 39588\_at Cluster Incl. AF055872:Homo sapiens Apo3/DR3 ligand (APO3L) mRNA,  
 compl; 37189\_at Cluster Incl. AL023553:dJ347H13.3 (phosphomannomutase 1 (PMMH-22, yeast;  
 37596\_at Cluster Incl. U09117:Human phospholipase c delta 1 mRNA, complete cds /; 38359\_at  
 Cluster Incl. Y12336:H.sapiens mRNA for F25B3.3 kinase like protein fro; 34859\_at Cluster Incl.
- 15 Z98046:dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) /; 37016\_at Cluster Incl.  
 D13900:Homo sapiens mRNA for mitochondrial short-chain en; 38795\_s\_at Cluster Incl.  
 X56687:H.sapiens mRNA for autoantigen NOR-90 /cds=(179; 38845\_at Cluster Incl.  
 R89044:ym99b08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 1782\_s\_at M31303  
 /FEATURE=mRNA /DEFINITION=HUMOP18A Human oncoprotein 18 (Op18) .
- 20 **Metagene** 485; 31636\_s\_at Cluster Incl. U09210:Human vesicular acetylcholine transporter mRNA,  
 ; 34557\_at Cluster Incl. X67594:H.sapiens mRNA for MSH receptor /cds=(168,1121) /g; 35674\_at  
 Cluster Incl. AB023211:Homo sapiens mRNA for KIAA0994 protein, partial ; 36643\_at Cluster Incl.  
 L20817:Homo sapiens tyrosine protein kinase (CAK) gene, c; 39828\_at Cluster Incl.  
 AA477714:zu44e09.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 1681\_at X03635
- 25 /FEATURE=cds /DEFINITION=HSERR Human mRNA for oestrogen receptor ; 780\_at X90978  
 /FEATURE= /DEFINITION=HSRNAML13 H.sapiens mRNA for an acute myeloi; 164\_at U47931  
 /FEATURE=mRNA /DEFINITION=HSU47931 Human G-protein beta-3 subunit .  
**Metagene** 486; 35497\_at Cluster Incl. AI924594:wn57a11.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 36371\_at Cluster Incl. L35251:Homo sapiens extracellular matrix protein (MFAP3) ;
- 30 36442\_g\_at Cluster Incl. U02632:Human calcium-activated potassium channel mRNA, ; 38503\_at  
 Cluster Incl. M63967:Human mitochondrial aldehyde dehydrogenase x gene,; 32626\_at Cluster Incl.  
 M90516:Human glutamine-fructose-6-phosphate amidotransfer; 36467\_g\_at Cluster Incl.  
 U26742:Human dystrobrevin-delta mRNA, complete cds /cds; 40148\_at Cluster Incl.  
 U62325:Human FE65-like protein (hFE65L) mRNA, partial cds; 32229\_at Cluster Incl.
- 35 AF038957:Homo sapiens translation initiation factor 4e mR; 41499\_at Cluster Incl. X15218:Human  
 ski oncogene mRNA /cds=(72,2258) /gb=X15218 ; 1335\_at X04434 /FEATURE=cds  
 /DEFINITION=HSIGFIRR Human mRNA for insulin-like gro; 785\_at U96114 /FEATURE=  
 /DEFINITION=HSU96114 Homo sapiens Nedd-4-like ubiquitin-; 369\_s\_at Z29331 /FEATURE=cds  
 /DEFINITION=HSUCEH3 H.sapiens (23k/3) mRNA for ubiq.

- Metagene 487**; 37078\_at Cluster Incl. J04132:Human T cell receptor zeta-chain mRNA, complete cd; 37196\_at Cluster Incl. X79981:H.sapiens VE-cadherin mRNA /cds=(24,2378) /gb=X799;  
37897\_s\_at Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IM; 41577\_at Cluster Incl. AB020630:Homo sapiens mRNA for KIAA0823 protein, partial ; 32580\_at Cluster Incl.
- 5 AF035152:Homo sapiens regulator of G-protein signalling 1.  
**Metagene 488**; 32393\_s\_at Cluster Incl. W27466:31c9 Homo sapiens cDNA /gb=W27466 /gi=1307270 /u; 41417\_at Cluster Incl. AC003108:Human Chromosome 16 BAC clone CIT987SK-327024 /c; 41453\_at Cluster Incl. U49089:Human neuroendocrine-dlg (NE-dlg) mRNA, complete c; 41635\_at Cluster Incl. D14661:Human mRNA for KIAA0105 gene, complete cds /cds=(1; 41855\_at Cluster Incl.
- 10 AF030424:Homo sapiens histone acetyltransferase 1 mRNA, c; 31879\_at Cluster Incl. U69127:Human FUSE binding protein 3 (FBP3) mRNA, partial ; 32665\_at Cluster Incl. AJ005801:Homo sapiens mRNA for protein phosphatase 2C (be; 33741\_at Cluster Incl. AI741756:wg22c12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33811\_at Cluster Incl. AI761567:wg66a05.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 34192\_at Cluster Incl.
- 15 AB011104:Homo sapiens mRNA for KIAA0532 protein, partial ; 34258\_at Cluster Incl. W28205:43g5 Homo sapiens cDNA /gb=W28205 /gi=1308171 /ug=; 34274\_at Cluster Incl. AB029039:Homo sapiens mRNA for KIAA1116 protein, complete; 34723\_at Cluster Incl. U79270:Human clone 23707 mRNA, partial cds /cds=(0,460) /; 35177\_at Cluster Incl. AB018268:Homo sapiens mRNA for KIAA0725 protein, partial ; 35702\_at Cluster Incl.
- 20 M76665:Human 11-beta-hydroxysteroid dehydrogenase (HSD11); 35973\_at Cluster Incl. AB023163:Homo sapiens mRNA for KIAA0946 protein, partial ; 38353\_at Cluster Incl. AF042378:Homo sapiens spindle pole body protein spc98 hom; 39005\_s\_at Cluster Incl. AB018257:Homo sapiens mRNA for KIAA0714 protein, partial; 39794\_at Cluster Incl. D29956:Human mRNA for KIAA0055 gene, complete cds /cds=(3; 40801\_at Cluster Incl.
- 25 AA643063:nr95e11.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 41733\_at Cluster Incl. AC003007:Human Chromosome 16 BAC clone CIT987SK-A-61E3 /c; 33368\_at Cluster Incl. X76040:H.sapiens mRNA for Lon protease-like protein /cds=; 34359\_at Cluster Incl. AA524058:ng33b12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 34401\_at Cluster Incl. L32977:Homo sapiens (clone f17252) ubiquinol cytochrome c; 34813\_at Cluster Incl.
- 30 AL079283:Homo sapiens mRNA full length insert cDNA clone ; 35356\_at Cluster Incl. W21884:58c2 Homo sapiens cDNA /clone=(not-directional) /g; 35364\_at Cluster Incl. U50939:Human amyloid precursor protein-binding protein 1 ; 37352\_at Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete ; 37357\_at Cluster Incl. D00723:Homo sapiens mRNA for hydrogen carrier protein, a ; 37389\_at Cluster Incl.
- 35 AI346580:qp51f08.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 37715\_at Cluster Incl. AF045184:Homo sapiens nuclear receptor coactivator NCoA-6; 37752\_at Cluster Incl. M15353:Homo sapiens cap-binding protein mRNA, complete cd; 37755\_at Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete; 37762\_at Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein ; 40229\_at Cluster Incl.

- AJ010071:Homo sapiens for TOM1-like protein /cds=(30,1460; 40577\_at Cluster Incl.  
 AI951046:wx62g06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41557\_at Cluster Incl.  
 D29641:Human mRNA for KIAA0052 gene, partial cds /cds=(0; 32541\_at Cluster Incl.  
 S46622:calcineurin A catalytic subunit [human, testis, mR; 1891\_at D14497 /FEATURE=  
 5 /DEFINITION=HUMPOPSTK Human mRNA for proto-oncogene pro; 674\_g\_at J04031  
 /FEATURE= /DEFINITION=HUMMDMCSF Human methylenetetrahydrofolate .  
**Metagene** 489; 31554\_at Cluster Incl. X55019:H.sapiens mRNA for acetylcholine receptor delta su;  
 31930\_f\_at Cluster Incl. X63096:H.sapiens mRNA for rhesus polypeptide (RhVIII) /; 40381\_at  
 Cluster Incl. AB023189:Homo sapiens mRNA for KIAA0972 protein, complete; 31821\_at Cluster  
 10 Incl. AB011167:Homo sapiens mRNA for KIAA0595 protein, partial ; 38724\_at Cluster Incl.  
 AB011087:Homo sapiens mRNA for KIAA0515 protein, partial ; 39735\_at Cluster Incl.  
 AF069987:Homo sapiens nitrilase 1 (NIT1) mRNA, complete c; 33934\_at Cluster Incl.  
 AB018340:Homo sapiens mRNA for KIAA0797 protein, partial ; 37734\_at Cluster Incl.  
 D80006:Human mRNA for KIAA0184 gene, partial cds /cds=(0; 40538\_at Cluster Incl.  
 15 AL050358:Homo sapiens mRNA; cDNA DKFZp564M1916 (from clon; 1071\_at M77810  
 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor GATA-2; 948\_s\_at  
 D63861 /FEATURE=expanded\_cds /DEFINITION=D63861 Homo sapiens DNA for cy.  
**Metagene** 490; 32004\_s\_at Cluster Incl. W32483:zc67e07.r1 Homo sapiens cDNA, 5 end  
 /clone=IMAG; 33679\_f\_at Cluster Incl. X02344:Homo sapiens beta 2 gene /cds=(0,1337)  
 20 /gb=X0234; 41717\_at Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8  
 (B; 33781\_s\_at Cluster Incl. AF075599:Homo sapiens ubiquitin conjugating enzyme 12 (; 34669\_at  
 Cluster Incl. X96717:H.sapiens mRNA for transcription factor TFE3 /cds=; 39685\_at Cluster Incl.  
 AL050282:Homo sapiens mRNA; cDNA DKFZp586H2219 (from clon; 40845\_at Cluster Incl.  
 U10324:Human nuclear factor NF90 mRNA, complete cds /cds=; 33414\_at Cluster Incl.  
 25 X57398:Human mRNA for pM5 protein /cds=(0,3572) /gb=X5739; 33818\_at Cluster Incl.  
 AC004472:Homo sapiens chromosome 9, P1 clone 11659 /cds=(; 36158\_at Cluster Incl.  
 AF086947:untitled /cds=(334,4119) /gb=AF086947 /gi=413912; 39159\_at Cluster Incl.  
 X99656:H.sapiens mRNA for protein containing SH3 domain, ; 39518\_at Cluster Incl.  
 H97470:yw11b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-; 39521\_at Cluster Incl.  
 30 U55054:Human K-Cl cotransporter (hKCC1) mRNA, complete cd; 40619\_at Cluster Incl.  
 M91670:Human ubiquitin carrier protein (E2-EPF) mRNA, com; 1813\_at Epidermal Growth Factor  
 Receptor-Related Protein ; 1751\_g\_at AD000092 /FEATURE=cds#5 /DEFINITION=CH19HHR23  
 Homo sapiens DNA from ch; 1218\_at X12794 /FEATURE=cds /DEFINITION=HSEAR2 Human v-  
 erbA related ear-2 gene ; 1224\_at X66363 /FEATURE=cds /DEFINITION=HSSTHPKD H.sapiens  
 35 mRNA PCTAIRE-1 for se; 922\_at J02902 /FEATURE=mRNA /DEFINITION=HUMP2A Human  
 protein phosphatase 2A regu; 893\_at M91670 /FEATURE= /DEFINITION=HUME2EPI Human  
 ubiquitin carrier protein (E2; 518\_at U07132 /FEATURE= /DEFINITION=HSU07132 Human  
 steroid hormone receptor Ner-; 423\_at X66899 /FEATURE=cds /DEFINITION=HSEWS H.sapiens  
 EWS mRNA ; 391\_at X89416 /FEATURE=cds /DEFINITION=HSRNAPPP5 H.sapiens mRNA for

- protein phos; 399\_at X99325 /FEATURE=cds /DEFINITION=HSSTE20 H.sapiens mRNA for Ste20-like kin; 294\_s\_at Protein Kinase Pitslre, Alpha, Alt. Splice 1-Feb ; 163\_at U46461 /FEATURE= /DEFINITION=HSU46461 Human dishevelled homolog (DVL) mRN; 146\_at U81802 /FEATURE= /DEFINITION=HSU81802 Human PtdIns 4-kinase (PI4Kb) mRNA.; 110\_at X96753
- 5 /FEATURE=cds /DEFINITION=HSMCSP H.sapiens mRNA for melanoma-associ; 160044\_g\_at NM\_001098 /FEATURE=mRNA /DEFINITION=Homo sapiens aconitase 2, mitoch.
- Metagene 491;** 37418\_at Cluster Incl. M36653:Human Oct-2 factor mRNA, complete cds /cds=UNKNOWN; 41152\_f\_at Cluster Incl. T89651:yd99a05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36104\_at Cluster Incl. AA526497:ni96d07.s1 Homo sapiens cDNA, 3 end
- 10 /clone=IMAG; 1313\_at D38048 /FEATURE= /DEFINITION=D38048 Human mRNA for proteasome subunit z; 360\_at Y11999 /FEATURE=cds /DEFINITION=HSINSP3KN H.sapiens mRNA for inositol 1,4.
- Metagene 492;** 35451\_s\_at Cluster Incl. AA280726:zs96g08.s1 Homo sapiens cDNA, 3 end /clone=IM; 35942\_at Cluster Incl. A1183417:qd24c11.x1 Homo sapiens cDNA, 3 end /clone=IMAG;
- 15 36330\_at Cluster Incl. Y17448:Homo sapiens CCBL1 gene, last two exons /cds=(0,14; 35253\_at Cluster Incl. AB011143:Homo sapiens mRNA for KIAA0571 protein, complete; 38830\_at Cluster Incl. U66685:HSU66685 Homo sapiens cDNA /gb=U66685 /gi=1906570 ; 1233\_s\_at M76125 /FEATURE= /DEFINITION=HUMTYRKINR Human tyrosine kinase receptor; 392\_g\_at X89416 /FEATURE=cds /DEFINITION=HSRNAPPP5 H.sapiens mRNA for protein ph; 144\_at U80628
- 20 /FEATURE= /DEFINITION=HSU80628 Human thymidine kinase 2 isoform B .
- Metagene 493;** 41382\_at Cluster Incl. AJ000342:Homo sapiens mRNA for DMBT1 6 kb transcript vari; 39144\_at Cluster Incl. U59736:Human transcription factor (NFATc.b) mRNA, complet.
- Metagene 494;** 36368\_at Cluster Incl. AF054998:Homo sapiens clone 24479 mRNA sequence /cds=UNKN; 34031\_i\_at Cluster Incl. U90268:Human Krit1 mRNA, complete cds /cds=(25,1614)
- 25 /g; 36720\_at Cluster Incl. AA873266:oh68e03.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38224\_at Cluster Incl. U71300:Human snRNA activating protein complex 50kD subuni; 33805\_at Cluster Incl. AB007949:Homo sapiens mRNA for KIAA0480 protein, complete; 34718\_at Cluster Incl. X04434:Human mRNA for insulin-like growth factor I recept; 39401\_at Cluster Incl. W28264:44c9 Homo sapiens cDNA /gb=W28264 /gi=1308212 /ug=; 34381\_at Cluster Incl.
- 30 AI708889:as86g01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35373\_at Cluster Incl. M61906:Human P13-kinase associated p85 mRNA sequence /cds; 36573\_at Cluster Incl. U78524:Human Gu binding protein mRNA, partial cds /cds=(0; 38765\_at Cluster Incl. AB028449:Homo sapiens mRNA for Helicase-MOI, complete cds; 33173\_g\_at Cluster Incl. T75292:yc89b05.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 1785\_at S66431 /FEATURE=
- 35 /DEFINITION=S66431 RBP2=retinoblastoma binding protein .
- Metagene 495;** 39628\_at Cluster Incl. AI671547:wb33e07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 33704\_at Cluster Incl. AB011111:Homo sapiens mRNA for KIAA0539 protein, complete; 36494\_at Cluster Incl. AF058918:Homo sapiens unknown mRNA /cds=(212,634) /gb=AF0; 32572\_at Cluster Incl. X98296:H.sapiens mRNA for ubiquitin hydrolase /cds=(59,77.

- Metagene 496;** 39316\_at Cluster Incl. AI935153:wp14c12.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 39647\_s\_at Cluster Incl. U95019:Human voltage-dependent calcium channel beta-2c ; 1452\_at U24576 /FEATURE= /DEFINITION=U24576 Homo sapiens breast tumor autoantigen; 903\_at L42373 /FEATURE=mRNA /DEFINITION=HUMPP2A Homo sapiens phosphatase 2A B56-  
 5 .
- Metagene 497;** 41395\_at Cluster Incl. AB003791:Homo sapiens mRNA for keratan sulfate Gal-6-sulf; 33272\_at Cluster Incl. AA829286:of08a01.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 36555\_at Cluster Incl. AF044311:Homo sapiens gamma-synuclein gene, complete cds ; 37587\_at Cluster Incl. S43855:recoverin=photoreceptor protein [human, retina, mR; 38261\_at Cluster Incl. AF085692:Homo sapiens multidrug resistance-associated protein; 41123\_s\_at Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796; 41124\_r\_at Cluster Incl. L35594:Human autotaxin mRNA, complete cds /cds=(49,2796; 34311\_at Cluster Incl. X76648:H.sapiens mRNA for glutaredoxin /cds=(63,383) /gb=; 38118\_at Cluster Incl. U73377:Human p66shc (SHC) mRNA, complete cds /cds=(194,19; 40541\_at Cluster Incl.
- 10 X01630:Human mRNA for argininosuccinate synthetase /cds=(; 1930\_at U83659 /FEATURE= /DEFINITION=HSU83659 Human multidrug resistance-associated; 1731\_at M21574 /FEATURE=mRNA /DEFINITION=HUMPDGFRAA Human platelet-derived growth; 707\_s\_at Mucin 6, Gastric ; 411\_i\_at X57351 /FEATURE=cds /DEFINITION=HS18D Human 1-8D gene from interferon- $\gamma$ ; 291\_s\_at J04152 /FEATURE=mRNA /DEFINITION=HUMGA733A Human
- 20 gastrointestinal tumor.
- Metagene 498;** 32168\_s\_at Cluster Incl. U85267:Homo sapiens down syndrome candidate region 1 (D); 36638\_at Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor; 37028\_at Cluster Incl. U83981:Homo sapiens apoptosis associated protein (GADD34); 38772\_at Cluster Incl. Y11307:H.sapiens CYR61 mRNA /cds=(223,1368) /gb=Y11307 /g.
- 25 **Metagene 499;** 32424\_at Cluster Incl. D84424:Homo sapiens mRNA for hyaluronan synthase, complete; 36214\_at Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) ; 40375\_at Cluster Incl. X63741:H.sapiens pilot mRNA /cds=(353,1516) /gb=X63741 /g; 32065\_at Cluster Incl. S68134:CREM=cyclic AMP-responsive element modulator beta ; 37623\_at Cluster Incl. X75918:H.sapiens mRNA for NOT /cds=(317,2113) /gb=X75918 ; 33439\_at Cluster Incl.
- 30 D15050:Human mRNA for transcription factor AREB6, complete; 36669\_at Cluster Incl. L49169:Human G0S3 mRNA, complete cds /cds=(593,1609) /gb=; 38037\_at Cluster Incl. M60278:Human heparin-binding EGF-like growth factor mRNA; 41483\_s\_at Cluster Incl. X56681:Human junD mRNA /cds=(174,1217) /gb=X56681 /gi=3; 547\_s\_at S77154 /FEATURE= /DEFINITION=S77154 TINUR= NGFI-B/nur77 beta-type trans; 279\_at L13740 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, complete; 280\_g\_at L13740
- 35 /FEATURE= /DEFINITION=HUMTR3A Human TR3 orphan receptor mRNA, complete.
- Metagene 500;** 38913\_at Cluster Incl. U60319:Homo sapiens haemochromatosis protein (HLA-H) mRNA; 39633\_at Cluster Incl. Z18948:H.sapiens mRNA for S100E calcium binding protein ; 31868\_at Cluster Incl. AF060798:Homo sapiens myristylated and palmitylated serin; 32632\_g\_at



- Cluster Incl. J03060:Human glucocerebrosidase (GCB) gene /cds=(229,17; 32670\_at Cluster Incl.  
 L38969:Homo sapiens thrombospondin 3 (THBS3) gene, comple; 34181\_at Cluster Incl.  
 X55330:H.sapiens mRNA for aspartylglucosaminidase /cds=(1; 36497\_at Cluster Incl.  
 W28438:47g10 Homo sapiens cDNA /gb=W28438 /gi=1308449 /ug; 38697\_at Cluster Incl.
- 5 AL050274:Homo sapiens mRNA; cDNA DKFZp566C243 (from clone; 39069\_at Cluster Incl.  
 AF053944:Homo sapiens aortic carboxypeptidase-like protei; 40136\_at Cluster Incl.  
 AB014576:Homo sapiens mRNA for KIAA0676 protein, partial ; 32181\_at Cluster Incl.  
 M60922:Human surface antigen mRNA, complete cds /cds=(126; 36126\_at Cluster Incl.  
 U18919:Human chromosome 17q12-21 mRNA, clone pOV-2, parti; 39910\_at Cluster Incl.
- 10 AA663800:ae72g12.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 32502\_at Cluster Incl.  
 AL041124:DKFZp434D0316\_s1 Homo sapiens cDNA, 3 end /clon; 33132\_at Cluster Incl.  
 U37012:Human cleavage and polyadenylation specificity fac; 2020\_at M73554 /FEATURE=  
 /DEFINITION=HUMBCL1 Human bcl-1 mRNA, complete CDS .  
**Metagene** 501; 34771\_at Cluster Incl. AF035959:Homo sapiens type-2 phosphatidic acid  
 15 phosphatas; 37974\_at Cluster Incl. AL050178:Homo sapiens mRNA; cDNA DKFZp586J1822 (from  
 clon; 39787\_at Cluster Incl. AB029821:Homo sapiens mRNA for phosphatidylethanolamine N;  
 34866\_at Cluster Incl. AF055029:Homo sapiens clone 24711 mRNA sequence /cds=UNKN;  
 33202\_f\_at Cluster Incl. U43747:Human frataxin (FRDA) mRNA, complete cds /cds=(5.  
**Metagene** 502; 35503\_at Cluster Incl. M81590:Homo sapiens serotonin 1D receptor (5-HT1D~)  
 20 mRNA;; 32332\_at Cluster Incl. X69433:H.sapiens mRNA for mitochondrial isocitrate dehydr;  
 33480\_at Cluster Incl. X15393:H.sapiens motilin gene exon 2 (and joined CDS) /cd; 37510\_at  
 Cluster Incl. AF036715:Homo sapiens syntaxin 8 mRNA, complete cds /cds=; 37880\_at Cluster Incl.  
 X53414:Human mRNA for peroxisomal L-alanine-glyoxylate am; 38517\_at Cluster Incl.  
 M87503:Human IFN-responsive transcription factor subunit ; 38531\_at Cluster Incl.
- 25 AA428150:zw57c05.s1 Homo sapiens cDNA, 3 end /clone=IMAG; 38865\_at Cluster Incl.  
 AJ011736:Homo sapiens mRNA for growth factor receptor bin; 41108\_at Cluster Incl.  
 Y14391:Homo sapiens mRNA for putative GTP-binding protein; 36058\_at Cluster Incl.  
 AL096741:Homo sapiens mRNA; cDNA DKFZp586O0223 (from clon; 37214\_g\_at Cluster Incl.  
 X90392:H.sapiens mRNA for DNase X gene /cds=(794,1702) ; 38966\_at Cluster Incl.
- 30 AF038958:Homo sapiens synaptic glycoprotein SC2 spliced v; 40089\_at Cluster Incl.  
 AJ224442:Homo sapiens mRNA for putative methyltransferase; 40104\_at Cluster Incl.  
 D63780:Homo sapiens mRNA for YSK1, complete cds /cds=(114; 40866\_at Cluster Incl.  
 AJ001258:Homo sapiens mRNA for NIPSNAP1 protein /cds=(254; 41776\_at Cluster Incl.  
 U70660:Human copper transport protein HAH1 (HAH1) mRNA, c; 35796\_at Cluster Incl.
- 35 Y17169:Homo sapiens mRNA for A6 related protein /cds=(104; 35835\_at Cluster Incl.  
 AB019409:Homo sapiens mRNA, expressed in fibroblasts of p; 36574\_at Cluster Incl.  
 Z68907:H.sapiens mRNA for NAD (H)-specific isocitrate deh; 37311\_at Cluster Incl.  
 AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878; 37706\_at Cluster Incl.  
 U28811:Human cysteine-rich fibroblast growth factor recep; 38787\_at Cluster Incl.

- X63131:H.sapiens Myl (PML) mRNA /cds=(141,2042) /gb=X6313; 39867\_at Cluster Incl.  
 S75463:P43=mitochondrial elongation factor homolog [human; 1980\_s\_at X58965 /FEATURE=  
 /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene ; 1855\_at X14445  
 /FEATURE=expanded\_cds /DEFINITION=HSINT2 Human int-2 proto-oncogene; 982\_at X74795  
 5 /FEATURE=cds /DEFINITION=HSP1CDC46 H.sapiens P1-Cdc46 mRNA .  
**Metagene 503**; 31935\_s\_at Cluster Incl. U75968:Human clone C3 CHL1 protein (CHLR1) mRNA,  
 altern; 34167\_s\_at Cluster Incl. AA984230:am82g03.s1 Homo sapiens cDNA, 3 end /clone=IM;  
 35124\_at Cluster Incl. M62982:Human arachidonate 12-lipoxygenase mRNA, complete ; 32879\_at  
 Cluster Incl. AL080233:Homo sapiens mRNA; cDNA DKFZp586L111 (from clone; 35013\_at  
 10 Cluster Incl. AF013512:untitled /cds=(106,1551) /gb=AF013512 /gi=265381; 35883\_at Cluster Incl.  
 X66079:H.sapiens Spi-B mRNA /cds=(5,793) /gb=X66079 /gi=3; 38558\_at Cluster Incl.  
 M29273:Human myelin-associated glycoprotein (MAG) mRNA, c; 36826\_at Cluster Incl.  
 X64037:H.sapiens mRNA for RNA polymerase II associated pr; 36883\_at Cluster Incl.  
 X14640:Human mRNA for keratin 13 /cds=(42,1418) /gb=X1464; 39802\_at Cluster Incl.  
 15 X72308:Homo sapiens mRNA for monocyte chemotactic protein; 33377\_at Cluster Incl.  
 X03168:Human mRNA for S-protein /cds=(61,1497) /gb=X03168; 34405\_at Cluster Incl.  
 U47927:Human isopeptidase T (ISOT) mRNA, complete cds /cd; 37339\_at Cluster Incl.  
 U20657:Human ubiquitin protease (Unph) proto-oncogene mRN; 40558\_at Cluster Incl.  
 W28227:43h1 Homo sapiens cDNA /gb=W28227 /gi=1308175 /ug=; 40598\_at Cluster Incl.  
 20 W20138:zb40d12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-; 41793\_at Cluster Incl.  
 AI288757:qm11h01.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 1804\_at X07730 /FEATURE=  
 /DEFINITION=HSPSA Human mRNA for prostate specific anti; 912\_s\_at M21056 /FEATURE=cds  
 /DEFINITION=HUMPLA2A2 Human pancreatic phospholipas.  
**Metagene 504**; 31810\_g\_at Cluster Incl. Z21488:H.sapiens contactin mRNA /cds=(121,3177)  
 25 /gb=Z21; 33155\_at Cluster Incl. M95740:Human alpha-L-iduronidase gene /cds=(0,1961) /gb=M.  
**Metagene 505**; 35101\_at Cluster Incl. X52997:Human mRNA for platelet glycoprotein IX  
 /cds=(222,; 35131\_at Cluster Incl. J05213:Homo sapiens sialoprotein precursor (IBSP) mRNA, c;  
 37176\_at Cluster Incl. U96078:Homo sapiens hyaluronoglucosaminidase 1 (HYAL1) mR; 37929\_at  
 Cluster Incl. AB017563:Homo sapiens IGSF4 gene /cds=(0,1328) /gb=AB0175.  
 30 **Metagene 506**; 35941\_f\_at Cluster Incl. U91329:Human kinesin-like motor protein KIF1C mRNA,  
 com; 41407\_at Cluster Incl. L03411:Human RD protein (RD) mRNA, complete cds /cds=(86,;  
 35169\_at Cluster Incl. AI982638:wt53c06.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35701\_at  
 Cluster Incl. AI038821:ox96d03.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 35723\_at Cluster  
 Incl. D16581:Human mRNA for 8-oxo-dGTPase, complete cds /cds=(2; 38725\_s\_at Cluster Incl.  
 35 N36295:yx99b12.r1 Homo sapiens cDNA, 5 end /clone=IMAG; 39074\_at Cluster Incl.  
 U79241:Human clone 23759 mRNA, partial cds /cds=(0,1315) ; 39342\_at Cluster Incl.  
 X94754:H.sapiens mRNA for yeast methionyl-tRNA synthetase; 39363\_at Cluster Incl.  
 AF042384:Homo sapiens BC-2 protein mRNA, complete cds /cd; 40056\_at Cluster Incl.  
 D87989:Human mRNA for UDP-galactose transporter related i; 40837\_at Cluster Incl.

- M99436:Human transducin-like enhancer protein (TLE2) mRNA; 41163\_at Cluster Incl.  
 AL109672:Homo sapiens mRNA full length insert cDNA clone ; 41732\_at Cluster Incl.  
 AA310786:EST181572 Homo sapiens cDNA, 5 end /clone=ATCC-; 33824\_at Cluster Incl.  
 X74929:H.sapiens KRT8 mRNA for keratin 8 /cds=(59,1510) /; 33906\_at Cluster Incl.
- 5 AB001740:Homo sapiens mRNA for p27, complete cds /cds=(20; 35269\_at Cluster Incl.  
 AF093420:Homo sapiens Hsp70 binding protein HspBP1 mRNA ; 35823\_at Cluster Incl.  
 M63573:Human secreted cyclophilin-like protein (SCYLP) mR; 36135\_at Cluster Incl.  
 U86602:Human nucleolar protein p40 mRNA, complete cds /cd; 36613\_at Cluster Incl.  
 U09585:Homo sapiens putative interferon-related protein (; 38076\_at Cluster Incl. X69907:H.sapiens
- 10 gene for mitochondrial ATP synthase c su; 38808\_at Cluster Incl. D64154:Human mRNA for Mr  
 110,000 antigen, complete cds /c; 40956\_at Cluster Incl. X90857:H.sapiens mRNA for -14 gene,  
 containing globin reg; 41259\_at Cluster Incl. AI553745:tn28c11.x1 Homo sapiens cDNA, 3 end  
 /clone=IMAG; 41332\_at Cluster Incl. D38251:Homo sapiens mRNA for RPB5 (XAP4), complete  
 cds /c; 32518\_at Cluster Incl. AF019767:Homo sapiens zinc finger protein (ZPR1) mRNA, co;
- 15 2035\_s\_at M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding protein  
 (MBP; 1878\_g\_at M13194 /FEATURE=mRNA /DEFINITION=HUMERCC1 Human excision  
 repair protei; 1322\_at U47677 /FEATURE=mRNA /DEFINITION=HSE2F1S03 Human  
 transcription factor E2; 1309\_at D26598 /FEATURE= /DEFINITION=HUMPSH1 Human mRNA  
 for proteasome subunit H; 1154\_at J02645 /FEATURE=mRNA /DEFINITION=HUMEIF2A Human
- 20 translational initiation; 503\_at U37690 /FEATURE= /DEFINITION=HSU37690 Human RNA  
 polymerase II subunit (hs; 241\_g\_at M64231 /FEATURE=mRNA /DEFINITION=HUMSPERSYN  
 Human spermidine synthase g.
- Metagene** 507; 36336\_s\_at Cluster Incl. AC005390:Homo sapiens chromosome 19, cosmid R31180  
 /cds; 37101\_at Cluster Incl. AL050008:Homo sapiens mRNA; cDNA DKFZp564A063 (from clone;  
 25 40297\_at Cluster Incl. AC005053:Homo sapiens BAC clone RG041D11 from 7q21 /cds=(; 40695\_at  
 Cluster Incl. J05272:Human IMP dehydrogenase type 1 mRNA complete cds /; 41415\_at Cluster  
 Incl. L36720:Homo sapiens bystin mRNA, complete cds /cds=(64,98; 31856\_at Cluster Incl.  
 Z24680:H.sapiens garp gene mRNA, complete CDS /cds=(94,20; 34273\_at Cluster Incl.  
 AI267373:aq64c09.x1 Homo sapiens cDNA /clone=IMAGE-203569; 34293\_at Cluster Incl.
- 30 AF004426:Homo sapiens microtubule-based motor (HsKIFC3) m; 37893\_at Cluster Incl.  
 AI828880:wj37b02.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 38617\_at Cluster Incl.  
 D45906:Homo sapiens mRNA for LIMK-2, complete cds /cds=(1; 38969\_at Cluster Incl.  
 AI828168:wk32h09.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 41728\_at Cluster Incl.  
 D63486:Human mRNA for KIAA0152 gene, complete cds /cds=(1; 34830\_at Cluster Incl.
- 35 W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=; 36678\_at Cluster Incl.  
 D21261:Human mRNA for KIAA0120 gene, complete cds /cds=(7; 38393\_at Cluster Incl.  
 D87434:Human mRNA for KIAA0247 gene, complete cds /cds=(2; 38417\_at Cluster Incl.  
 M91029:Human AMP deaminase (AMPD2) mRNA /cds=(0,2282) /gb; 40169\_at Cluster Incl.  
 AF057140:Homo sapiens cargo selection protein TIP47 (TIP4; 40635\_at Cluster Incl.

- AF089750:Homo sapiens flotillin-1 mRNA, complete cds /cds; 40964\_at Cluster Incl.  
 Z46376:H.sapiens HK2 mRNA for hexokinase II /cds=(1490,42; 40986\_s\_at Cluster Incl.  
 AA058852:zf65a11.s1 Homo sapiens cDNA, 3 end /clone=IM; 41246\_at Cluster Incl.  
 AI743134:wg87f07.x1 Homo sapiens cDNA, 3 end /clone=IMAG; 32562\_at Cluster Incl.
- 5 X72012:H.sapiens end mRNA for endoglin /cds=(281,2158) /g; 33131\_at Cluster Incl.  
 X70683:H.sapiens mRNA for SOX-4 protein /cds=(350,1774) /; 33143\_s\_at Cluster Incl.  
 U81800:Homo sapiens monocarboxylate transporter (MCT3) ; 33214\_at Cluster Incl. Y11681:Homo sapiens mRNA for mitochondrial ribosomal prot; 1693\_s\_at D11139 /FEATURE=exons#1-4  
 /DEFINITION=HUMTIMP Human gene for tissue in; 1385\_at M77349 /FEATURE=
- 10 /DEFINITION=HUMTGFBIG Human transforming growth factor-; 1138\_at L20859 /FEATURE=  
 /DEFINITION=HUMGLVR1X Human leukemia virus receptor 1 ( ; 1020\_s\_at U85611 /FEATURE=  
 /DEFINITION=HSU85611 Human DNA-PK interaction protein; 892\_at M90657 /FEATURE=  
 /DEFINITION=HUML6A Human tumor antigen (L6) mRNA, comple; 793\_at X54936  
 /FEATURE=cds /DEFINITION=HSPLGF H.sapiens mRNA for placenta growth; 691\_g\_at J02783
- 15 /FEATURE=mRNA /DEFINITION=HUMTHBP Human thyroid hormone binding ; 404\_at X52425  
 /FEATURE=mRNA /DEFINITION=HSIL4R Human IL-4-R mRNA for the interle; 333\_s\_at Single-Stranded Dna-Binding Protein Mssp-1 .  
**Metagene** 508; 33632\_g\_at Cluster Incl. AF023612:Homo sapiens Dim1p homolog mRNA, complete cds ; 36450\_at Cluster Incl. D13897:Human DNA for peptide YY, complete cds  
 /cds=(91,36; 39426\_at Cluster Incl. AF017789:Homo sapiens putative transcription factor CA150; 40449\_at Cluster Incl. L23320:Human replication factor C large subunit mRNA, com; 34796\_at Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /; 37030\_at Cluster Incl. AB020694:Homo sapiens mRNA for KIAA0887 protein, partial ; 37377\_i\_at Cluster Incl. M13452:Human lamin A mRNA, 3end /cds=(0,1547) /gb=M1345; 38031\_at Cluster Incl.
- 25 D21853:Human mRNA for KIAA0111 gene, complete cds /cds=(2; 38815\_at Cluster Incl. Y08999:H.sapiens mRNA for Sop2p-like protein /cds=(33,114.  
**Metagene** 509; 31864\_at Cluster Incl. X98263:H.sapiens mRNA for M-phase phosphoprotein, mp.  
**Metagene** 509; 31864\_at Cluster Incl. X98263:H.sapiens mRNA for M-phase phosphoprotein, mp;

#### 30 4. DISCUSSION

Applicants have described a novel and unbiased approach for developing detailed genomic phenotypes that are exquisitely predictive for clinical disease states in human aorta samples. Importantly, the analysis is driven by the ability to predict phenotypic characteristics rather than merely identifying genes whose expression differs by an arbitrary amount for a given clinical

35 phenotype. Applicants identified patterns of gene expression involving multiple, interacting genes that define the association with the clinical phenotypes. Most importantly, our analytic approach is rigorous in assessing the validity of these patterns through cross-validation analyses. This establishes the robust conclusion that these patterns of gene expression have the capacity to accurately predict the clinical phenotype, and hence underpins the inferred validity of the connection between these

genes and the phenotype. The method described could serve as a model for studying other complex cardiovascular diseases where target tissues are genomically phenotyped to identify high priority candidate genes. These genes are now the focus of SNP studies and the basis for studying clinical patient populations.

5           The statistical methodology described in this report has been successfully applied to identify gene expression patterns capable of discriminating breast cancer samples on the basis of estrogen receptor status and predicting both recurrence and extent of lymph node metastasis in primary breast cancer. The use of metagenes in our statistical approach places the emphasis on the differential co-expression of multiple genes acting in concert - consonant with the biological model of complex  
10       diseases. The decision tree models used in this study showed considerable predictive value using the metagene patterns identified. In the cross validation analysis, applicants were able to correctly classify unknown samples with 93.5% accuracy for extent of disease severity and 93.6% accuracy for aortic location. Even with the heterogeneous nature of human aorta tissues and of atherosclerotic lesions therein, the metagenes identified through this approach clearly exhibit reliable discriminatory  
15       patterns. One point in the disease burden analysis is that applicants used sections from two different locations within multiple aortas. Because applicants did not use a single location, the inherent heterogeneity within an individual aorta could have influenced our results. However, the genes that predicted aortic location in our second analysis were quite different from those in our first analysis suggesting that location was not a major factor in the burden analysis.

20           Our disease burden analysis identified genes associated with minimal vs. severe atherosclerosis as measured, primarily, by the extent of advanced disease plaques. The samples included in the analysis were classified by quantitative measures of atherosclerosis identifying genes that reflect extent of disease. Although our analysis did identify genes whose expression is limited in the tissue (i.e. endothelium-derived), it may be biased toward genes expressed in the more abundant  
25       media, especially the inner media which may be most interactive with the atheromas. Still, applicants intentionally used the full thickness of the vessel wall in this initial analysis as the disease process likely involves complex interactions across the tissue layers through autocrine and other mechanisms. The expression patterns identified therefore may represent the net gene expression effect contributed from the different tissue layers.

30           The second analysis identified genes associated with location within the aortas. The regional differences within an aorta could be related to disease susceptibility given results from the PDAY study that showed atherosclerotic development progresses from the distal to the proximal aorta. Cornhill JF et al, *Monogr Atheroscler.* 1990;15:13-19. In our analysis of the proximal and distal sections of the human aortas, there was no significant difference in the age of the donor patients  
35       and the atherosclerotic burden of the proximal and distal sections used by Sudan IV and raised lesion scores. This would seem to indicate that the differential gene expression patterns applicants found were indicative of location rather than age or presence of disease. This may reflect inherent differences in the mechanical stress from hemodynamic factors experienced by the different locations or possibly differences in the clonal origin of the cells populating the proximal or distal areas. See

Nakashima Y, Raines EW, Plump AS, Breslow JL, Ross R. Upregulation of VCAM-1 and ICAM-1 at atherosclerosis-prone sites on the endothelium in the ApoE-deficient mouse. *Arterioscler Thromb Vasc Biol.* 1998;18:842-851; Passerini AG, Polacek DC, Shi C, Francesco NM, Manduchi E, Grant GR, Pritchard WF, Powell S, Chang GY, Stoeckert CJ, Jr., Davies PF. Coexisting proinflammatory and antioxidative endothelial transcription profiles in a disturbed flow region of the adult porcine aorta. *Proc Natl Acad Sci U S A.* 2004;101:2482-2487; Schwartz SM, deBlois D, O'Brien ER. The intima. Soil for atherosclerosis and restenosis. *Circ Res.* 1995;77:445-465.

Our first analysis for extent of disease identified genes reproducibly associated with atherosclerosis in the literature such as *apoE*, *osteopontin*, and *olr1*. See Chen M, Masaki T, Sawamura T. LOX-1, the receptor for oxidized low-density lipoprotein identified from endothelial cells: implications in endothelial dysfunction and atherosclerosis. *Pharmacol Ther.* 2002;95:89-100; de Knijff P, van den Maagdenberg AM, Frants RR, Havekes LM. Genetic heterogeneity of apolipoprotein E and its influence on plasma lipid and lipoprotein levels. *Hum Mutat.* 1994;4:178-194; Ilveskoski E, Perola M, Lehtimäki T, Laippala P, Savolainen V, Pajarinen J, Penttilä A, Lähdesmäki KH, Mannikko A, Liesto KK, Koivula T, Karhunen PJ. Age-dependent association of apolipoprotein E genotype with coronary and aortic atherosclerosis in middle-aged men: an autopsy study. *Circulation.* 1999;100:608-613; Kwon HM, Hong BK, Kang TS, Kwon K, Kim HK, Jang Y, Choi D, Park HY, Kang SM, Cho SY, Kim HS. Expression of osteopontin in calcified coronary atherosclerotic plaques. *J Korean Med Sci.* 2000;15:485-493; Mahley RW. Apolipoprotein E: cholesterol transport protein with expanding role in cell biology. *Science.* 1988;240:622-630; Bini A, Mann KG, Kudryk BJ, Schoen FJ. Noncollagenous bone matrix proteins, calcification, and thrombosis in carotid artery atherosclerosis. *Arterioscler Thromb Vasc Biol.* 1999;19:1852-1861. As one would expect from a biological context, these genes were upregulated in the diseased sections of the aorta. Importantly for our study, applicants also identified genes such as *capg*, *gm2*, *mmp9* and *ccl12* that encode proteins whose function is consistent with a role in atherogenesis but have not been previously linked to atherosclerosis. CapG is a key regulatory protein for actin and membrane phospholipids within migrating phagocytes. See Witke W, Li W, Kwiatkowski DJ, Southwick FS. Comparisons of CapG and gelsolin-null macrophages: demonstration of a unique role for CapG in receptor-mediated ruffling, phagocytosis, and vesicle rocketing. *J Cell Biol.* 2001;154:775-784. The gene *gm2* has been well studied in the oncology field for its role in cell proliferation, adhesion and chemotaxis. See Garner B, Priestman DA, Stocker R, Harvey DJ, Butters TD, Platt FM. Increased glycosphingolipid levels in serum and aortae of apolipoprotein E gene knockout mice. *J Lipid Res.* 2002;43:205-214; Gouni-Berthold I, Seul C, Ko Y, Hescheler J, Sachinidis A. Gangliosides GM1 and GM2 induce vascular smooth muscle cell proliferation via extracellular signal-regulated kinase 1/2 pathway. *Hypertension.* 2001;38:1030-1037; Sachinidis A, Kraus R, Seul C, Meyer zu Brickwedde MK, Schulte K, Ko Y, Hoppe J, Vetter H. Gangliosides GM1, GM2 and GM3 inhibit the platelet-derived growth factor-induced signaling transduction pathway in vascular smooth muscle cells by different mechanisms. *Eur J Cell Biol.* 1996;71:79-88. In addition, it has been shown to be present

in aorta of apoE knock-out mice. The proteins MMP1, MMP2, MMP9 and MMP13 have all been associated with atheroma progression presumably through vascular remodeling. See Jeng AY, Chou M, Sawyer WK, Caplan SL, Von Linden-Reed J, Jeune M, Prescott MF. Enhanced expression of matrix metalloproteinase-3, -12, and -13 mRNAs in the aortas of apolipoprotein E-deficient mice with advanced atherosclerosis. *Ann N Y Acad Sci.* 1999;878:555-558; Prescott MF, Sawyer WK, Von Linden-Reed J, Jeune M, Chou M, Caplan SL, Jeng AY. Effect of matrix metalloproteinase inhibition on progression of atherosclerosis and aneurysm in LDL receptor-deficient mice overexpressing MMP-3, MMP-12, and MMP-13 and on restenosis in rats after balloon injury. *Ann N Y Acad Sci.* 1999;878:179-190; Lee RT, Schoen FJ, Lorce HM, Lark MW, Libby P. Circumferential stress and matrix metalloproteinase 1 in human coronary atherosclerosis. Implications for plaque rupture. *Arterioscler Thromb Vasc Biol.* 1996;16:1070-1073. The gene product of *ccrl2* serves as a receptor for monocyte chemotactic protein 1 (MCP1) and other chemokines, and may be important for processes such as vascular infiltration by monocytes and intimal hyperplasia. See Perez de Lema G, Maier H, Nieto E, Vielhauer V, Luckow B, Mampaso F, Schlondorff D. Chemokine expression precedes inflammatory cell infiltration and chemokine receptor and cytokine expression during the initiation of murine lupus nephritis. *J Am Soc Nephrol.* 2001;12:1369-1382; Bush E, Maeda N, Kuziel WA, Dawson TC, Wilcox JN, DeLeon H, Taylor WR. CC chemokine receptor 2 is required for macrophage infiltration and vascular hypertrophy in angiotensin II-induced hypertension. *Hypertension.* 2000;36:360-363. An ontologic analysis of the gene list confirmed much of what has already been reported regarding the processes involved in atherosclerosis. Although, the number of genes related to cell growth/motility, transcriptional regulation and signal transduction seem to indicate that even in the advanced stages, the disease is active and proliferating. This would suggest that molecular, targeted interventions could still be of some benefit to this population of patients.

The second analysis looked for genes related to disease susceptibility. As before, there were genes whose translated products are directly associated with atherosclerosis such as *sod3* and *procr*. See Laszik ZG, Zhou XJ, Ferrell GL, Silva FG, Esmon CT. Down-regulation of endothelial expression of endothelial cell protein C receptor and thrombomodulin in coronary atherosclerosis. *Am J Pathol.* 2001;159:797-802; Hink HU, Santanam N, Dikalov S, McCann L, Nguyen AD, Parthasarathy S, Harrison DG, Fukai T. Peroxidase properties of extracellular superoxide dismutase: role of uric acid in modulating in vivo activity. *Arterioscler Thromb Vasc Biol.* 2002;22:1402-1408.

In addition, the analysis identified genes whose function has been described in other human disorders, but are involved in inflammatory, growth signaling, and cell-cell communication pathways that would be important for early atherosclerosis initiation and progression. Key examples are a number of homeobox-containing genes, that have been found in vascular smooth muscle and endothelial cells and have been linked to cellular proliferation, migration and differentiation as well as vascular remodeling. See Gorski DH, Walsh K. The role of homeobox genes in vascular remodeling and angiogenesis. *Circ Res.* 2000;87:865-872. Another gene, *gata2*, is a transcription factor that regulates endothelin-1 production in endothelial cells. Endothelin-1 is a vasoactive peptide that has been highly associated with atherosclerosis. See Fadel BM, Boutet SC, Quertermous

T. Endothelial cell-specific regulation of the murine endothelin-1 gene. *J Cardiovasc Pharmacol.* 2000;35:S7-11; Kawana M, Lee ME, Quertermous EE, Quertermous T. Cooperative interaction of GATA-2 and AP1 regulates transcription of the endothelin-1 gene. *Mol Cell Biol.* 1995;15:4225-4231.

5           An intriguing observation is the great percentage of genes that are related to regulation of transcription and signal transduction without a great number of genes related to inflammation. One explanation could be that the genes identified by our analysis could be upstream effectors that modulate the inflammatory pathways. For example, the identification of the homeobox genes and *gata2* is intriguing given the potential role in modulation of VCAM1 and ICAM1 – two proteins  
10       linked to atherosclerotic pre-lesion and early lesion formation. Homeobox genes, particularly the C class, have been associated with the increased and decreased expression of ICAM1. See Cillo C. HOX genes in human cancers. *Invasion Metastasis.* 1994;14:38-49; Cillo C, Cantile M, Mortarini R, Barba P, Parmiani G, Anichini A. Differential patterns of HOX gene expression are associated with specific integrin and ICAM profiles in clonal populations isolated from a single human melanoma metastasis. *Int J Cancer.* 1996;66:692-697. The gene, *gata2* has been shown to mediate VCAM  
15       induction in response to thrombin, estrogen and glucocorticoids. See Minami T, Aird WC. Thrombin stimulation of the vascular cell adhesion molecule-1 promoter in endothelial cells is mediated by tandem nuclear factor-kappa B and GATA motifs. *J Biol Chem.* 2001;276:47632-47641; Minami T, Abid MR, Zhang J, King G, Kodama T, Aird WC. Thrombin stimulation of vascular adhesion  
20       molecule-1 in endothelial cells is mediated by protein kinase C (PKC)-delta-NF-kappa B and PKC-zeta-GATA signaling pathways. *J Biol Chem.* 2003;278:6976-6984; Simoncini T, Maffei S, Basta G, Barsacchi G, Genazzani AR, Liao JK, De Caterina R. Estrogens and glucocorticoids inhibit endothelial vascular cell adhesion molecule-1 expression by different transcriptional mechanisms. *Circ Res.* 2000;87:19-25.

25           The identification of genes that predict atherosclerotic phenotypes, whether they are genes already known to function in the disease process or novel genes not previously linked to the disease, represents an important initial step towards an improved understanding of the disease. Our method as described is not meant initially to serve as a diagnostic test, but rather as a means to prioritize genes  
30       and allow us to focus our research efforts for identification of SNPs for large-scale analyses of gene variants. As well, identification of important genes advances our understanding of the biological pathways relevant to atherosclerosis. Importantly, our analytical approach may identify not only the initial steps in biological pathways but the secondary and tertiary events as well. As such, the analysis provides a much richer dataset than merely identifying the immediate effectors of a process. Many of the genes applicants have identified are likely to be causative and may be relevant to future  
35       therapeutic interventions. Furthermore, by finding the polymorphisms within these high priority genes, applicants may begin to identify combinations of SNPs, when taken in concert with clinical cardiovascular risk factors that may lead to the development of new diagnostic and prognostic tools for cardiovascular events. Clearly, a next step must be to develop a deeper understanding of the biological pathways implicated by these analyses and to begin the process of investigating the role of



these genes in the development of vascular disease.

The following attached documents, cited throughout the specification, are incorporated by reference:

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- The following reference is specifically incorporated by reference: Seo D, Wang T, Dressman H, Herderick EE, Iversen ES, Dong C, Vata K, Milano CA, Rigat F, Pittman J, Nevins JR, West M, Goldschmidt-Clermont PJ. "Gene expression phenotypes of atherosclerosis." *Arterioscler Thromb Vasc Biol.* 2004 Oct;24(10):1922-7. Instant figures 11-13 correspond to Figures 2-4 of Seo *et al.*, respectively, also incorporated by reference.
- 35

## CLAIMS:

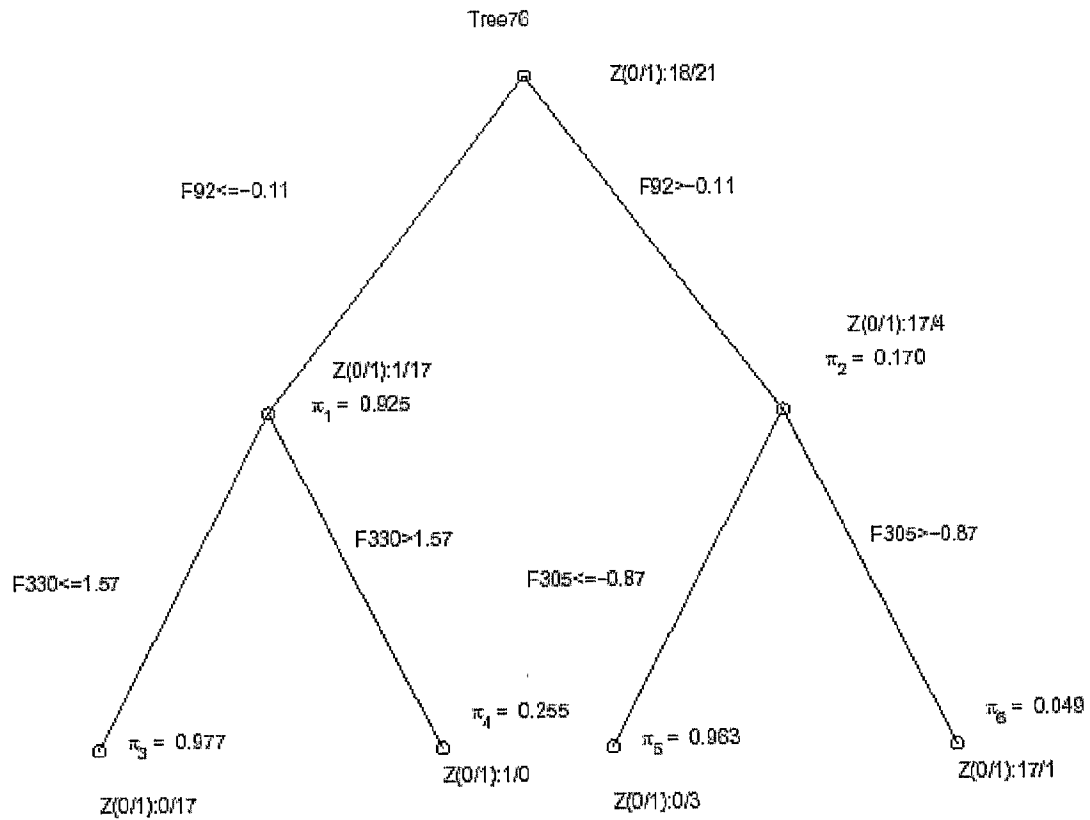
1. A method of estimating whether a sample is from tissue having an atherosclerotic phenotype, said method comprising:
  - 5 (a) obtaining an expression profile for said sample from at least two of said genes listed in Table I;
  - (b) providing one or more predictive statistical tree models, each model including one or more nodes, each node representing a metagene, each node including a statistical predictive probability of the having an atherosclerotic phenotype, each metagene representing a dominant factor from a group of genes associated with having an atherosclerotic phenotype, wherein at least two genes in the group of genes are selected from those listed in Table I; and
  - 10 (c) determining an estimate of the sample having the atherosclerotic phenotype by averaging the predictions of one or more of the tree models applied to the expression profile of the sample.
2. The method of claim 1, wherein at least two of the genes are selected from genes having Genbank accession numbers selected from Y09445, AF053233, U43185, AL050008, AB022718, L10333, M80634, AF044896, X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, AB014574, L13939, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271, J03011, D12485, U88629, U75308, J03600, AF004709, AB002361, X90858, Z29067, U00952, M80254, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, L10678, Z98046, D79994, D87074, X81109, AL049946, U78556, M63603, X12451, U89606, AB029018, AF095791, X74039, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AB015718, X78817, AJ000534, M63835, M16336, U32324, M22324, X54162, U57911, M64571, AC005546, AC005546, Y13622, L76191, U60060, AJ011497, D64142, D26350, X15414, D87434, X79204, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, U56833, J05070, AF093118, U12707, M55531, AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, X97074, D89016, AF022797, M33552, U09578, M21186, M64925, U10906, U83993, AF022789, L35249, M61916, AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193, D84110, AJ006973, AB002318, U51333, U09577 and U00672.
3. The method of claim 1, wherein at least two of the genes are selected from genes having Genbank accession numbers selected from Y09445, AF053233, U43185, AL050008,

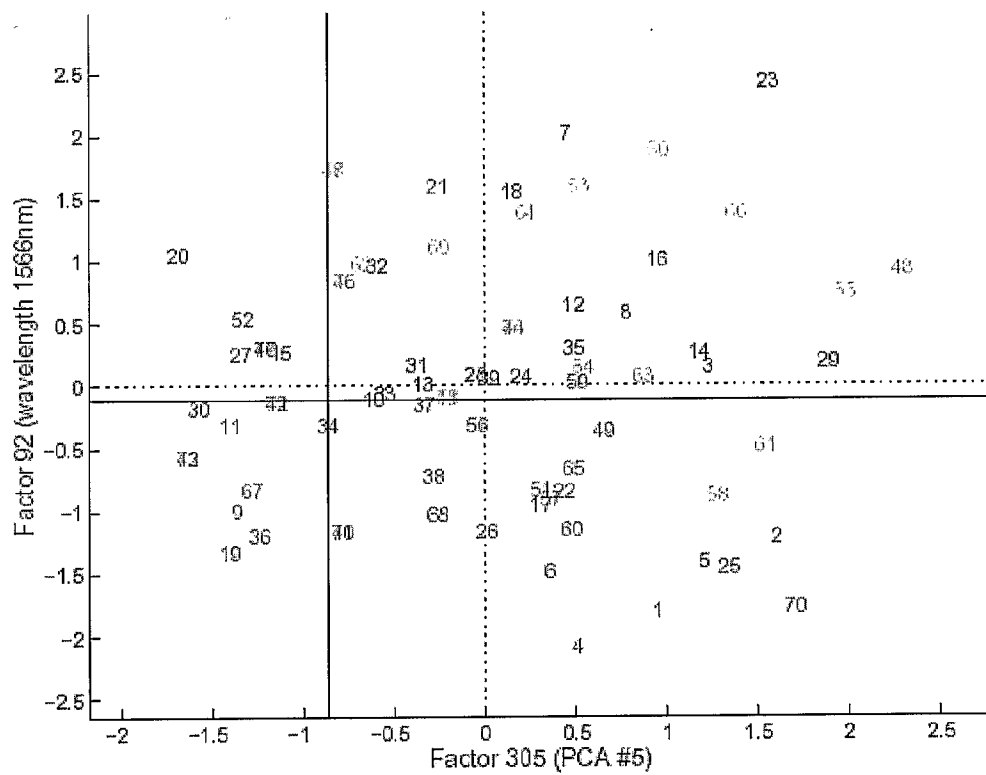
- AB022718, L10333, M80634, AF044896, X78565, AB011143, X69819, J02947, U78095, D67029, AF013249, AB014574, L13939, L06797, D89077, Y08374, X02317, AB002365, AF084481, D34625, AB011103, AF041259, J05037, AF056087, U81800, AL050262, AB018271, J03011, D12485, U88629, U75308, J03600, AF004709, AB002361, X90858, Z29067, U00952, M80254, AF030339, AJ007395, AF013570, Z22555, L22524, Y07512, Y00093, AB007889, Y08136, L10678, Z98046, D79994, D87074, X81109, AL049946, U78556, M63603, X12451, U89606, AB029018, AF095791, X74039, X90976, U00802, X96752, Z49107, AL080235, AF051851, AF062075, AB000220, AB015718, X78817, AJ000534, M63835, M16336, U32324, M22324, X54162, U57911, M64571, AC005546, AC005546, Y13622, L76191, U60060, AJ011497, D64142, D26350, X15414, D87434, X79204, AB014513, U63127, S59184, X53587, Z84718, AF030409, J04621, U56833, J05070, AF093118, U12707, M55531, AB019527, X62055, D83004, X76534, U45285, X63657, L09708, AB020316, AF112219, Y14768, Y14768, Y14768, Y14768, Y14768, AL031846, AL031846, AF036927, D49400, M55210, X97074, D89016, AF022797, M33552, U09578, M21186, M64925, U10906, U83993, AF022789, L35249, M61916, AB011155, X91809, U20158, S59049, U13991, X93498, M87770, AL050139, M73720, U35451, M32315, Y13710, AB008109, M60830, X71874, AB007972, X16663, M63193, D84110, AJ006973, AB002318, U51333, U09577 and U00672.
4. The method according to Claim 1, wherein said tissue is a vascular tissue.
5. The method according to Claim 2, wherein said vascular tissue is aortic tissue.
6. The method of claim 1, wherein the sample is from a mammal suspected of having tissue having an atherosclerotic phenotype.
7. The method of claim 6, wherein the mammal is at risk of being afflicted with atherosclerosis.
8. The method of claim 7, wherein the mammal has being treated with an anti-atherosclerosis agent.
9. The method of claim 1, wherein at least one metagene is Metagene n, wherein n is an integer between 1 and 509.
10. The method of claim 1, wherein the one or more predictive statistical tree models correctly classify samples with greater than 85% accuracy.
11. The method of claim 1, wherein the one or more predictive statistical tree models correctly

classify samples with greater than 90% accuracy.

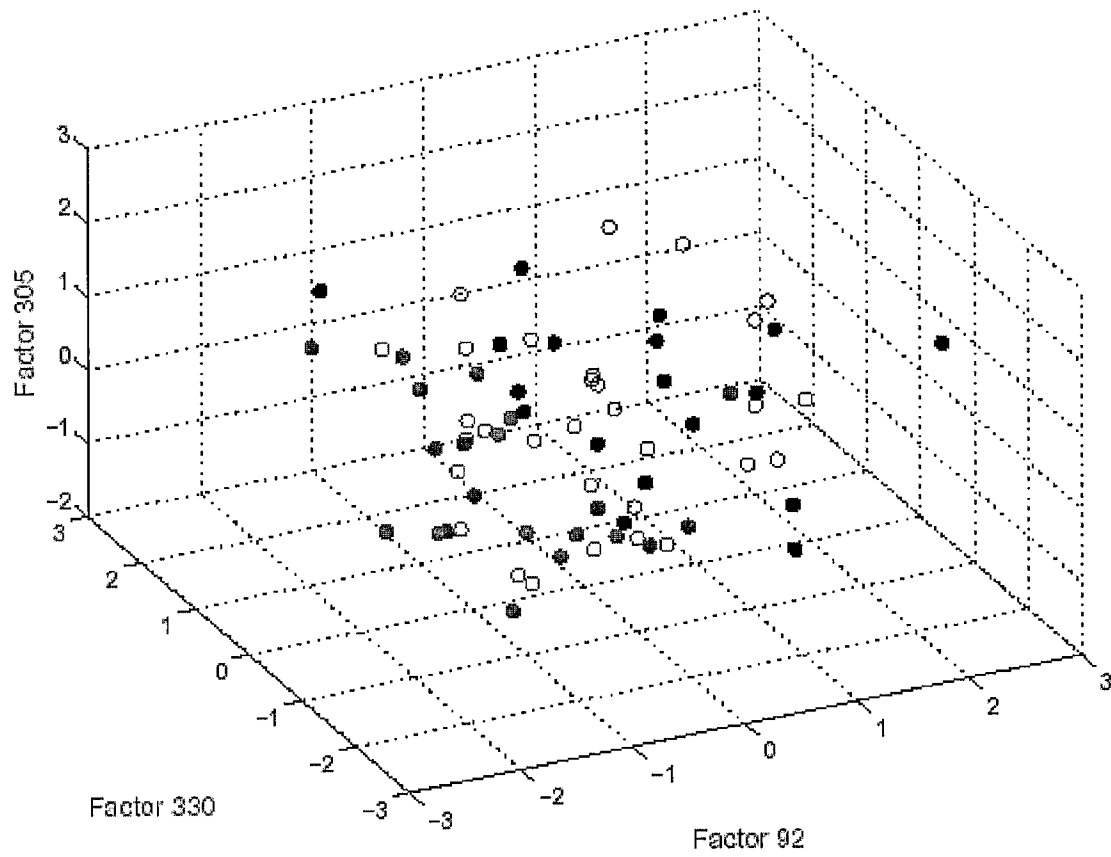
12. A method of predicting the susceptibility of a mammal for developing atherosclerosis, the method comprising:
  - 5 (a) obtaining an expression profile of at least two of said genes listed in Table II from a sample from the mammal;
  - (b) providing one or more predictive statistical tree models, each model including one or more nodes, each node representing a metagene, each node including a statistical predictive probability of being susceptible to developing atherosclerosis, each metagene representing a dominant factor from a group of genes associated with
    - 10 susceptible to developing atherosclerosis, wherein at least two genes in the group of genes are selected from those listed in Table II; and
  - (c) determining an estimate of the sample being susceptible to developing atherosclerosis by averaging the predictions of one or more of the tree models
    - 15 applied to the expression profile of the sample.
13. The method of claim 12, wherein at least two of the genes are selected from genes having Genbank accession numbers selected from M68891, X51757, D83004, X06256, Z22865, X75918 and M55153.
  - 20
14. The method of claim 12, wherein at least seven genes are selected from genes having Genbank accession numbers M68891, X51757, D83004, X06256, Z22865, X75918 and M55153.
- 25 15. The method according to claim 12, wherein the sample is a sample of vascular tissue.
16. The method according to claim 12, wherein the vascular tissue is aortic tissue.
17. The method of claim 12, wherein at least one metagene is Metagene n, wherein n is an integer between 1 and 509.
  - 30
18. The method of claim 12, wherein the one or more predictive statistical tree models correctly classify samples with greater than 85% accuracy.
- 35 19. The method of claim 12, wherein the one or more predictive statistical tree models correctly classify samples with greater than 90% accuracy.

Fig. 1



**Fig. 2**



**Fig. 3**

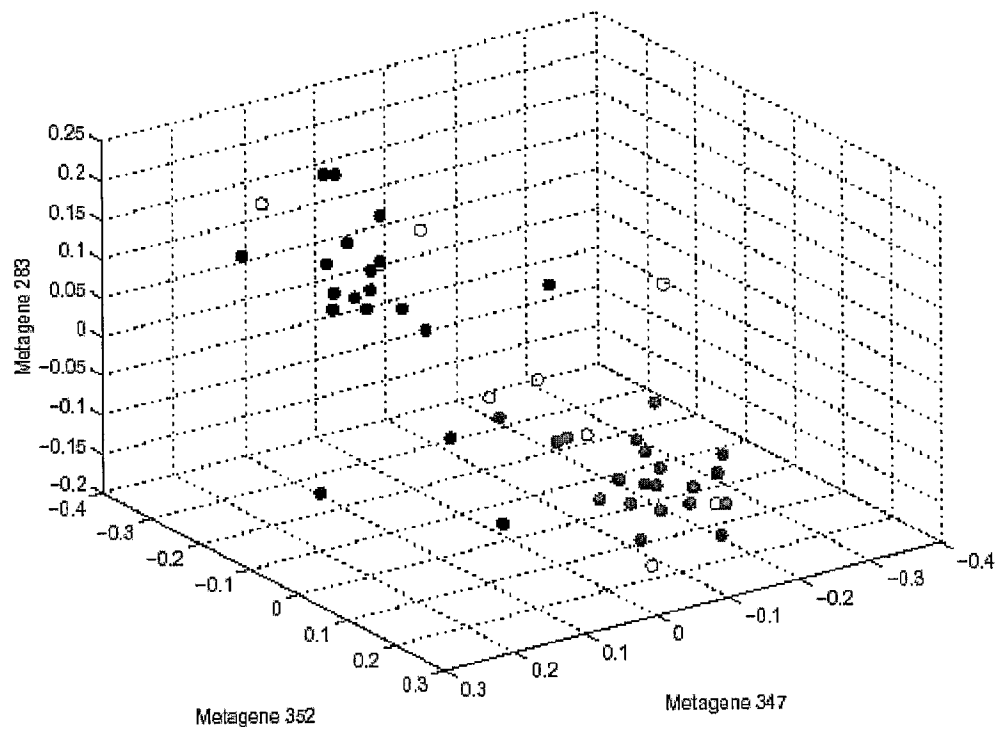
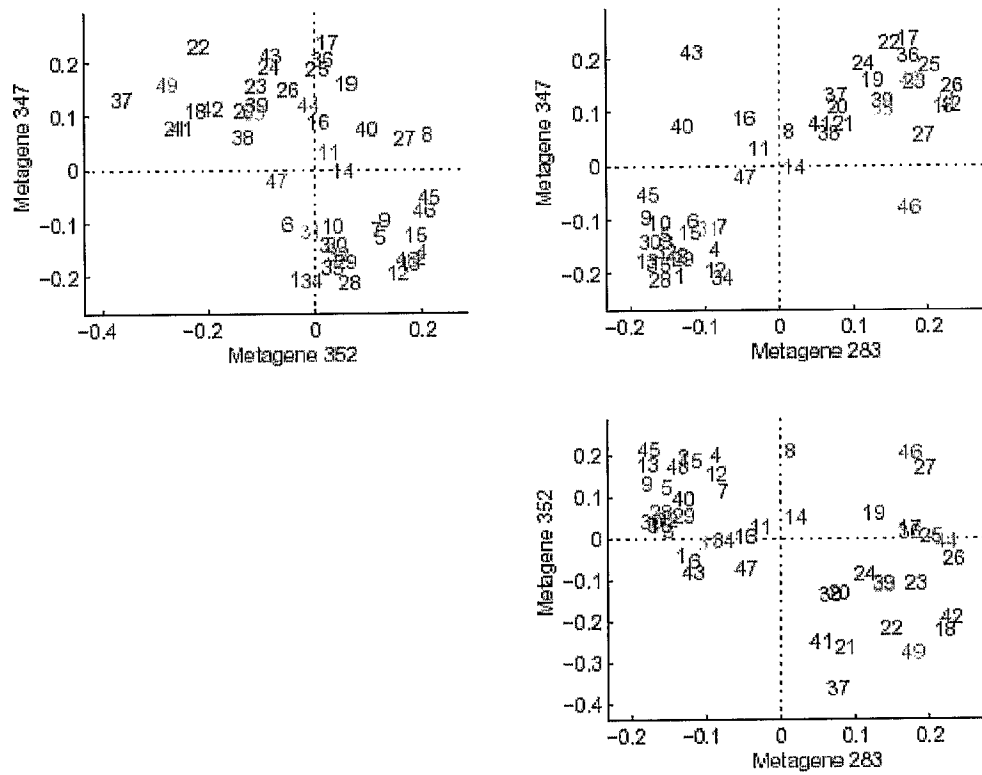
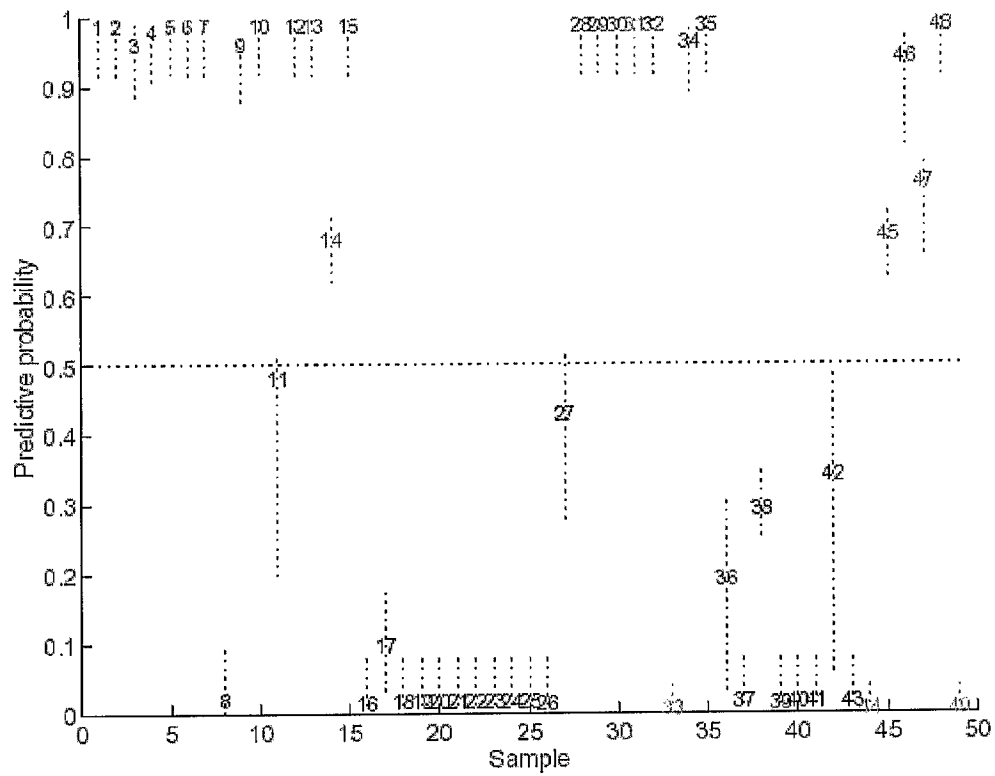
**Fig. 4**

Fig. 5



**Fig. 6**

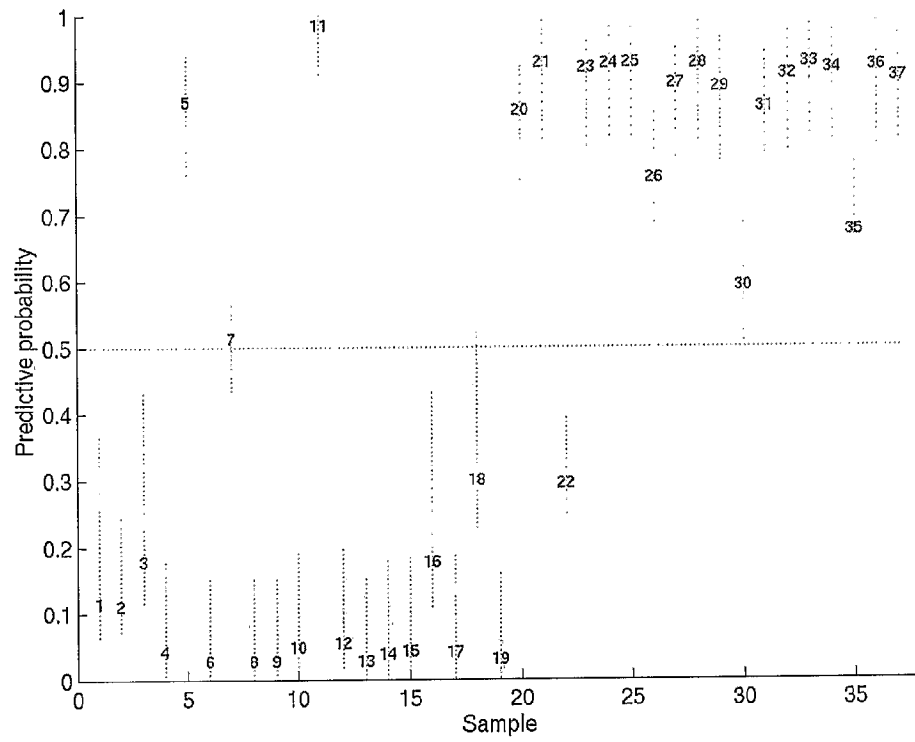
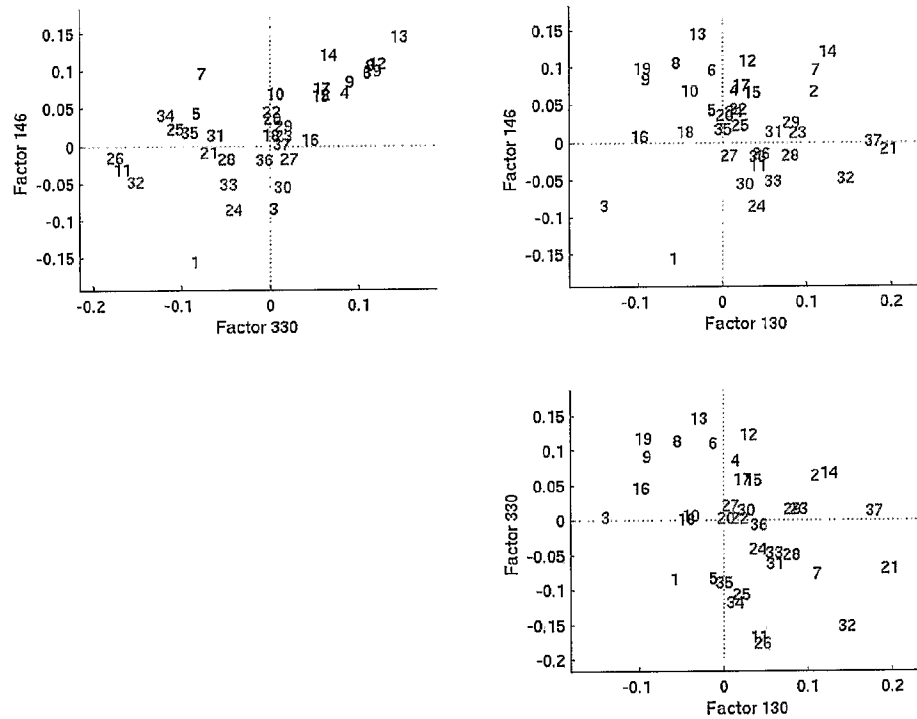
**Fig. 7**

Fig. 8



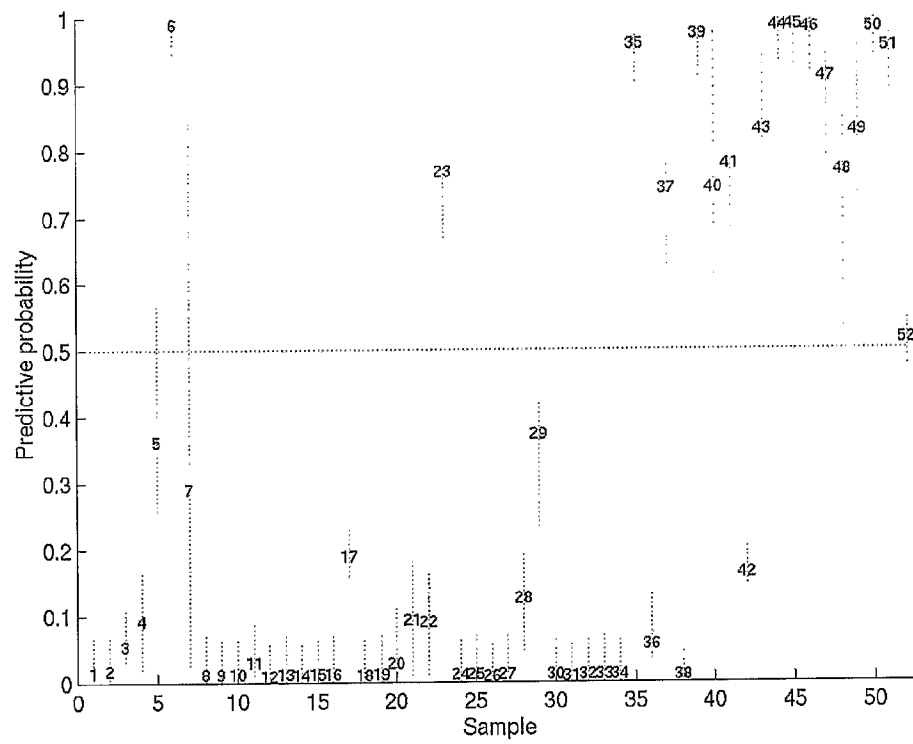
**Fig. 9**

Fig. 10

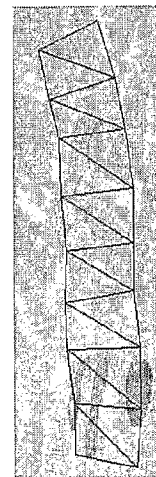
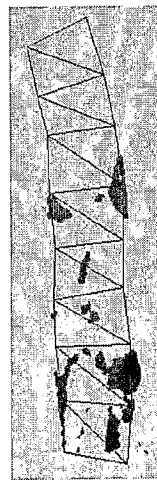
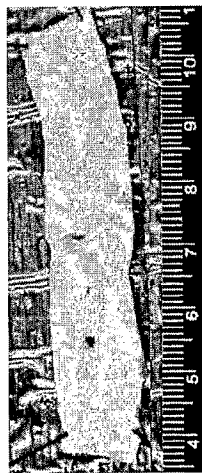
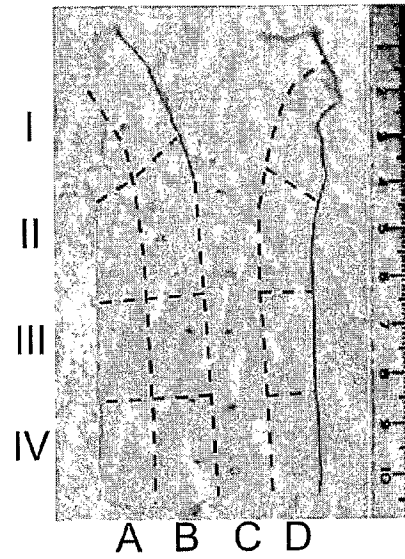
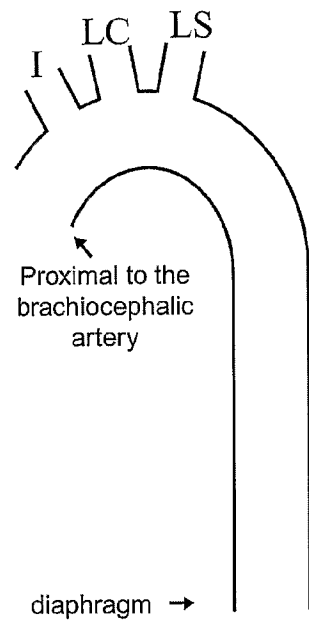




Fig. 11

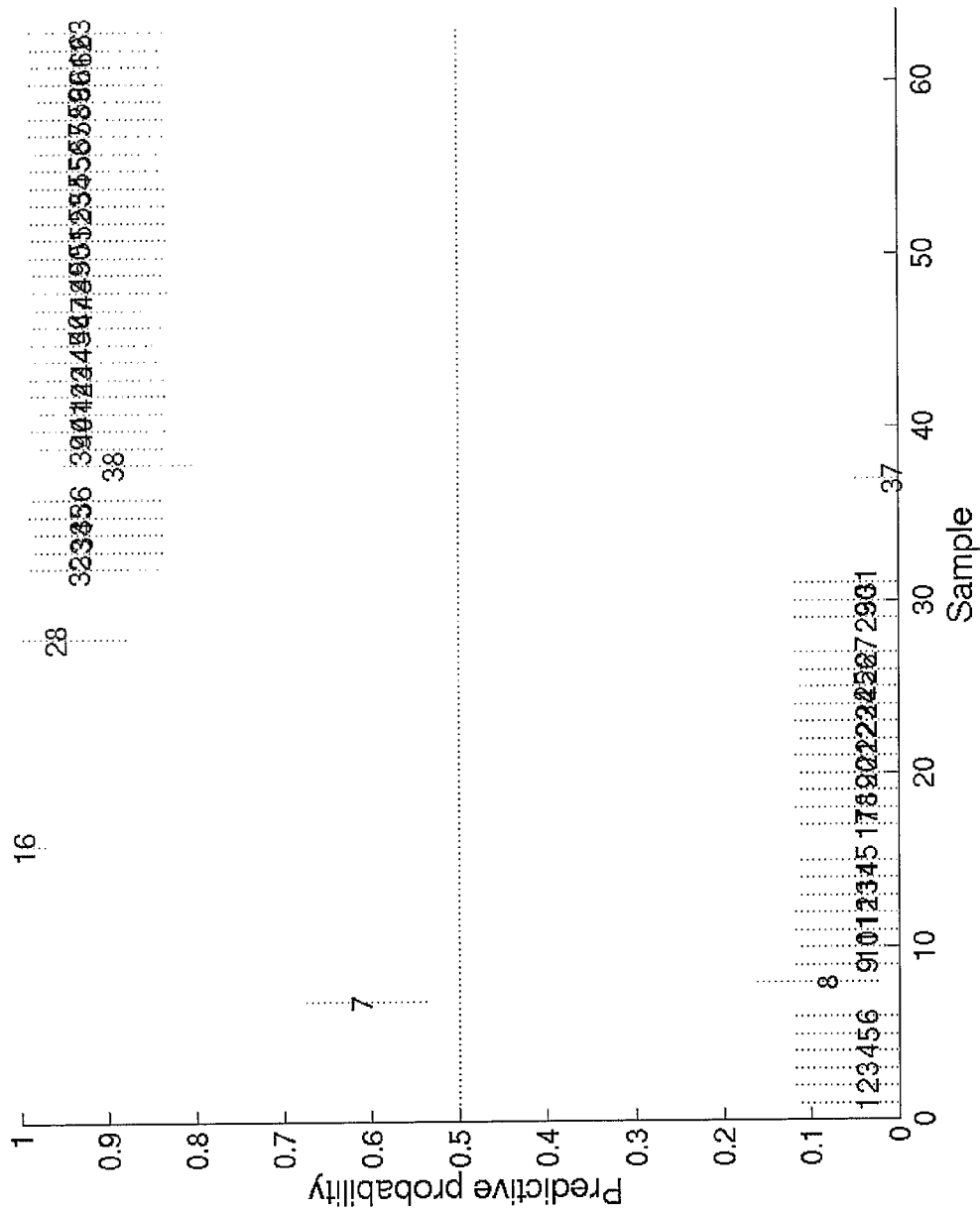
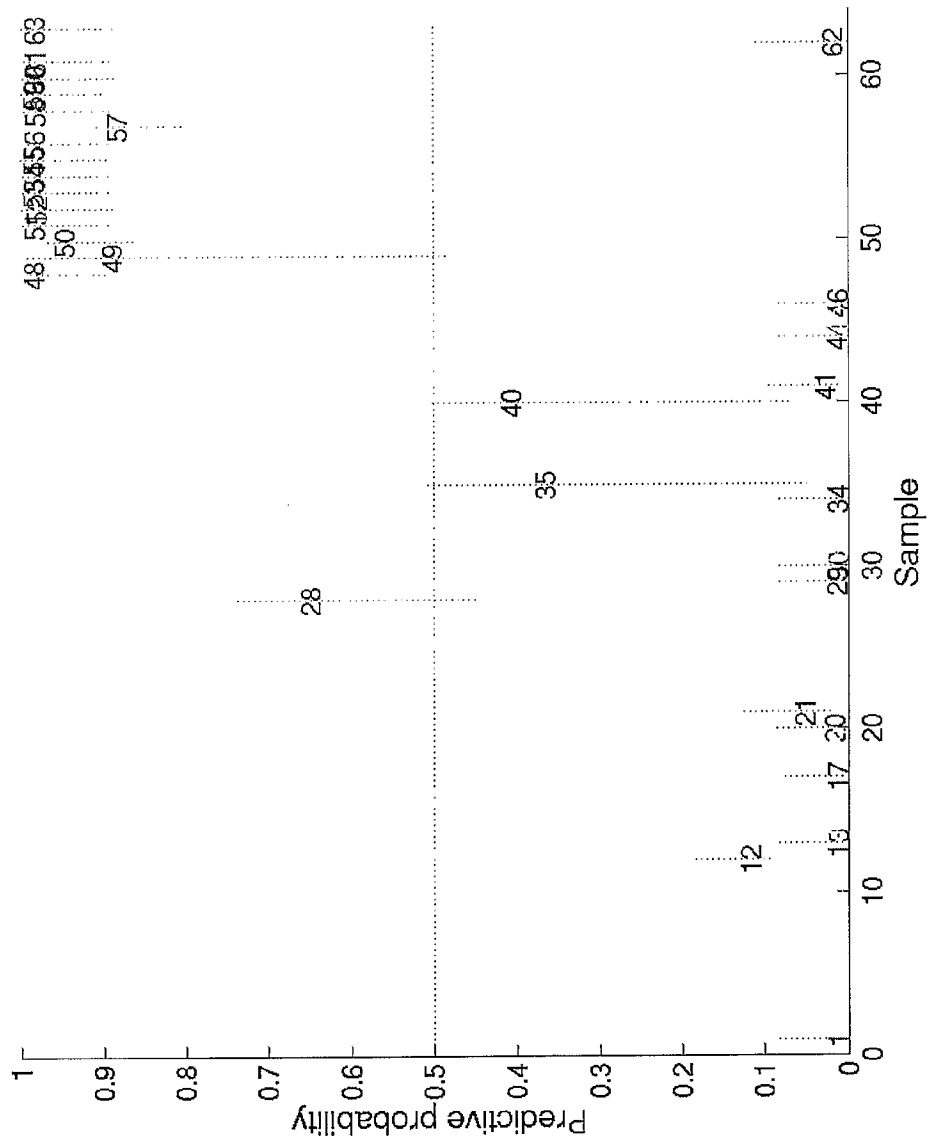


Fig. 12



**Fig. 13**